Rare and low-frequency coding variants alter human adult height

CHD Exome+ Consortium; ExomeBP Consortium; T2D-Genes Consortium; GoT2D Genes Consortium; Global Lipids Genetics Consortium; ReproGen Consortium

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Supplementary Table 1. Information on genotyping methods, quality control of SNPs, imputation, and statistical analysis for ExomeChip study cohorts

Short name	Study Full name	Study design	Ethnicity	Total sample size (N)	Call rate*	Sample QC other exclusions	Samples in analyses (N)	Anthropometric assessment method	Discovery/Validation	References
ADDITION	Anglo–Danish–Dutch Study of Intensive Treatment in People with Screen-Detected Diabetes in Primary Care	Population-based screening of T2D	European	2,347	≥ 98%	1) Missing body weight and height. 2) Heterozygosity were calculated separately for maf < 1% and maf > 1% and samples were dropped judged by plots 3) Cryptic relatedness (related to 20 or more individuals) 3) Technical duplicates 4) Non-European population outliers from PCA plot (based on AIM SNPs) 5) Sex discrepancy	2,313	measured	Discovery	[PMID 11063270] Lauritzen T, et al. (2000) The ADDITION study: proposed trial of the cost-effectiveness of an intensive multifactorial intervention on morbidity and mortality among people with Type 2 diabetes detected by screening. Int J Obes Relat Metab Disord 24 (Suppl 3): 6-11
ADH	National longitudinal Study of Adolescent and Young Adult Health (Add Health)	Population-based	European American (EA) African American (AA) Hispanic American (HA)	3,866 (EA) 2,119 (AA) 1,669 (HA)	≥ 95%	1) call rate <95%; 2) PCA outliers; 3)sex mismatch 4) inbreeding coefficient +/ 6SD from mean of ancestry distribution 5) first degree relatedness 6) comparison with taqman genotyped SNPs, exclude if >40% mismatch 7) missing height, weight measures (only exclude from analyses missing respective phenotype trait, no hip measure available to get WHR)	2,992 (EA) 1,762 (AA) 1,369 (HA)	measured	Discovery	[PMID: 19884593] Harris, K.M., K.M. Perreira, and D. Lee, Obesity in the transition to adulthood: predictions across race/ethnicity, immigrant generation, and sex. Arch Pediatr Adolesc Med, 2009. 163(11): p. 1022-8. [PMID: 20155681] Harris, K.M., *An integrative approach to health*. Demography, 2010. 47(1): p. 1-22.
AEwS	Athero-Express Exome Study	Cohort-study	European	3,265	≥ 97%	1) Missing body weight and height. 2) Heterozygosity (outliers >3SD) 3) Relatedness (>0.2) 4) PCA (non-Eurpoean descent)	1,364	measured	Discovery	[PMID: 15678794] Verhoeven, B.A.N. et al. Athero-express: differential atherosclerotic plaque expression of mRNA and protein in relation to cardiovascular events and patient characteristics. Rationale and design. Eur J Epidemiol. 2004;19(12):1127-33.
AGES-Reykjavik	Age, Gene/Environment Susceptibility study	Population-based	European	2,983	≥ 95%	1) Individuals with high degree of mismatches between GWAS and EC genotypes removed (1 person) 2) Sex mismatches removed (1 person) 3) low genotype success rate (NO person) 4) Missine phenotypes or covariates	2,983	measured	Discovery	[PMID 17551290] Harris TB, Launer LJ, Eiriksdottir G, Kjartansson O, Jonsson PV, Sigurdsson G, Thorgeirsson G, Aspelund T, Garcia ME, Cotch MF, Hoffman HJ, Gudnason V. Age, Gene/Environment Susceptibility-Reykjavik Study: multidisciplinary applied phenomics. Am J Epidemiol. 2007;165(9):1076-87
AIRWAVE	The Airwave Health Monitoring Study	Population-based	European	14804	≥ 95%	missing body weight and height	14,892	measured	Validation	[PMID: 21194656] Elliott P et al. The Airwave health Monitoring Study of police officers and staff in Great Britain: Rationale, design and methods. Environmental Research 2014; 134: 280-285
AMISH	Amish	Population-based	white European	1633	≥ 95%	1) MAF <1% 2) HWE <1E-06	1,630 (BMI) 1,610 (weight) 1,613 (WHR)	measured	Discovery	[PMID: 26174108] Bizzi, L.M. et al. The Pharmacogenomics of Anti-Platelet Intervention (PAPI) Study: Variation in Platelet Response to Clopidogrel and Aspirin. Curr Vasc Pharmacol 14(3), 236-24 (2016). [PMID: 18460328] Mitchell, B.D. et al.: The genetic response to short-term interventions affecting cardiovascular function: rationale and design of the Heredity and Phenotype Intervention (HAPI) Heart Study. Am Heart J. 155(5), 823-8 (2008) [PMID: 17161662] Post, W. et al.: Determinants of coronary artery and aortic calcification in the Old Order Amish. Circulation 115(2), 717-24 (2007). [PMID: 15621237] Sorkin J et al : Exclorine the genetics of lonewhr in the Old Order Amish Mech Aeeine Dev. 126(2): 347-50 (2005)
ARIC	Atherosclerosis Risk in Communities	Population-based	European American (EA) African American (AA)	11,071 (EA) 3,564 (AA)	≥ 95%	1) call rate <95% 2) PCA outliers 3)sex mismatch 4) inbreeding coefficient +/ 6SD from mean of ancestry distribution 5) first degree relatedness 6) comparison with GWAS data, exclude if >40% mismatch 7) (p10GC) genotype quality score, representing the 10th percentile of the distribution of GenCall scores across all SNPs 8) missing height, weight, or waist-hip measures (only exclude from analyses missing respective phenotype trait)	10,870 (EA) 3,564 (AA)	measured	Discovery	[PMID: 2646917] The Atherosclerosis Risk in Communities (ARIC) Study: design and objectives. The ARIC investigators. Am J Epidemiol. 1989 ;129(4):687-702. [PMID: 23874163] Grove ML, Yu B, Cochran BJ, Haritunians T, Bis JC, et al. (2013) Best Practices and Joint Calling of the HumanExome BeadChip: The CHARGE Consortium. PLoS ONE 8(7): e68095. doi: 10.1371/journal.pone.0068095
ASCOT-SC	Anglo-Scandinavian Cardiac Outcome Trial (Scandinavians)	Randomised control clinical trial	European	2,976	≥ 95% from GenCall, then ≥ 99% post zCall	1) Missing phenotypes & covariates 2) Heterozygosity 3) Ancestry outliers 4) Gender mismatch 5) Duplicates & relateds	2,468	measured	Discovery	[PMID: 11685901] Sever P.S.,et al, Rationale, design, methods and baseline demography of participants of the anglo-scandinavian cardiac outcomes trial. Ascot investigators. Journal of hypertension. 19:1139-1147 (2001)
ASCOT-UK	Anglo-Scandinavian Cardiac Outcome Trial (UK/Ireland)	Randomised control clinical trial	European	3,942	≥ 98% from GenCall, then ≥ 99% post zCall	1) Missing phenotypes & covariates 2) Heterozygosity 3) Ancestry outliers 4) Gender mismatch 5) Duplicates & relateds	3,246	measured	Discovery	[PMID: 11685901] Sever P.S.,et al, Rationale, design, methods and baseline demography of participants of the anglo-scandinavian cardiac outcomes trial. Ascot investigators. Journal of hypertension. 19:1139-1147 (2001)
BBMRI-NL	Biobanking and Biomolecular Resources Research Infrastructure	Compedium of 8 different studies	European	7,140	≥ 99%	1) Missing body weight and height 2) Heterozygosity 3) duplicate samples	5,242	measured	Discovery	NA
BC1958	British 1958 Birth Cohort	Population-based	European	5,945	≥ 98%	Genomatrix QC GSP >5 applied	5,945	measured	Discovery	[PMID 17554300] Nature. 2007 Jun 7;447(7145):661-78. Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Wellcome Trust Case Control Consortium
BioMe	IPM BioMe Biobank	Population-based	African American (AA) European American (EA) Hispanic American (HA)	4,680 (AA) 2,645 (EA) 6,204 (HA)	≥ 99%	1) Missing body weight and height. 2) Heterozygosity. 3) Ancestry outliers. 4) Relatedness	4,211 (AA) 2,609 (EA) 5,335 (HA)	self-reported	Discovery	[PMID: 23745551; PMCID: PMC3769282] Gottesman O, et al. The Electronic Medical Records and Genomics (eMERGE) Network: past, present and future. Genet Med 15:761-771, 2013.
BioVU	Vanderbilt University DNA data bank	Cross-sectional	African American (AA) European American (EA)	h genetic data, prior to QC. Race,	≥ 97.5%	1) Information missing on height & BMI 2) Low genotyping call rate 3) Gender inconsistency 4) Cryptic relatedness	1,894/1,886 (AA) 21,213/21,133 (EA)	measured	Discovery	[PMID: 20461953] Pulley J, Clayton E, Bernard GR, Roden DM, Masys DR. Principles of human subjects protections applied in an opt-out, de-identified biobank. *Clinical and translational science*. 2010;3:42-48
BMES	Blue Mountains Eye Study	Population-based	European	1,020	>95%	1) Missing phenotype 2) Population outliers 3) Heterozygosity	821	measured	Discovery	[PMID: 8097791] Mitchell P et al. Prevalence of age-related maculopathy in Australia. The Blue Mountains Eye Study. Ophthalmology 102, 1450-60 (1995). [PMID: 26691988] Fritsche LG et al. A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. Nat Genet 48, 134-43 (2016).
BRAVE	Bangladeshi Risk of Acute Ventricular Events	Case-control	South-Asian (Bangladesh)	~6,143	~> 97%	1) Intensity Outliers (2) Gender mismatch (3) Non-concordance with previous genotyping (4) Duplicates or twins (5) Excess sample Heterozygosity (6) Ancestry outliers from PCA (7) Missine phenotype within each analysis	5,756	measured	Discovery	[PMID: 25930055] Chowdhury R et al. The Bangladesh Risk of Acute Vascular Events (BRAVE) Study: objectives and design.
BRIGHT	British Genetics of Hypertension	Hypertensive Cases	European	1,452	≥ 98% from GenCall, then ≥ 99% post zCall	1) Missing age 2) Heterozygosity 3) Ancestry outliers 4) Gender mismatch 5) Duplicates & relateds	1,361	measured	Discovery	[PMID: 12826435] Caulfield, M.C. et al. Genome-wide mapping of human loci for essential hypertension. Lancet. 361(9375):2118-23 (2003).
CAMCANCER	Cambridge Cancer Studies (SEARCH, SIBS, UKO and UKGPCS)	Population-based	>85% European ancestry	7,958	≥ 99%	1)missing weight and height 2) heterozygosity +0.35 (n=2) 3) mismatched sex(n=12) 4) related*** (n=68) or duplicates (n=18)	7,958	self-reported (SEARCH, UKO and UKGPCS) or measured (SIBS)	Discovery	[PMID: 17327212] Pharoah PD et al. Association between common variation in 120 candidate genes and breast cancer risk. PLoS Genet. 2007 Mar 16;3(3):e42. [PMID: 17369409] Gayther SA et al. Tagging single-nucleotide polymorphisms in cell cycle control genes and susceptibility to invasive epithelial ovarian cancer. Cancer Res. 2007 Apr 1;67(7):3027-35. [PMID: 23076296] Varghese JS et al. The heritability of mammographic breast density and circulating sex-hormone levels: two independent breast cancer risk factors. Cancer Epidemiol Biomarkers Prev. 2012 Dec;21(12):2167-75. [PMID: 19127258] Rosie-Jane 2 et al. A recurrent truncating germline mutation in the BRIP1/FANCJ gene and susceptibility to prostate cancer. Br J Cancer. 2009 Jan 27;100(2):426-30.
CARDIA	The Coronary Artery Risk Development in Young Adults	Population-based	European American (EA) African-American (AA)	5,115 total participants at CARDIA baseline examination; 4,191 genotyped	≥ 95%	1) Missing body weight and height 2) sex mismatch 3) high heterozygosity 4) Outlier in PCA	1,971 (AA) 2,180 (EA)	measured	Discovery	[PMID: 23874568] Grove, Megan L., et al. "Best practices and joint calling of the HumanExome BeadChip: the CHARGE Consortium." PloS one 8.7 (2013): e68095. [PMID: 12046120] Friedman, Gary D., et al. "CARDIA: study design, recruitment, and some characteristics of the examined subjects." Journal of clinical epidemiology 41.11 (1988): 1105-1116.
CARL	INGI-Carlantino	Population-based	European	820	≥ 99%	1) Missing phenotypes 2) Heterozygosity 3) Ethnic outliers	573	measured	Discovery	[PMID: 23248956] Meozzella,M. et al. Genetic characterization of northeastern Italian population isolates in the context of broader European genetic diversity. Eur J Hum Genet. 2013 Jun; 21(6): 659–665.
CCHS	Copenhagen City Heart Study	Prospective cohort study	European	~9,735	~> 97%	(1) Intensity Outliers (2) Gender mismatch (3) Non-concordance with previous genotyping (4) Duplicates or twins (5) Excess sample Heterozygosity (6) Ancestry outliers from PCA (7) Missine phenotype within each analysis	8,107	measured	Discovery	[PMID: 16757268] Schnohr P, Lange P, Scharling H, Jensen JS. Long-term physical activity in leisure time and mortality from coronary heart disease, stroke, respiratory diseases, and cancer. The Copenhagen City Heart Study.
CGPS	Copenhagen General Population Study	Cross-sectional	European	~12,941	~> 97%	(1) Intensity Outliers (2) Gender mismatch (3) Non-concordance with previous genotyping (4) Duplicates or twins (5) Excess sample Heterozygosity (6) Ancestry outliers from PCA (7) Missine phenotype within each analysis	11,821	measured	Discovery	http://biosric.com/CGPS/Design.htm
CHS	Cardiovascular Health Study	Population-based	European American (EA) African-American (AA)	5,088 (3064A, 1,845EA)	≥ 95%	Following the central QC and joint variant calling, additional QC steps were applied to the CHS data using PLINK. SNPs with a missingness rate of >95% were removed and individuals meeting the following criteria were excluded from analysis. We further excluded individuals with low P10GC call, a missing genotype rate of > 97%, gender mis-matches identified by X chromosome homozygosity rates. The sample was limited to those of self-described European-ancestry (EA) and African-American (AA) participants. Principal components analysis was performed using a subset of common LD-pruned variants from the Exome Chip both for the full sample as well as in EA and AA strata. Individuals whose full-sample first principal component suggested a different ancestry from their self-reported ancestry were excluded as were individuals who were outliers for the first 10 ancestry-specific principal components. Pair-wise IBD measures were calculated and outliers with high levels of IBD were removed.	5,059	measured	Discovery	[PMID: 23874568] Grove ML, Yu B, Cochran BJ, Haritunians T, Bis JC, Taylor KD, Hansen M, Borecki IB, Cupples LA, Fornage M *et al*: *Best Practices and Joint Calling of the HumanExome BeadChip: The CHARGE Consortium*. *PLoS One* 2013, 8(7):e68095. [PMID: 16495077] Fried, L. P., Borhani, N. O., Enright, P. et al. The Cardiovascular Health Study: design and rationale. Ann.Epidemiol., Feb, 1991. Vol. 1, Issue 3, pp.263-276. PM: 16495077.
CHOS	Copenhagen Ischaemic Heart Disease Study	Case-series	European	~7,617	~> 97%	(1) Intensity Outliers (2) Gender mismatch (3) Non-concordance with previous genotyping (4) Duplicates or twins (5) Excess sample Heterozygosity (6) Ancestry outliers from PCA (7) Missine phenotype within each analysis	6,625	measured	Discovery	[PMID: 18232221] Frikke-Schmidt R et al. Association of loss-of-function mutations in the ABCA1 gene with high-density lipoprotein cholesterol levels and risk of ischemic heart disease.
CLEAR	The Carotid Lesion Epidemiology And Risk Study	Case-Control	European	271	≥ 95%	Missing height or weight, duplicate, gender discordant	271	measured	Discovery	[PMID: 16476172] Carlson, C.S. et al. TagSNP analysis of the PON gene cluster: effects on PON1 activity, LDL oxidative susceptibility, and vascular disease. J Lipid Res. 47(5):1014-1024 (2006)
CLHNS	Cebu Longitudinal Health and Nutrition Survey	Population-based	Asian (Filipino)	1,798	≥ 98%	gender; heterozygosity	1,785	measured	Discovery	[PMID: 20507864] Adair, L.S. et al. Cohort Profile: the Cebu Longitudinal health and nutrition survey. Int J Epidemiol 40, 619-625 (2011)
CROATIA-Korcula	CROATIA-Korcula	Population-based	European	955	>-99%	1) Missing phenotype	~ 800	measured	Discovery	[PMID:19260143] Zemunik. T. et al. Genome-wide association study of biochemical traits in Korcula Island. Croatia. Croat Med J. 2009. 50(1): p. 23-33.
dbCDDR	dbCDDR anthropometric study	Population-based	White European	192,857	>98%	Non-Icelandic individual and individuals without anthropometric measurements excluded.	76,460	Measured or self-reported	Discovery	**[PMID: 19390583]** Thorleifsson G, et al. Genome-wide association yields new sequence variants at seven loci that associate with measures of obesity. Nat Genet. 2009 Jan;41(1):18-24. doi: 10.1038/ng.274. Epub 2008Dec 14. **[PMID: 18385351]** Gudbjartsson DF, et al. Many sequence variants affecting diversity of adult human height. Nat Genet. 2008 May;40(5):609-15. doi: 10.1038/ng.122. Epub 2008Apr 6.
DHS	Diabetes Heart Study	Family-based	European	1,191	≥ 98%	1) Missing body weight and height 2) Gender discordant 3) Mendelian inconsistency 4) non-diabetic	1,189	measured	Discovery	[PMID: 18460048] Bowden,D.W. et al. Genetic epidemiology of subclinical cardiovascular disease in the diabetes heart study. Ann Hum Genet. 72, 598-610 (2008). [PMID: 21408311] Bowden,D.W. et al. Review of the Diabetes Heart Study (DHS) family of studies: a comprehensively examined sample for genetic and epidemiological studies of type 2 diabetes and its complications. Rev Diabet Stud 7, 188-201 (2010).
DIABNORD	Diabetes Register in Northern Sweden (DiabNorth)	Incident type 2 diabetes cases	European	1,000	≤ 95%	1) Missing body weight and height 2) Heterozygosity 3) Gender discordance 4) Duplicates samples	928	measured	Discovery	[PMID: 16602243] Hallmans,G. et al. Cardiovascular disease and diabetes in the Northern Sweden Health and Disease Study Cohort - evaluation of risk factors and their interactions. Scandinavian journal of public health Supplement. 2003;61:18-24. Epub 2003/12/09.
Dicore	DiMerter. COhoRtE	Prospective cohort study of patients with diabetes mellitus type 2	European	1,523	>-98%	1) Missing phenotype 2) Ancestry not European 3) Relatedness 2nd degree or closer 4) Genetic gender discordant with phenotypic gender 5) Gonosomal aberation 6) Excess of Heterozygosity 7) low call rate 8) Heterozygosity >median + 3*IQR	BMI: 1,515 Height:1,523 WHR:1,505	measured	Discovery	[PMID: 23409724] Dorhofer, L., Lammert, A., Krone, V., Gorski, M., Banas, B., Wanner, C., Kramer, B.K., Heid, I.M., and Boger, C.A. (2013). Study design of DIACORE (DiMerter COhoRtE) - a cohort study of patients with diabetes mellitus type 2. BMC Med Genet 14, 25.
DPS	The Finnish Diabetes Prevention Study	Randomised controlled trial	European	686	≥ 99%	1) Technical duplicates with lower call rate 2) Non-European population outliers 4) Sex discrepancy 5) Contamination score >10% 6) Exclusion of first-degree relateds across multiple Finnish studies	621	measured	Discovery	[PMID: 11333990] Tuomilehto, J. et al. Prevention of type 2 diabetes mellitus by changes in lifestyle among subjects with impaired glucose tolerance. N Engl J Med. 2001 May 3;344(18):1343-50.
DR's EXTRA Study	The Dose Responses to Exercise Training Study	Randomised controlled trial	European	1,243	≥ 99%	1) Heterozygosity >median + 3*IQR 2) Technical duplicates with lower call rate 3) Non-European population outliers 4) Sex discrepancy 5) Contamination score >10% 6) Exclusion of first-degree relateds across multiple Finnish studies (kinship > 0.177 IBNG software) 7) Outliers from population clustering	740	measured	Discovery	[PMID: 21186108] Kouki, A. et al. Diet, fitness and metabolic syndrome--the DR's EXTRA study. Nutr Metab Cardiovasc Dis. 2012 Jul;22(7):553-60.
DUKE	Duke Cathgen	MI Case-Control	European American (EA), African American (AA)	~2,600	≥ 99%	1) Gender mismatch 2) Heterozygosity	2,307	measured	Discovery	NA
EFSOCH	The Exeter Family Study of Childhood Health	Family-based	European	1,528	≥ 99%	heterozygosity, duplicates, relatedness	1,528	measured	Discovery	[PMID:16466433] Knight B, Shields BM, Hattersley AT. The Exeter Family Study of Childhood Health (EFSOCH): study protocol and methodology. Paediatr Perinat Epidemiol. 2006 Mar;20(2):172-9.
EGCUT	Estonian Genome Center of University of Tartu	Nested case-control	European	4,788	≥ 99%	1) Missing fenotype 2) Heterozygosity 3) No duplicates 4) Gender mismatch 5) Population Outliers (Principal components obtained from MDS analysis)	3,510	measured	Discovery	[PMID: 24518929] Leitsalu et al, Cohort Profile: Estonian Biobank of the Estonian Genome Center, University of Tartu. Int J Epidemiol. 2014 Feb 11
EGCUT CORE	Estonian Genome Center of University of Tartu	Population-based	European	4,916	≥ 99%	1) Missing fenotype 2) Heterozygosity 3) No duplicates 4) Gender mismatch 5) Population Outliers (Principal components obtained from MDS analysis)	3,887	measured	Discovery	[PMID: 24518929] Leitsalu et al, Cohort Profile: Estonian Biobank of the Estonian Genome Center, University of Tartu. Int J Epidemiol. 2014 Feb 11
EPIC-CVD	European Prospective Investigation into diet and Cancer Cardiovascular Disease case-cohort study	Case-cohort	European	~23,749	~> 97%	1) Intensity Outliers (2) Gender mismatch (3) Non-concordance with previous genotyping (4) Duplicates or twins (5) Excess sample Heterozygosity (6) Ancestry outliers from PCA (7) Missing phenotype within each analysis	22,412	measured	Discovery	[PMID: 16512959] Gonzalez CA. The European Prospective Investigation into Cancer and Nutrition (EPIC).
EPIC-Potsdam	European Prospective Investigation into Cancer and Nutrition - Potsdam Study	Population-based	European	2,482	≥ 99%	Heterozygosity , sex mismatch, population outliers	2,449	measured	Discovery	[PMID: 10592368] Boeing H, Wahrendorf J, Becker N (1999) EPIC-Germany--A source for studies into diet and risk of chronic diseases. European Investigation into Cancer and Nutrition. Ann Nutr Metab 43: 195-204
EpiHealth	Epidemiology for Health	Population-based	European	2,500	≥ 98%	1) Gender mismatch. 2) Ethnic outliers. 3) Heterozygosity > 5 s.d. 4) Cryptic relatedness. 5) Misstae of anthropometric measures	2,373	measured	Discovery	[PMID: 23435790] Lind,L. et al. EpiHealth: a large population-based cohort study for investigation of gene-lifestyle interactions in the pathogenesis of common diseases. Eur J Epidemiol. 28(2):189-97 (2013).
EUGENDA_UK	The European Genetic Database (age-related macular degeneration)	AMD cases and controls	European	790	≥ 98%	1) Missing body weight and height. 2) Gender mismatch. 3) Population PCA clustering. 4) Deviation from HWE. 5) Duplicated individuals. 6) Missine genotype data	430 cases 546 controls	measured	Discovery	Fritsche et al. 2016. A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. Nat Genet. 2016 Feb;48(2):134-43. doi: 10.1038/ng.3448. Epub 2015 Dec 21.
EUGENDA_UMCN	The European Genetic Database (age-related macular degeneration)	AMD cases and controls	European	933	≥ 98%	1) Missing body weight and height. 2) Gender mismatch. 3) Population PCA clustering. 4) Deviation from HWE. 5) Duplicated individuals. 6) Missine genotype data.	472 cases 363 controls	measured	Discovery	Fritsche et al. 2016. A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. Nat Genet. 2016 Feb;48(2):134-43. doi: 10.1038/ng.3448. Epub 2015 Dec 21.
EXTEND	Exeter 10,000	Population-based	European	1,590	≥ 99%	heterozygosity, duplicates, relatedness	1,579	measured	Discovery	http://www.exeter.crf.nihr.ac.uk/node/155
FamHS (AA)	Family Heart Study	Family-based	African American	608	≥ 96%	1) Missing body weight, height, waist and hip 2) Heterozygosity 3)Mendell errors	608	measured	Discovery	[PMID:8601220] Higgins M et al. NHLBI Family Heart Study: objectives and design. Am J Epidemiol 143, 1219-28 [PMID: 18200598] Zhang Q,et al. Genome-wide admixture mapping for coronary artery calcification in African Americans: the NHLBI Family Heart Study. Genet Epidemiol 2008, 32: 264-72
FamHS (EA)	Family Heart Study	Family-based	European American	4,135	≥ 99%	1) Missing body weight, height, waist and hip 2) Heterozygosity 3) Mendell errors	3,749	measured	Discovery	[PMID:8601220] Higgins M et al. NHLBI Family Heart Study: objectives and design. Am J Epidemiol 143, 1219-28 [PMID: 18200598] Zhang Q,et al. Genome-wide admixture mapping for coronary artery calcification in African Americans: the NHLBI Family Heart Study. Genet Epidemiol 2008, 32: 264-72
Fenland	Fenland Study	Population-based	white European	1,650	? 98%	1) heterozygosity outliers (>3.5 SDs) 2) ethnic outliers 3) sex discrepancy 4) unusually high number of singleton genotypes 5) related (IBD > 0.1875) 6) missing phenotypes required for the analyses	1,341	measured	Discovery	[PMID:20519500] Ede, L. et al. Association between birth weight and visceral fat in adults. Am J Clin Nutr 92(2), 347-352 (2010)
FIA3	Förstagångsinfarkt hjärtinfarkt i AC-län 3 (First myocardial infarction in AC county 3)	Incident myocardial infarction cases	European	2,017	≥ 95%	1) Missing body weight and height 2) Heterozygosity 3) Gender discordance 4) Duplicate samples	2,338	measured	Discovery	[PMID: 16602243] Hallmans,G. et al. Cardiovascular disease and diabetes in the Northern Sweden Health and Disease Study Cohort - evaluation of risk factors and their interactions. Scandinavian journal of public health Supplement. 2003;61:18-24. Epub 2003/12/09.
FINCAVAS	The Finnish Cardiovascular Study	Population-based	European	1,032	≥ 98%	1) Missing body height, weight or waist-hip ratio. 2) Heterozygosity 3) Gender mismatch 4) MDS outliers	938	measured	Discovery	[PMID: 16515496] Nieminen T, Lehtinen R, Viik J, Lehtimäki T, Niemelä K, Nikus K, Niemi M, Kalilo J, Kööbi T, Turjanmaa V, Kähönen M. The Finnish Cardiovascular Study (FINCAVAS): characterizing patients with high risk of cardiovascular morbidity and mortality. BMC Cardiovasc Disord. 2006 Mar 3;6:9
FIN-D2D 2007	National type 2 diabetes prevention programme in Finland: FIN-D2D	Population-based survey	European	2,690	≥ 99%	1) Heterozygosity >median + 3*IQR 2) Technical duplicates with lower call rate 3) Non-European population outliers 4) Sex discrepancy 5) Contamination score >10% 6) Exclusion of first-degree relateds across multiple Finnish studies (kinship > 0.177, IBNG software)	2,585	measured	Discovery	[PMID: 20459722] Kotronen, A. et al. Non-alcoholic and alcoholic fatty liver disease - two diseases of affluence associated with the metabolic syndrome and type 2 diabetes: the FIN-D2D survey. BMC Public Health. 2010 May 10;10:237.

FINRISK 2007	National FINRISK 2007 Study	T2D case-control study	European	1,212	≥ 99%	1) Heterozygosity >median + 3*IQR 2) Technical duplicates with lower call rate 3) Non-European population outliers	1,091	measured	Discovery	[PMID: 19936602] Vartiainen, E. et al. Thirty-five-year trends in cardiovascular risk factors in Finland. Int J Epidemiol. 2010 Apr;39(2):504-18.
FINRISKEXTREMES	Samples are Height and BMI extremes from four Finnish T2D Case Control cohorts: Finrisk 1992, Finrisk 1997, Finrisk 2002, Finrisk 2007.	T2D case-control studies	European	29,287	≥ 95%	1) Heterozygosity >median + 3*IQR 2) Duplicate samples 3) MDL outliers 4) Exclusion of first-degree relateds across multiple Finnish studies Kinship >0.177 KING software	774	measured	Discovery	[PMID: 25422363] Borodulin K, Vartiainen E, Peltonen M, et al. Forty-year trends in cardiovascular risk factors in Finland. Eur J Public Health 2015;25:539-46. doi:10.1093/eurpub/cku174
FRAM	Framingham Heart Study	Population-based	European	8,153	≥ 90%	1) GWAS discordance 2) heterozygosity 3)missingness 4) sex heterozygosity 5) missing trait and/or covariates	7,715	measured	Discovery	[PMID 14023561] Dawber TR, Kannel WB, Lyell LP. An approach to longitudinal studies in a community: the Framingham Study. Ann N Y Acad Sci. 1963;107:539-556. [PMID 12838613] Feinleib M, Kannel WB, Garrison RJ, McNamara PM, Castelli WP. The Framingham Offspring Study. Design and preliminary data. Prev Med. 1975;4:518-525. [PMID 17372189] Splansky GL, Corey D, Yang Q et al. The Third Generation Cohort of the National Heart, Lung, and Blood Institute's Framingham Heart Study: design, recruitment, and initial examination. Am J Epidemiol. 2007;165:1328-1335.
FTCS	Finnish Twin Cohort Study	Family-based	European	4,384	> 95%	1) Missing genotype 2) Missing weight and height 3) Missing age	1,792	measured	Discovery	1: Kaprio J, Pulkkinen L, Rose RJ. Genetic and environmental factors in health-related behaviors: studies on Finnish twins and twin families. Twin Res. 2002 Oct;5(5):366-71. Review. PubMed PMID: 12537860. 2: Kaprio J, Koskenvuo M. Genetic and environmental factors in complex diseases: the older Finnish Twin Cohort. Twin Res. 2002 Oct;5(5):358-65. Review. PubMed PMID: 12537859.
FUSION	Finland-United States Investigation of NIDDM Genetics Study	T2D case-control study	European	4,839	≥ 99%	1) Heterozygosity >median + 3*IQR 2) Technical duplicates with lower call rate 3) Non-European population outliers 4) Sex discrepancy 5) Contamination score >10% 6) Exclusion of first-degree relateds across multiple Finnish studies Kinship >0.177 KING software	4,361	measured	Discovery	[PMID: 9614613] Valle, T. et al. Mapping genes for NIDDM. Design of the Finland-United States Investigation of NIDDM Genetics (FUSION) Study. Diabetes Care. 1998 Jun;21(6):949-58. [PMID: 17463248] Scott, L.J., et al. A genome-wide association study of type 2 diabetes in Finns detects multiple susceptibility variants. Science. 2007 Jun 1;316(5829):1341-5.
FVG	INGI-FVG	Population-based	European	1,581	≥ 99%	1) Missing phenotypes 2) Heterozygosity 3) ethnic outliers	775	measured	Discovery	[PMID: 23249956] Meszaros,M. et al. Genetic characterization of northeastern Italian population isolates in the context of broader European genetic diversity. Eur J Hum Genet. 2013 Jun; 21(6): 659–665.
GBTDS	Guizhou-Bijie Type 2 Diabetes Study	Type 2 diabetes case-control	Chinese Han	846 T2D cases 829 controls	≥ 98%	1) Heterozygosity 2) Duplications 3) Gender mismatches	838 T2D cases 824 controls	measured	Discovery	[PMID:22961080] Li H, Gan W, Lu L, et al. A genome-wide association study identifies GNKS and RASGRP1 as type 2 diabetes loci in Chinese Hans. Diabetes, 2013, 62(1): 291-298.
GECCO	Genetics and Epidemiology of Colorectal Cancer Consortium	Consortium of population-based studies	European	20,637	≥ 98%	1) individual study IRB excludes non-colorectal cancer analyses 2) missing body weight and body height 3) duplicate errors 4) sex discrepancies 5) high proportion of identity-by-descent sharing (as assessed among GWAs with MAF > 5%) 6) heterozygosity outliers 7) samples not clustering with the Utah residents with Northern	7,469	measured or self-reported	Validation	[PMID: 23266554] Peters U, et al. Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-wide Meta-analysis. Gastroenterology. 2012. [PMID: 22367214] Hutter CM, et al. Characterization of gene-environment interactions for colorectal cancer susceptibility loci. Cancer research. 2012;72:2056-64.
GENDEP	Genome-Based Therapeutic Drugs for Depression	Pharmacogenetic study	European	868	≥ 99%	1) Missing body weight and height 2) Discordant Gender 3) Discordant with GWAS data 4) Heterozygosity 5) Population Outlier	668	measured	Discovery	[PMID: 20360315] Uher,R. et al. Genome-wide pharmacogenetics of antidepressant response in the GENDEP project. Am J Psychiatry 167, 555-64 (2010). [PMID: 23091423] Tansey,K.E. et al. Genetic predictors of response to serotonergic and noradrenergic antidepressants in major depressive disorder: a genome-wide analysis of individual-level data and a meta-analysis. PLoS Med 9 (2012). [PMID: 21502950] Rivera,M. et al. Depressive disorder moderates the effect of the FTO gene on body mass index. Mol Psych, 17, 1604-11. (2012).
GENOA	Genetic Epidemiology Network of Arteriopathy	Cohort of sibships enriched for hypertension	European American (EA) African American (AA)	1,544 (EA) 1,392 (AA)	≥ 95%	Gender inconsistency >4sd from mean of inbreeding coefficient >4sd from mean heterozygosity >4sd from mean of singleton count >4sd from IBS 0	1,512 (EA) 1,126 (AA)	measured	Discovery	[PMID: 11796073] FBPP Investigators. Multi-center genetic study of hypertension: The Family Blood Pressure Program (FBPP). Hypertension. 2002 Jan;39(1):3-9. [PMID: 15122484] Daniels PR, Kardia SL, Hanis CL, Brown CA, Hutchinson R, Boerwinkle E, Turner ST; Genetic Epidemiology Network of Arteriopathy study. Familial aggregation of hypertension treatment and control in the Genetic Epidemiology Network of Arteriopathy (GENOA) study. Am J Med. 2004 May 15;116(10):676-81. PubMed PMID:
GHS	Geisinger ExomeChip Study	Population-based	European	7,808	≥ 99%	1) Missing body weight and height. 2) Heterozygosity. 3) Ancestry outliers. 4) Relatedness	7,406	measured	Discovery	[PMID: 23746552; PMCID: PMC3769328]
GLACIER	The Gene-Lifestyle Interactions And Complex traits Involved in Elevated disease Risk Study	Population-based	European	1,000	≤ 95%	1) Missing body weight and height 2) Heterozygosity 3) Gender discordance 4) Duplicate samples 5) Missing Height, BMI or WHR 6) Heterozygosity 7) Ethnic outliers (using HapMap)	927	measured	Discovery	[PMID: 16560243] Hallmans,G. et al. Cardiovascular disease and diabetes in the Northern Sweden Health and Disease Study Cohort - evaluation of risk factors and their interactions. Scandinavian journal of public health Supplement. 2003;61:18-24. Epub 2003/12/09.
GRAPHIC	Genetic Regulation of Arterial Pressure in Humans in the Community	Family-based	European	2,037	≥ 98%	1) Missing phenotype 2) Duplicate checks 3) Identity checks 4) Gender checks 5) IDs <95% in GenCall	1,910	measured	Discovery	[PMCID: PMC3019594] Tomaszewski M et al. Genetic architecture of ambulatory blood pressure in the general population: insights from cardiovascular gene-centric array. Hypertension. 2010;56:1069-76.
GS:SHS	Generation Scotland: Scottish Family Health Study	Population-based	European	9,947	> 99%	1) Missing phenotype	Height: 9,914 BMI: 9,881 WHR:9,743	measured	Discovery	[PMID:22786799] Smith, B.H. et al. Generation Scotland: Scottish family health study. A profile of the study, its participants, and their potential for genetic research on health and illness. Int J Epidemiol (2013).
HABC	Health Aging and Body Composition	Population-based	European	1,648	≥ 95%	1) Missing body weight and height. 2) Heterozygosity 3) Cryptic relatedness or ancestry outlier based on 1000 Genomes reference populations	2,753	measured	Discovery	NA
Health	Health 2006 and 2008	Population-based	European	4,037	≥ 98%	1) Missing body weight and height. 2) Heterozygosity were calculated separately for maf < 1% and maf > 1% and samples were dropped judged by plots 3) Cryptic relatedness (related to 20 or more individuals) 4) Technical duplicates 5) Non-European population outliers from PCA plot (based on AIM SNPs) 6) Sex discrepancy	3,676	measured	Discovery	[PMID: 23615486] Thuesen BH, et al. Cohort Profile: The Health2006 cohort, Research Centre for Prevention and Health. Int J Epidemiol. 2014, 568-75
HELIC MANOLIS	HELIC (Hellenic Isolated Cohorts) MANOLIS	Isolated population	European	1,267	GenCall 98% and zCall 99%	Sex check, heterozygosity at MAF<1% and MAF≥1%, duplicates, ethnic outliers, GWAS concordance, phenotype-missing	975 (height) 956 (BMI) 910 (WHR)	measured	Discovery	NA
HELIC Pomak	HELIC (Hellenic Isolated Cohorts) Pomak	Isolated population	European	1,012	GenCall 98% and zCall 99%	Sex check, heterozygosity at MAF<1% and MAF≥1%, duplicates, ethnic outliers, GWAS concordance, phenotype-missing	904 (height) 903 (BMI) 841 (WHR)	measured	Discovery	NA
HRS	Health and Retirement Study	Population-based	European American (EA) African American (AA)	10,566 (EA) 2,319 (AA)	≥ 98%	1) participants with non-European (EA) or non-African American (AA) ethnicity 2) ethnic outliers within the European American sample 3) related individuals and duplicates 4) missing body weight and/or height. 5) Missing body weight and height	EA: 9,925 (BMI); 10,273 (height) AA: 2,103 (BMI); 2,230 (height)	measured	Discovery	Juster, F. T., Suzman, R. (1995). An Overview of the Health and Retirement Study. Journal of Human Resources: 30 Suppl: S7-S56. [PMID: 24676015] Gonneaja A, Faul JD, Ofstedal MB, Langa KM, Phillips JWR, Weir DR. Cohort Profile: the Health and Retirement Study (HRS). Int. J Epidemiol. 2014; 43 (2): 576-585. Crimmins, E.M., Guyer H., Langa K.M., Ofstedal M.B., Wallace R.B., and Weir D.R. (2008). Documentation of Physical Measures, Anthropometrics and Blood Pressure in the Health and Retirement Study. HRS Documentation Report DR-011. http://hrsonline.isr.umich.edu/sitedocs/userdr/dr-011.pdf
HUNT Study	Nord-Trøndelag Health Study	MI cases and control, sepsis cases and control	European	Total N=17,834: MI cases (N=2,865), MI controls (N=12,249), sepsis cases (N=1362), control (N=1359)	≥ 98%	1) Heterozygosity 2) Deviation from HWE P < 1e-06 3) Duplicate samples with lower call rate 4) Ethnic outliers (non-European) 5) Missing body weight and height. 6) Missing body weight and height 7) heterozygosity were calculated separately for maf < 1% and maf > 1% and samples were dropped judged by plots 8) Cryptic relatedness (related to 20 or more individuals) 9) Technical duplicates	15,114	measured	Discovery	[PMID: 22679362] Krokstad, S. et al. Cohort profile: the HUNT Study, Norway. Int. J. Epidemiol. 42, 968–977 (2013).
Inter99	Inter99	Population-based	European	6,141	≥ 98%	1) sex mismatch 2) het outlier 3) ear allele count outlier 4) IBD relatedness (0.1875) 5) missing phenotypes required for the analyses	5,991	measured	Discovery	[PMID: 16663300] Jørgensen T, et al. (2003) A randomized non-pharmacological intervention study for prevention of ischaemic heart disease: Baseline results Inter99 (1). Eur J Cardiovasc Prev Rehab 10:377-386
InterAct	European Prospective Investigation into Cancer and Nutrition - InterAct	Case-cohort	white European	2,712 (non-subcohort cases)	? 98%	1) missing phenotype 2) Gender mismatch 3) Discordance with GWAS data 4) Population clustering outliers 5) Individuals with high inbreeding coefficients or heterozygote rates 6) Duplicate samples 7) Individuals with an unexpectedly high proportion of identity-by-descent sharing (CHARGE protocol Grouve et al 2013)	2,641	measured	Discovery	[PMID: 21717716] Design and cohort description of the InterAct Project: an examination of the interaction of genetic and lifestyle factors on the incidence of type 2 diabetes in the EPIC Study. Diabetologia. 2011 Sep;54(9):2272-82
IRASFS	Insulin Resistance Atherosclerosis Family Study	Population-based	Hispanic American (HA) African American (AA)	2,010 (HA) 596 (AA)	≥99%	1) Gender inconsistencies 2) Mendelian inconsistencies 3) Missing body weight and height. 3) Missing body weight and height. 3) Missing analysis variables 5) Missing outcome or covariate 2) Heterozygosity 3) PC outlier 4) Half of overlap with AARC African Americans (coordinated with AARC)	1,260 (HA) 596 (AA)	measured	Discovery	[PMID: 15269185] Henkin L. et al. Genetic epidemiology of insulin resistance and visceral adiposity. The IRAS Family Study design and methods. Ann Epidemiol. 2003 Apr;13(4):211-7. [PMID: 15146617] Norris JM et al. Quantitative trait loci for abdominal fat and BMI in Hispanic-Americans and African-Americans: the IRAS Family study. Norris JM, Langefeld CD, Schwenzer AL, Rich SS, Bookman E Beck SR Saad MF Haffner SM Bergman RN Bowden DW Wagenknecht LE
JHS	Jackson Heart Study	Population-based	African American	2,803	≥ 95%	1) Heterozygosity >median + 3*IQR 2) Technical duplicates with lower call rate 3) Non-European population outliers 4) Sex discrepancy 5) Contamination score >10% 6) Exclusion of first-degree relateds across multiple Finnish studies Kinship >0.177 KING software	2,317	measured	Discovery	[PMID: 16320381] Taylor, H.A., Jr. et al. Toward resolution of cardiovascular health disparities in African Americans: design and methods of the Jackson Heart Study. *Ethn Dis* 15, S6-4-17 (2005).
KORA-F4	Cooperative Health Research in the Region of Augsburg	Population-based	European	2,921	≥ 98%	1) excess heterozygosity [i.e. (het_rate) > (mean+7·6sd)] 2) no German passport	2,847	measured	Discovery	[PMID: 16032514] Wichmann HE et al. KORA-gen--resource for population genetics, controls and a broad spectrum of disease phenotypes. Gesundheitswesen 67 Suppl 1, S26-30 (2005).
LBC 1921	Lothian Birth Cohort 1921	Population-based birth cohort	European	550	≥ 95%	1) Missing phenotype 2) Gender mismatch 3) Discordance with GWAS data 4) Population clustering outliers 5) Individuals with high inbreeding coefficients or heterozygote rates 6) Duplicate samples 7) Individuals with an unexpectedly high proportion of identity-by-descent sharing (CHARGE protocol Grouve et al 2013)	490	measured	Discovery	[PMID: 14717632] Deary I.et al. The impact of childhood intelligence on later life: following up the Scottish Mental Surveys of 1932 and 1947. J Pers Soc Psychol 2004; 86: 130-147. [PMID: 22253330] Deary I.et al. Cohort profile: The Lothian Birth Cohorts of 1921 and 1936. Int J Epidemiol 2012; 41(6): 1576-1584.
LBC 1936	Lothian Birth Cohort 1936	Population-based birth cohort	European	1,091	≥ 95%	1) Missing phenotype 2) Gender mismatch 3) Discordance with GWAS data 4) Population clustering outliers 5) Individuals with high inbreeding coefficients or heterozygote rates 6) Missing phenotype 2) Heterozygosity 3) Non-European population outliers	988	measured	Discovery	[PMID: 18052258] Deary I.et al. The Lothian Birth Cohort 1936: a study to examine influences on cognitive ageing from age 11 to age 70 and beyond. *BMC Geriatrics* 2007; 7: 28. [PMID: 22253330] Deary I.et al. Cohort profile: The Lothian Birth Cohorts of 1921 and 1936. Int J Epidemiol 2012; 41(6): 1576-1584.
Leipzig-adults	LeipzigAdults	Populations-based	European	902	≥ 99%	1) Missing phenotype 2) Heterozygosity 3) Non-European population outliers	902	measured	Discovery	[PMID: 20935630] Speliotes, Elizabeth K., et al. Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature genetics 42.11, 937-948 (2010)
LOLIPOP-Exome	London Life Sciences Prospective Population Study	Population-based	South-Asian (Indian Asians)	1,664	≥ 98%	Duplicates, gender discrepancy, ethnic outliers, contaminated samples, relatedness, extreme heterozygosity	1,664	measured	Discovery	[PMID:18193048] Kooner JS, Chambers JC, Aguilar-Salinas CA, et al. Genome-wide scan identifies variation in MLXIPL associated with plasma triglycerides. Nat Genet. 40:149-151 (2008). [PMID:18654146] Chambers JC, Elliott P, Zabaneh D, Zhang W, Li Yun, Froguel Philippe, Balding D, Scott J, Kooner JS. Common genetic variation near MC4R is associated with waist circumference and insulin resistance. Nat Genet 40, 716-718 (2008). [PMID:21222517] van der Harst P, et al. Seventy-five genetic loci influencing the human red blood cell. Nature 492:369-375 (2012).
LOLIPOP-OmniEE	London Life Sciences Prospective Population Study	Population-based	South-Asian (Indian Asians)	977	≥ 98%	Duplicates, gender discrepancy, ethnic outliers, contaminated samples, relatedness, extreme heterozygosity	977	measured	Discovery	[PMID:18193048] Kooner JS, Chambers JC, Aguilar-Salinas CA, et al. Genome-wide scan identifies variation in MLXIPL associated with plasma triglycerides. Nat Genet. 40:149-151 (2008). [PMID:18654146] Chambers JC, Elliott P, Zabaneh D, Zhang W, Li Yun, Froguel Philippe, Balding D, Scott J, Kooner JS. Common genetic variation near MC4R is associated with waist circumference and insulin resistance. Nat Genet 40, 716-718 (2008). [PMID:21222517] van der Harst P, et al. Seventy-five genetic loci influencing the human red blood cell. Nature 492:369-375 (2012).
Marshfield PMRP Exomechip	Marshfield Clinic Personalized Medicine Research Project (PMRP) Biobank	Population-based	98% European	10,016	≥ 98.5%	1) Missing body weight and height 2) AGE - Joined our cohort at age 80 or above. 3) Ancestry - Non white-European	8,570	measured	Discovery	McCarty, C.A. et al. Marshfield Clinic Personalized Medicine Research Project (PMRP): design, methods and recruitment for a large population-based biobank. Future Medicine, 2(1):69-79 (2005).
MESA	Multi-Ethnic Study of Atherosclerosis (MESA) Cohort	Population-based	European American (EA), Asian American (Chinese) (AAS), Hispanic American (HA), and African American (AA) were recruited from six field centers	6,375	≥ 95%	Ethnic outliers; duplicates; gender mismatch; Phenoty outliers	EA 2,497 IAS 769 AA 1,615 HA 1435	measured	Discovery	Bild DE, Bluemke DA, Burke GL, Detrano R, Diez Roux AV, Folsom AR, Greenland P, Jacob DR Jr, Kronmal R, Liu K, Nelson JC, O'Leary D, Saad MF, Shea S, Szklo M, Tracy RP. Multi-ethnic study of atherosclerosis: objectives and design. Am J Epidemiol. 2002 Nov 1;156(9):871-81. PubMed PMID: 12397006.
METSIM	Metabolic Syndrome in Men Study	Population-based cross-sectional study	European	9,765	≥ 99%	1) Heterozygosity >median + 3*IQR 2) Technical duplicates with lower call rate 3) Non-European population outliers 4) Sex discrepancy 5) Contamination score >10% 6) Exclusion of first-degree relateds across multiple Finnish studies Kinship >0.177 KING software	8,414	measured	Discovery	[PMID: 19221568] Stancáková, A. et al. Changes in insulin sensitivity and insulin release in relation to glycemia and glucose tolerance in 6,414 Finnish men. Diabetes. 2009 May;58(5):1212-21.
MGH-CAMP	Massachusetts General Hospital (MGH) Cardiology and Metabolic Patient Cohort (CAMP)	Population-based	European	3,756	≥ 98%	1) Missing body weight and height 2) Sample call rate <98% 3) HWE P<1E-6 4) DNP call rate <95% 5) Pregnancy: pregnant women, under medication to treat obesity (Orlistat or Rimonabant), History of bariatric surgery, Down Syndrome, Cushing Syndrome, Polycystic Ovary Syndrome 2) Missing body weight, height and waist-hip ratio.	3,242	measured	Discovery	NA
MHIBB	Montreal Heart Institute Biobank	Population-based	European	10,506	≥ 95%	(1) Intensity Outliers (2) Gender mismatch (3) Non-concordance with previous genotyping (4) Duplicates or twins (5) Excess sample Heterozygosity	9,634	measured	Discovery	[PMID: 24777453] Auer, P.L. et al. Rare and low-frequency coding variants in CXCR2 and other genes are associated with hematological traits. Nature Genetics (2014) doi:10.1038/ng.2962.
MORGAM	MOnica Risk, Genetics, Archiving and Monograph	Case-cohort	European	~6,869	~> 97%	(1) Intensity Outliers (2) Gender mismatch (3) Non-concordance with previous genotyping (4) Duplicates or twins (5) Excess sample Heterozygosity (6) Ancestry outliers from PCA (7) Missing phenotype within each analysis	6,128	measured	Discovery	[PMID: 15561751] Evans A et al. MORGAM (an international pooling of cardiovascular cohorts).
NEO Study	The Netherlands Epidemiology of Obesity Study	Population-based	European	6,604	≥ 98%	1) remove duplicate/swap samples 2) remove samples with gender mismatch 3) remove outliers in PCA	6,127	measured	Discovery	[PMID: 23576214] de Mutsert R, et al.(2013).The Netherlands Epidemiology of Obesity (NEO) study: study design and data collection.*Eur J Epidemiol.* 2013 Jun;28(6):513-23.
NHAPC	Nutrition and Health of Ageing Population in China	Population-based	East Asian (Chinese-Han)	3,161	≥ 98%	1) Heterozygosity 2) Duplications 3) Gender mismatches	3,138	measured	Discovery	[PMID:18633108] Wu Y, Li H, Loos R J F, et al. Common variants in CDKAL1, CDKN2A/B, IGF2BP2, SLC30A8, and HHEX/IDE genes are associated with type 2 diabetes and impaired fasting glucose in a Chinese Han population. Diabetes, 2008, 57(10): 2834-2842. [PMID:22961080] Li H, Gan W, Lu L, et al. A genome-wide association study identifies GNKS and RASGRP1 as type 2 diabetes loci in Chinese Hans. Diabetes, 2013, 62(1): 291-298.
Nijmegen	Nijmegen Biomedical Study & Nijmegen Bladder Cancer Study	Case-Control	European	3,509	≥ 99%	1) Missing body weight and height. 2) Heterozygosity 3) duplicate samples	3,509	measured	Discovery	[PMID: 21750108] Rafnar T, Vermeulen SH, Sulem P, Thorleifsson G, Aben KK, Witjes JA, Grotenhuis AJ, Verhaegh GW, Hulsbergen-van de Kaa CA, Besenbacher S, Gudbjartsson D, Stacey SN, Gudmundsson J, Johannsdottir H, Bjarnason H, Zanon C, Hedgedottir H, Jonasson JG, Tryggvadottir L, Jonsson S, Gelinson G, Nikulasson S, Petursdottir V, Bishop DT, Chung-Gak S, Choudhury A, Elliott F, Barrett JH, Knowles MA, Kiemeney LA, Thorlacius S, Thorgeirsson A, Rudnai P, Gurzau E, Koppova K, Vineis P, Polidoro S, Guarrera S, Saieva C, Peeraden A, Sanz-Velez JI, Sanchez M, Valdivia G, Garcia-Prats MD, Hengstler JG, Selinski S, Gerullis H, Ovsiannikov D, Khorst A, Aminsharifi A, Malekzadeh M, van den Berg LH, Ophoff RA, Veldink JH, Zeegers MP, Kellen E, Fostinelli J, Andreoli D, Arsi C, Porru S, Buntinx F, Ghadirian A, Golka K, Mayordomo JI, Matullo G, Kumar R, Steineck G, Kiltie AE, Kong A, Thorsteinsdottir U, Stefansson K, Kiemeney LA. European genome-wide association study identifies SLC14A1 as a new urinary bladder cancer susceptibility gene. Hum Mol Genet. 2011 Nov 1;20(21):4268-81. doi: 10.1093/hmg/ddr303.
NMCCS	The Norwegian Mother and Child Cohort Study	Population-based	European	1,904	≥ 98%	1) Missing body weight and height. 2) Heterozygosity outliers >3.SD (rare and common evaluated separately, split by maf 0.01) 3) Gender discordance (thr: 0.3, 0.7)	1,835 (BMI) 1,866 (WEIGHT)	self-reported	Validation	[PMID: 16926217] Magnus, Per, et al. "Cohort profile: the Norwegian mother and child cohort study (MoBa)." International journal of Epidemiology 35.5 (2006): 1146-1150.
NWIGM	Northwest Institute of Genetic Medicine	Cohort	European	1,314	≥ 95%	Missing height or weight, duplicate, gender discordant	1,314	measured	Discovery	[PMID: 21269477] McCarty, C.A., Chisholm, R.L., Chute, C.G., Kullo, I.J., Jarvik, G.P., Larson, E.B., Li, R., Masys, D.R., Ritchie, M.D., Roden, D.M. et al. (2011) The eMERGE Network: a consortium of biorepositories linked to electronic medical records data for conducting genomic studies. *BMC Med. Genomics*, 4, 13
OMICS-EPICNorfolk	European Prospective Investigation into Cancer and Nutrition - Obesity Study	Population-based	European	21,044	≥ 97%	1) Duplicates, 2) Sex discordance, 3) Heterozygosity 98%	21,044	measured	Validation	[PMID: 10465767] Day,N.E. et al. EPIC-Norfolk: study design and characteristics of the cohort. European Prospective Investigation of Cancer. British Journal of Cancer 80, 95-103 (1999).
OMICS-Fenland	Fenland Study	Population-based	European	8,984	>97%	Heterozygosity check; Ethnic outliers; sex discrepancy; unusually high number of singleton genotypes; impossible BD values; phenotype missing; excluding overlap exomechip samples	7,845	measured	Validation	[PMID: 20519568] Rolfe Ede L, Loos RJ, Druet C, Stolk RP, Ekelund U, Griffin SJ, Forouhi NG, Wareham NJ, Ong KK. Association between birth weight and visceral fat in adults. Am J Clin Nutr. 2010 Aug;92(2):347-52. Epub 2010 Jun 2.
OWAB	Ophthalmic Western Australian Biobank	Case-Control	European	1,000	> 95%	1) Missing phenotype 2) Population outliers 3) Heterozygosity	678	measured	Discovery	[PMID: 26691988] Fritsche LG et al. A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. Nat Genet 48, 134-43 (2016).
Oxford Biobank	The Oxford Biobank	Populations-based	European	4,515	≥ 99%	1) Missing phenotype 2) Heterozygosity 3) Non-European population outliers 4) Technical duplicates with lower call rate 5) Sex discrepancy	4,515	measured	Discovery	http://www.oxfordbiobank.org.uk/
PCOS	Polycystic Ovary Syndrome	Population-based	European	647	≥ 99%	1) Missing phenotype 2) Heterozygosity 3) Non-European population outliers 4) technical duplicates with lower call rate 5) Sex discrepancy	582	measured	Discovery	NA
PIVUS	Prospective Investigation of the Vasculature in Uppsala Seniors	Population-based	European	961	≥ 99%	1) Missing phenotype 2) Heterozygosity 3) Non-European population outliers 4) technical duplicates with lower call rate 5) Sex discrepancy	961	measured	Discovery	Lind L, Fors N, Hall J, Marttala K, Stenborg A. A Comparison of Three Different Methods to Evaluate Endothelium-Dependent Vasodilation in the Elderly. The Prospective Investigation of the Vasculature in Uppsala Seniors (PIVUS) Study. Arterioscler Thromb Vasc Biol. 2005; 25:2368-75
PROMIS	Pakistani Risk of Miocardial Infection Study	Case-control	South-Asian (Pakistan)	~24,324	~> 97%	(1) Intensity Outliers (2) Gender mismatch (3) Non-concordance with previous genotyping (4) Duplicates or twins (5) Excess sample Heterozygosity (6) Ancestry outliers from PCA (7) Missing phenotype within each analysis	22,094	measured	Discovery	http://www.phpc.cam.ac.uk/ceu/research/promis/
PROSPER	The Prospective Study of Pravastatin in the Elderly at Risk	Nested case-control within trial	European	~1,763	~> 97%	(1) Intensity Outliers (2) Gender mismatch (3) Non-concordance with previous genotyping (4) Duplicates or twins (5) Excess sample Heterozygosity (6) Ancestry outliers from PCA (7) Missing phenotype within each analysis	1,279	measured	Discovery	[PMID: 12632846] Kuilbertus H, Scheen AJ. The PROSPER Study (PROspective study of pravastatin in the elderly at risk)
QIMR	QIMR Berghofer Medical Research Institute - Exome Study	Population-based	European	5,722	>98% based on autosomal genotypes	1) Ethnic outliers 2) Related individuals and duplicates 3) Missing body weight and height	5,721	measured or self-reported	Validation	[PMID: 19896111] MedlandS.E. et al. Common variants in the trichohyalin gene are associated with straight hair in Europeans. Am J Hum Genet 85(5), 750-755 (2009).
RAINE	Western Australian Pregnancy Cohort (RAINE) Study	Population-based	European	1,527	≥95%	1) Missing body weight and height 2) Heterozygosity 3) Gender discordance with GWAS data	1,078	self-reported	Validation	[PMID: 8105165] Newnham JP, Evans S., Michael CA, Stanley FJ, Landau LI. Effect of frequent ultrasound during pregnancy: A randomised controlled trial. Lancet 1993; 342: 887–891

RISC	Relationship between Insulin Sensitivity and Cardiovascular disease	Population-based	European	313	≥ 99%	heterozygosity, duplicates, relatedness	313	measured	Discovery	[PMID: 14968294] Hills SA et al. The EGIR-RISC STUDY (The European group for the study of insulin resistance: relationship between insulin sensitivity and cardiovascular disease risk): I. Methodology and objectives. Diabetologia. 2004 Mar;47(3):566-70. Epub 2004 Feb 14.
RSI	Rotterdam Study I	Population-based	European	3,163	≥ 98%	Heterozygosity, gender-check 1) Missing body weight and height. 2) Heterozygosity were calculated separately for maf < 1% and maf > 1% and samples were dropped judged by plots	3,163	measured	Discovery	http://www.ncbi.nlm.nih.gov/pubmed [PMID: 24756097] Ikram MA et al. The Rotterdam Study: 2014 objectives and design update. European Journal of Epidemiology 29: 865-876 (2014)
SDC	Steno Diabetes Center T2D Cases	Case study	European	1,418	≥ 98%	1) Cryptic relatedness (related to 20 or more individuals) 2) Technical duplicates 4) Non-European population outliers from PCA plot (based on AIM SNPs) 5) Sex discrepancy	1,390	measured	Discovery	[PMID:21606431] Albrechtsen A, et al. Exome-sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. Diabetologia 56, 297-310 (2013)
SHIP	Study of Health in Pomerania	Population-based	European	3,964	≥ 90%	1) missing data 2) duplicate samples (by estimated IBD) 3) reported and genotyped sex mismatch 4) Heterozygosity	3,878	measured	Discovery	[PMID: 20167617] Völzke H, et al. Cohort Profile: The Study of Health in Pomerania. Int J Epidemiol. 2011 Apr;40(2):294-307.
SHIP-TREND	Study of Health in Pomerania - TREND	Population-based	European	4,331	≥ 90%	1) missing data 2) duplicate samples (by estimated IBD) 3) reported and genotyped sex mismatch 4) Heterozygosity	4,251	measured	Discovery	[PMID: 20167617] Völzke H, et al. Cohort Profile: The Study of Health in Pomerania. Int J Epidemiol. 2011 Apr;40(2):294-307.
SOLID-TIMI 52	The Stabilization Of pLaques using Darapladib-Thrombolysis in Myocardial Infarction 52 Trial (SOLID-TIMI 52)	Interventional Clinical Trial	AA, SA, EAS, SA, HA	200 AA, 8,102 EA, 255 EAS, 118 SA, 893 HA	≥ 94.5%	Sample call rate < 94.5% Heterozygosity; Cryptically related Not consented for genetic research; Only consented for genetic research of resource to drug 1) Missing phenotype 2) Heterozygosity 3) Non-European population outliers 4) Technical duplicates with lower call rate 5) Sex discrepancy	200 AA, 8,102 EA, 255 EAS, 118 SA, 893 HA	measured	Discovery	[PMID: 25175516] O'Donoghue ML et al; SOLID-TIMI 52 Investigators. Effect of darapladib on major coronary events after an acute coronary syndrome: the SOLID-TIMI 52 randomized clinical trial. JAMA. 2014 Sep 10 [PMID: 21982431] O'Donoghue ML, et al. Study design and rationale for the Stabilization of pLaques using Darapladib-Thrombolysis in Myocardial Infarction (SOLID-TIMI 52) trial in patients after an acute coronary syndrome Am Heart J 2011 Oct
Sorbs	Sorbs	Populations-based	white European	1,015	≥ 99%	1) Heterozygosity 2) Non-European population outliers 4) Technical duplicates with lower call rate 5) Sex discrepancy	1,015	measured	Discovery	NA
SR	Silk Road	Population-based	Central Asian	831	≥ 99%	1) Missing phenotypes 2) Heterozygosity 3) ethnic outliers	732	measured	Discovery	[PMID: 25476266] Mezzavilla,M. et al. Genetic landscape of populations along the Silk Road: admixture and migration patterns. BMC Genet. 2014 Dec 5;15:133. doi: 10.1186/s12863-014-0131-6.
STABILITY	The Stabilization of Atherosclerotic Plaque by Initiation of Darapladib Therapy Trial (STABILITY)	Interventional Clinical Trial	African American (AA), European American (EA), Asian American (EAS), Hispanic American (HA),	123 AA, 8,789 EA, 724 EAS, 380 SA, 518 HA	≥ 93.5%	Sample call rate < 94.5% Heterozygosity; Cryptically related Not consented for genetic research; Only consented for genetic research of resource to drug 1) Gender Mismatches 2) Heterozygosity 3) Missing body weight and height.	123 AA, 8,789 EA, 724 EAS, 380 SA, 518 HA	measured	Discovery	[PMID: 26176955] STABILITY Investigators, White HD, et al. Darapladib for preventing ischemic events in stable coronary heart disease. N Engl J Med. 2014 May 1;370(18):1702-11. doi: 10.1056/NEJMoa1315878. Epub 2014 Mar 30. [PMID: 22496275] Vedin O, Hagström E, Stewart R, Brown R, Krug-Gourley S, Davies R, Wallentin L, White H, Held C. Secondary prevention and risk factor target achievement in a global, high-risk population with established coronary heart disease: baseline results from the STABILITY study. Eur J Prev Cardiol. 2013 Aug;20(4):678-85. doi: 10.1177/2047487312464995. Epub 2012 Apr 10.
TUDR	Taiwan USA Diabetes Retinopathy	Population-based	East Asian	560	≥ 95%	2) Heterozygosity 3) Missing body weight and height.	548	measured	Discovery	[PMID: 21562823] Sheu, Wayne H-H , et al. "Genome-wide association study in a Chinese population with diabetic retinopathy." Human molecular genetics 22.15 (2013): 3165-3173.
TwinsUK	Twins UK	Populations-based	European	999	≥ 99%	1) Missine phenotype	999	measured	Discovery	[PMID: 23088088] Moayeri A. Hammond CJ. Hart DJ. Spector TD. The UK Adult Twin Registry (TwinsUK Resource). Twin Res Hum
UCLA-NL	UCLA - The Netherlands	A combination of Population-based and case-control design. Including individuals with Schizophrenia and Bipolar disorder	European	1,292	≥ 98%	1) Missing/unavailable body weight and height. 2) Heterozygosity 3) Sample overlap 4) Inconsistent sex phenotype and genotype	1,255	measured	Discovery	[PMID: 23190000] Luykx, J.J. et al. Genome-wide association study of monoamine metabolite levels in human cerebrospinal fluid. Mol Psychiatry, 2014. 19(2): p. 228-34. Schizophrenia Working Group of the Psychiatric Genomics Consortium. Common Variant Association Meta-Analysis for Schizophrenia identifies 108 Genomic Loci. To appear, Nature, (2014).
UHP	Utrecht Health Project	Cohort	European	2,529	≥ 95%	1) Missing body weight and height, -ckil, pregnant 2) Heterozygosity 3) Ancestry 4) Relatedness (>0.2) - these samples were excluded in an very early stage of QC and therefore not included in the current study	2,095	measured	Discovery	[PMID: 15921047] Grobbee DE, Hoes AW, Verheij TJ, Schrijvers AJ, van Ameijden EJ, Numans ME. The Utrecht Health Project: optimization of routine healthcare data for research. Eur J Epidemiol. 2005;20(3):285-7.
UK Biobank	UK Biobank	Population-based	Caucasian (genetic)	120,286	? 95%	See UK Biobank Documentation: http://www.ukbiobank.ac.uk/wp-content/uploads/2014/04/UKBiobank_genotyping_QC_documentation-web.pdf 1st, 2nd and 3rd degree relatives Non-"white British" individuals	120,286	measured	Discovery	[PMID: 25826379] Sudlow C, Gallacher J, Allen N, et al., UK biobank: an open access resource for identifying the causes of a wide range of complex diseases of middle and old age. PLoS Med, 2015 12: e1001779
ULSAM	Uppsala longitudinal Study of Adult Men	Population-based	European	1,302	≥ 99%	1) Missing phenotype 2) Heterozygosity 3) Non-European population outliers 4) technical duplicates with lower call rate 5) Sex discrepancy	1,302	measured	Discovery	Hedstrand H. A study of middle-aged men with particular reference to risk factors for cardiovascular disease. Ups J Med Sci Suppl 1975; 19: 1-61.
Vejle	Vejle Biobank T2D Case-control study	Case-control	European	2,076 cases 416 controls	≥ 98%	1) Missing body weight and height. 2) Heterozygosity were calculated separately for maf < 1% and maf > 1% and samples were dropped judged by plots 3) Cryptic relatedness (related to 20 or more individuals) 3) Technical duplicates 4) Non-European population outliers from PCA plot (based on AIM SNPs) 5) Sex discrepancy	2,026 cases 416 controls	measured	Discovery	[PMID:21606431] Albrechtsen A, et al. Exome-sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. Diabetologia 56, 297-310 (2013)
WGHS	Women's Genome Health Study	Population-based	European	22,618	≥95%	missing outcome	22,618	self-reported	Discovery	[PMID: 18070814] Ridker PM et al. Women's Genome Health Study Working Group. Rationale, design, and methodology of the Women's Genome Health Study: a genome-wide association study of more than 25 000 initially healthy american women. Clin Chem. 2008 Feb;54(2):249-55. Epub 2007 Dec 10
WHI	Women's Health Initiative	Population-based cohort	European American and African American	21,858 (EA), 3,519 (AA)	≥ 95%	1) Missing body weight, waist circumference, hip circumference, and height	21,858 (EA) 3,519 (AA)	measured	Discovery	[PMID: 22021423] Carty CL, Johnson NA, Hutter CM, Reiner AP, Peters U, Tang H, Kooperberg C. (2012) Genome-wide association study of body height in African Americans: the Women's Health Initiative SNP Health Association Resource (SHARE). Hum Mol Genet. 2012 Feb 1;21(3):711-20. doi: 10.1093/hmg/ddr499 [PMID: 26757982] Kim M, Auer PL, Wang GT, et al. (2016) Rare variant associations with waist-to-hip ratio in European-American and African-American women from the NHLBI-Exome Sequencing Project Eur J Hum Genet 2016 Jan 13 doi: 10.1038/ejhg.2015.272
WOSCOPS	The West of Scotland Coronary Prevention Study	Nested case-control within trial	European	~1,531	~> 97%	(1) Intensity Outliers (2) Gender mismatch (3) Non-concordance with previous genotyping (4) Duplicates or twins (5) Excess sample Heterozygosity (6) Ancestry outliers from PCA (7) Missing phenotype which melt analysis	1,346	measured	Discovery	[PMID: 7566020] Shepherd J et al. Prevention of coronary heart disease with pravastatin in men with hypercholesterolemia. West of Scotland Coronary Prevention Study Group.
WTCCC/UKT2D	Wellcome Trust Case Control Consortium/United Kingdom Type 2 Diabetes Genetics consortium	Populations-based	European	2,016	≥ 99%	1) Missing phenotype 2) Heterozygosity 3) Non-European population outliers 4) Technical duplicates with lower call rate 5) Sex discrepancy	2,016	measured	Discovery	[PMID: 20581827] Voight BF et al. Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nat Genet. 2010 Jul;42(7):579-89.
YFS	The Young Finns Study	Population-based	European	1,988	≥ 95%	1) Missing body height, weight or waist-hip ratio. Pregnancy 2) Heterozygosity 3) Gender mismatch	1,893	measured	Discovery Discovery	[PMID: 18243651] Raitakari, O.T. et al. Cohort profile: The cardiovascular risk in Young Finns Study. Int J Epidemiol 37(6): 1220-1226.

*** Call rate to exclude individuals for whom genotyping success rate is less than a certain percentage (to exclude 'bad' samples/DNA)**

Supplementary Table 2. Information on genotyping methods, quality control of SNPs, imputation, and statistical analysis for ExomeChip study cohorts

Cohort	Genotyping Array	Genotype calling algorithm	Principal components		Inclusion criteria			SNPs that met QC criteria	Association analyses	
			Software	SNPs used from GWAS/ExomeCHIP/AIMS/Other	MAF	Call rate*	p for HWE		Polymorphic SNPs in meta-	Analyses software
ADDITION	Illumina HumanExome-12v1	GenCall + zCall	PLINK	AIM SNPs for outlier detection; ExomeCHIP fo adjustment	no filter	≥ 98%	$> 10^{-6}$	227842	113741	RareMetalWorker
ADH	Illumina ExomeChip V1.0	GenTrain 2.0 clustering algorithm	EIGENSOFT v3.0	AIMS	no filter	≥ 95%	$> 10^{-6}$ (Hispanic, no HWE cut-off used)	250762	136767(EA) 132054 (AA) 129611 (HA)	RvTest
AExoS	Illumina ExomeChip v1.2	GeneCall + Zcall	EIGENSTRAT	ExomeCHIP	no filter	≥ 95%	$> 10^{-5}$	242117	84933	RvTest
AGES-Reykjavik	Illumina ExomeChip V1.0	CHARGE common calling	EIGENSTRAT	ExomeChip	no filter	≥ 95%	$> 10^{-6}$	238015	72607	RvTest
AIRWAVE	IumanExome 12v1-1/HumanCoreExome-12v1-1_	GeneCall + Zcall	PLINK-PCA	ExomeCHIP/GWAS	no filter	≥ 95%	$> 10^{-5}$	233013	153987	RareMetalWorker
AMISH	Illumina Exome Chip V1.0	Genome Studio	NONE	NONE	no filter	≥ 95%	$> 10^{-6}$	223290	40905	RareMetalWorker
ARIC	Illumina ExomeChip V1.0	GenTrain 2.0 clustering algorithm	EIGENSOFT v3.0	Exomchip (MAF>5%)	no filter	≥ 95%	$> 10^{-6}$	237898	148699	RvTest
ASCOT-SC	Illumina Human Omni Exome Express v8.1	GeneCall + Zcall (Oxford Protocol)	PLINK	ExomeChip (1% MAF, LD pruned)	no filter	≥ 98%	$> 10^{-6}$	240041	103002	RvTest
ASCOT-UK	Illumina HumanExome v1.1	GeneCall + Zcall (Oxford Protocol)	PLINK	ExomeChip (1% MAF, LD pruned)	no filter	≥ 99%	$> 10^{-6}$	238866	115221	RvTest
BBMRI-NL	Illumina ExomeChip V1.1	GeneCall + Zcall (Exome-chip QC SOP v5.pdf)	PLINK	AIMS	no filter	≥ 95%	$> 10^{-6}$	242474	133040	RvTest
BC1958	Illumina ExomeChip V1.0	GenCall + Zcall (Oxford Protocol)	PLINK	ExomeCHIP	no filter	≥ 98%	$> 10^{-6}$	244669	139372	RareMetalWorker
BioMe	Illumina ExomeChip V1.0 + Illumina HumanOmniExpressExome	GeneCall + Zcall (Oxford Protocol)	EIGENSTRAT	SNPs with MAF > 1% in exome chip	no filter	≥ 95%	$> 10^{-6}$	238785 (AA) 238680 (EA) 238777 (HA)	161194 (AA) 127368 (EA) 167655 (HA)	RvTest
BioVU	Illumina HumanExome BeadChip v1.1_A	GenomeStudio	EIGENSOFT	AIMs	no filter	≥ 98%	$> 10^{-6}$	232364 (AA) 231987 (EA)	133578 (AA) 172481 (EA)	RvTest
BMES	customized Illumina HumanCoreExome array ("HumanCoreExome_Goncalo_15038949_A")	GeneCall + Zcall	PLINK 1.9	AIMS	no filter	≥ 98%	$> 10^{-6}$	139650	94240	RvTest
BRAVE	Customized Illumina ExomeChip V1.1	Opticall + Zcall	R	Other	no filter	≥ 97%	10^{-6} for MAF ≥5% / 10^{-20} for MAF < 5%	236737	82824	RareMetalWorker
BRIGHT	Illumina Human Exome BeadChip v1.0	GeneCall + Zcall (Oxford Protocol)	PLINK	ExomeChip (1% MAF, LD pruned)	no filter	≥ 99%	$> 10^{-5}$	245322	92641	RareMetalWorker
CAMCANCER	Illumina ExomeChip V1.0	GeneCall + Zcall (Oxford Protocol)	GenABEL	ExomeCHIP	no filter	≥ 95%	$> 10^{-6}$	247108	124290	RvTest
CARDIA	Illumina HumanExome BeadChip V1.0	GeneCall + Zcall	EIGENSTRAT	Exome Chip SNPs (MAF >1%)	no filter	≥ 95%	$> 10^{-6}$	237584 (AA) 237630 (EA)	139250 (AA) 122765 (EA)	RvTest
CARL	HumanExome-12v1-1 A.bpm	GenomeStudio + Zcall (Oxford Protocol)	GenABEL	ExomeCHIP	no filter	≥ 99%	$> 10^{-8}$	234995	64531	RareMetalWorker
CCHS	Customized Illumina ExomeChip V1.1	Opticall + Zcall	R	Other	no filter	≥ 97%	10^{-6} for MAF ≥5% / 10^{-20} for MAF < 5%	235219	132335	RareMetalWorker
CGPS	Customized Illumina ExomeChip V1.1	Opticall + Zcall	R	Other	no filter	≥ 97%	10^{-6} for MAF ≥5% / 10^{-20} for MAF < 5%	233203	134993	RareMetalWorker
CHS	Illumina ExomeChip V1.0	CHARGE joint calling	R	ExomeChip	no filter	≥ 97%	no filter	227061	113606	RareMetalWorker
CIHDS	Customized Illumina ExomeChip V1.1	Opticall + Zcall	R	Other	no filter	≥ 97%	10^{-6} for MAF ≥5% / 10^{-20} for MAF < 5%	232811	103110	RareMetalWorker
CLEAR	Illumina ExomeChip V1.0	GenomeStudio	SNPRelate (R package)	AIMS	no filter	≥ 90%	$> 10^{-6}$	242172	63996	RvTest
CLHNS	Asian_Vand_ExomeChipConsortium_15033784_A	GenomeStudio version 2011.1 + Genotyping Module version 1.9.4 + GenTrain Version 1.0	EIGENSOFT	GWAS	no filter	≥ 95%	$> 10^{-6}$	239844	55138	RvTest
CROATIA-Korcula	Illumina ExomeChip V1.0	Used the GenomeStudio cluster files provided by the CHARGE consortium from their joint calling	GenABEL	ExomeCHIP (only variants with MAF>5%)	no filter	> 98%	$> 10^{-6}$	234824	66897	RvTest
DHS	Illumina ExomeChip V1.0	GeneCall + Zcall	EIGENSOFT	GWAS	no filter	≥ 95%	$> 10^{-6}$	245370	89384	RvTest
deCODE	Illumina HumanHap and OmniExpress arrays (followed by imputation)	BeadStudio	EIGENSTRAT	Use 120,732 uncorrelated SNPs on the Illumina chips	NA	NA	NA	NA	Replication List	In-house software at deCode
DIABNORD	Illumina HumanExome v1.1	GeneCall + Zcall (Exome-chip QC SOP v5.pdf)	PLINK	AIMS	no filter	≥ 95%	$> 10^{-5}$	242022	71947	RvTest
Diacore	Axiom UK Biobank Array	Axiom GT1 in Genotyping Console 4.0	SNPRelate	Others:all pairwise independent (LD<0.5) variants on chip	no filter	≥ 95%	$> 10^{-6}$	799756	752829	RvTest
DPS	HumanExome-12v1_A	Genotype calls generated on cluster boundaries trained on using study samples + manual review of clusterplots	PLINK	ExomeCHIP	no filter	≥ 95%	$> 10^{-5}$	241972	62015	RvTest
DR's EXTRA Study	HumanExome-12v1-1_A	Illumina GenCall using standard Illumina cluster files + Zcall	PLINK	ExomeCHIP	no filter	≥ 95%	$> 10^{-5}$	101413	62002	RvTest
Duke	Illumina ExomeChip V1.0	GeneCall + Zcall (Oxford Protocol)	NA	AIMS	no filter	> 99%	NA	241680	117407 (AA-case) 86038 (EA-case) 121973 (AA-control) 78828 (EA-control)	RareMetalWorker
EFSOCH	Illumina Human Exome Beadchip v1	GenCall followed by zCall	PLINK	ExomeCHIP	no filter	≥ 99%	$> 10^{-6}$	234763	96644	RareMetalWorker
EGCUT	Illumina HumanExome-12v1-1	GeneCall +Zcall (Exome-chip QC SOP v5)	PLINK	ExomeCHIP	no filter	≥ 90%	$> 10^{-6}$	241834	102498	RareMetalWorker
EGCUT CORE	Illumina HumanCoreExome 12v1-1; PsychChip	GeneCall +Zcall (Exome-chip QC SOP v5)	PLINK	ExomeCHIP	no filter	≥ 95%	$> 10^{-6}$	198771	104575	RareMetalWorker
EPIC-CVD	Customized Illumina ExomeChip V1.1	Opticall + Zcall	R	Other	no filter	≥ 97%	10^{-6} for MAF ≥5% / 10^{-20} for MAF < 5%	228846	173971	RareMetalWorker
EPIC-Potsdam	Illumina ExomeChip V1.1	GeneCall + Zcall (calling QC procedure according to Grove et all	R version 3.0.3 / package SNPRelate 0.9.19 (PCs)	AIMs	no filter	≥ 99%	$> 10^{-6}$	240027	107789	RareMetalWorker
EpiHealth	Illumina HumanCoreExome	GenCall + zCall (Oxford protocol)	PLINK	HumanCoreExome SNPs after minor allele frequency filtererring and LD pruning.	no filter	≥ 97% (GenCall), ≥ 99% (zCall)	$> 10^{-6}$	233185	101355	RvTest
EUGENDA_UK	Illumina ExomeChip (custom made)	GeneCall + Zcall (Oxford Protocol)	PLINK	ExomeCHIP	no filter	≥ 95%	$> 10^{-6}$	499912	63949	RareMetalWorker
EUGENDA_UMCN	Illumina ExomeChip (custom made)	GeneCall + Zcall (Oxford Protocol)	PLINK	ExomeCHIP	no filter	≥ 95%	$> 10^{-6}$	499912	62896	RareMetalWorker
EXTEND	humanCore+exome	GenCall followed by zCall	PLINK	humanCore+exome	no filter	≥ 98%	$> 10^{-6}$	236695	97733	RvTest
FamHS	Illumina ExomeChip V1.0	Charge Exomechip Joint calling	EIGENSTRAT	GWAS	no filter	> 90% (AA) ≥ 99% (EA)	no filter	237729 (AA) 237376 (EA)	100012 (AA) 96310 (EA)	RareMetalWorker
Fenland	Illumina ExomeChip V1.0	GeneCall + Zcall (Oxford Protocol)	PLINK	ExomeChip	no filter	? 97%	> 10-6	241,979	99394	RareMetalWorker
FIA3	Illumina HumanExome v1.1	GeneCall + Zcall (Exome-chip QC SOP v5.pdf)	PLINK	AIMS	no filter	≥ 95%	$> 10^{-6}$	247413	84574	RvTest
FINCAVAS	Illumina CoreExome v1.1b	GenCall	PLINK	ExomeCHIP	no filter	≥ 98%	$> 10^{-6}$	242815	67996	RvTest
FIN-D2D 2007	HumanExome-12v1-1_A	Illumina GenCall using standard Illumina cluster files + Zcall	PLINK	ExomeCHIP	no filter	≥ 95%	$> 10^{-5}$	238984	81883	RvTest
FINRISK 2007	HumanExome-12v1-1_A	Illumina GenCall using standard Illumina cluster files + Zcall	PLINK	ExomeCHIP	no filter	≥ 95%	$> 10^{-5}$	238984	63310	RvTest
FINRISKEXTREMES	Illumina ExomeChip V1.2	GeneCall + Zcall (Oxford Protocol)	EIGENSTRAT	Principal components	no filter	> 95%	no filter	219702	66303	RareMetalWorker
FRAM	Illumina ExomeChip V1.0	GenTrain 2.0 clustering algorithm	EIGENSTRAT	GWAS	no filter	≥ 90%	$> 10^{-6}$	246673	133293	RareMetalWorker
FTCS	Illumina HumanCoreExome-12v1.0 beadchip	GeneCall + Zcall	NA (family-based, no outliers)	CoreExomeCHIP	no filter	NA	$> 10^{-6}$	529846	313496	RareMetalWorker
FUSION	HumanExome-12v1-1_A	Illumina GenCall using standard Illumina cluster files + Zcall	PLINK	ExomeCHIP	no filter	≥ 95%	$> 10^{-5}$	238984	80155	RvTest
FVG	HumanExome-12v1-1 A.bpm	GenomeStudio + Zcall (Oxford Protocol)	GenABEL	ExomeCHIP	no filter	≥ 99%	$> 10^{-6}$	239867	70386	RareMetalWorker
GBTDS	Illumina ExomeChip+ v1.0 (Asian Vand ExomeChipConsortium)	central calling effort (Grove etal. PloS One 8(7):e68095)	EIGENSOFT	ExomeCHIP	no filter	≥ 95%	$> 10^{-6}$	208635	85123	RareMetalWorker
GECCO	Illumina HumanExome BeadChip v1.0	GeneCall + Zcall (Oxford Protocol)	R	AIMs/Others	no filter	≥ 98%	$> 10^{-6}$	241090	130300	RareMetalWorker
GENDEP	Illumina ExomeChip V1.1	Zcall	EIGENSTRAT	GWAS	no filter	≥ 99%	$> 10^{-6}$	241254	76945	RvTest
GENOA	Illumina ExomeChip 12v1.1 Beadchip	GeneCall	R	Autosome SNPs with MAF > 0.05 and complete data for the entire samole	no filter	≥ 95%	No filter	233507 (AA) 240121 (EA)	114091 (AA) 91284 (EA)	RareMetalWorker
GHS	HumanExome-12v1.1	GeneCall + Zcall (Oxford Protocol)	EIGENSTRAT	SNPs with MAF > 1% in exome chip	no filter	≥ 99%	$> 10^{-6}$	238744	148950	RvTest
GLACIER	Illumina HumanExome v1.1	GeneCall + Zcall (Exome-chip QC SOP v5.pdf)	PLINK	AIMS	no filter	≥ 95%	$> 10^{-5}$	242022	70875	RvTest
GRAPHIC	Illumina HumanExomee 12v1.1	GenCall + zCall (Sanger/Oxford7 protocol)	NA - empirical kinship matrix modelled instead	NA - empirical kinship matrix modelled instead	no filter	≥ 99% (zCall)	$> 10^{-6}$	245901	96963	RareMetalWorker
GS:SFHS	Illumina ExomeChip V1.0	Used the GenomeStudio cluster files provided by the CHARGE consortium from their joint calling	GenABEL	ExomeCHIP (only variants with MAF>5%)	no filter	> 98%	$> 10^{-6}$	232931	136001	RvTest
HABC	Illumina ExomeChip V1.0	CHARGE+ZCALL	EIGENSTRAT	GWAS	no filter	≥ 95%	> 0	228661	135497 (AA) 106022 (EA)	RvTest
Health	Illumina HumanExome-12v1	GenCall + Zcall	PLINK	AIM SNPs for outlier detection, ExomeCHIP fo adjustment	no filter	≥ 98%	$> 10^{-6}$	227842	128036	RareMetalWorker
HELIC MANOLIS	Illumina HumanExome-12v1_A	GenCall and Zcall (UK exomechip protocol SOPv5)	PLINK	Exome chip SNPs -MAF ≥ 1%, complex regions excluded and LD pruned using r-squared 0.2	no filter	GenCall call rate 95% and zCall call rate 99%	$> 10^{-6}$	239497	60488	RareMetalWorker
HEUC Pomak	Illumina HumanExome-12v1_A	GenCall and Zcall (UK exomechip protocol SOPv5)	PLINK	Exome chip SNPs -MAF ≥ 1%, complex regions excluded and LD pruned using r-squared 0.2	no filter	GenCall call rate 95% and zCall call rate 99%	$> 10^{-6}$	239506	54882	RvTest
HRS	Illumina ExomeChip V1.1	GenTrain (GenomeStudio)	GCTA	ExomeCHIP	no filter	> 0	≥ 95%	229447	134060	RvTest
HUNT Study	Illumina HumanExome-12v1-1	GeneCall + Zcall (Oxford Protocol)	EIGENSOFT (smartpca)	ExomeCHIP SNPs that are polymorphisms 1000G ALL	no filter	≥ 99.9%	$> 10^{-6}$	231575	86581	RvTest
Inter99	Illumina HumanExome-12v1	GeneCall + Zcall	PLINK	AIM SNPs for outlier detection, ExomeCHIP fo adjustment	no filter	≥ 98%	$> 10^{-6}$	227842	139181	RareMetalWorker
InterAct	HumanCoreExome-12v1	GenCall + Zcall (Oxford Protocol)	PLINK	core exome chip	no filter	≥ 95%	> 10-6	237967	128317	RareMetalWorker
IRASFS	Illumina ExomeChip V1.0 and V1.1	GeneCall + zCall	ADMIXTURE	ExomeCHIP	no filter	≥ 99%	no filter	93966 (AA) 83337 (HA)	93168 (AA) 80791 (HA)	RareMetalWorker
JHS	Illumina ExomeChip V1.0	CHARGE joint calling (Illumina GenomeStudio v2011.1 software was utilized with the GenTrain 2.0 clustering algorithm)	EIGENSTRAT - smartpca	Bi-allelic ExomeChip SNPs with MAF > 0.05, HWE p > 0.000001, callrate > 99%, pruned to be pairwise independent with r = 0.3 in plink.	no filter	≥ 95%	no filter	246669	136949	RareMetalWorker
KORA-F4	Illumina ExomeChip V1.0	GeneCall + Zcall (Oxford Protocol)	PLINK	AIMS	no filter	≥ 98%	$> 10^{-7}$	245976	66896	RvTest
LBC 1921	Illumina ExomeChip v1.0	Illumina GenomeStudio v2011.1 + GenTrain2.0 (CHARGE protocol, Grove et al 2013)	MDS	GWAS	no filter	> 95%	no filter	236753	70837	RvTest
LBC 1936	Illumina ExomeChip v1.0	Illumina GenomeStudio v2011.1 + GenTrain2.0 (CHARGE protocol. Grove et al 2013)	MDS	GWAS	no filter	> 95%	no filter	237571	82405	RvTest
Leipzig-adults	Illumina HumanExome-12v1_A	GeneCall + Zcall (Oxford Protocol)	PLINK	ExomeCHIP	no filter	≥ 99%	$> 10^{-6}$	231460	82683	RareMetalWorker
LOLIPOP-Exome	Illumina Human Exome BeadChip	GeneCall + Zcall (Oxford Protocol)	EIGENSOFT - smartpca	GWAS	no filter	≥ 95%	$> 10^{-6}$	240270	73936	RareMetalWorker
LOLIPOP-OmniEE	Illumina OmniExpressExome BeadChip	GeneCall + Zcall (Oxford Protocol)	EIGENSOFT - smartpca	GWAS	no filter	≥ 95%	$> 10^{-6}$	240115	67834	RareMetalWorker
Marshfield PMRP Exomechip	Illumina HumanCoreExome HumanCoreExome Goncalo 15038949 A	GeneCall + Zcall (University of Michigan Abecasis Protocol)	PLINK 1.9	ExomeCHIP	no filter	≥ 98.5%	$> 10^{-6}$	207677	100900	RvTest
MESA	Illumina Exome Chip v1.0	Illumina GenomeStudio2011.1	EIGENSTRAT	ExomeCHIP	no filter	≥ 95%	$> 10^{-6}$	238876	136368	RvTest
METSIM	HumanExome-12v1_A	Genotype calls generated on cluster boundaries trained on using study samples + manual review of clusterplots	PLINK	ExomeCHIP	no filter	≥ 95%	$> 10^{-5}$	241972	91099	RvTest
MGH-CAMP	Infinium HumanCoreExome-24 BeadChips	GeneCall + Zcall	PLINK	AIMS	no filter	≥ 95%	$> 10^{-6}$	235081	140285	RareMetalWorker
MHIBB	Illumina ExomeChip V1.0	GeneCall + Zcall (Oxford Protocol)	PLINK (MDS)	AIMS	no filter	≥ 90%	$> 10^{-6}$	245241	136395	RvTest
MORGAM	Customized Illumina ExomeChip V1.1	Opticall + Zcall	R	Other	no filter	≥ 97%	10^{-6} for MAF ≥5% / 10^{-20} for MAF < 5%	233874	131212	RareMetalWorker
NEO Study	Illumina HumanCoreExomeChip-24V1.0	GeneCall (SOP v5)	PLINK	Based on LD prune	no filter	≥ 98%	$> 10^{-6}$	209874	105552	RvTest
NHAPC	Illumina ExomeChip+ v1.0 (Asian Vand ExomeChioConsortium)	central calling effort (Grove etal. PloS One 8(7):e68095)	EIGENSOFT	ExomeCHIP	no filter	≥ 95%	$> 10^{-6}$	208635	110204	RareMetalWorker
Nijmegen	Illumina ExomeChip V1.1	GeneCall + Zcall (Exome-chip QC SOP v5.pdf)	PLINK	AIMS	no filter	≥ 95%	$> 10^{-6}$	242474	114532	RvTest
NMCCS	Illumina HumanCoreExome-12 V1.1	GeneCall + Zcall (Oxford Protocol)	EIGENSTRAT	AIMS	no filter	≥ 98%	$> 10^{-6}$	245394	94752	RvTest
NWIGM	Illumina ExomeChip V1.0	GenomeStudio	SNPRelate (R package)	AIMS	no filter	≥ 90%	$> 10^{-6}$	241794	100816	RvTest
OMICS-EPICNorfolk	Affymetrix Axiom UKBiobank	Axiom GT1	PLINK v1.9beta	GWAS	no filter	≥ 95%	$> 10^{-6}$	728244	57836	RareMetalWorker
OMICS-Fenland	Affymetrix Axiom UKBiobank	Axiom GT1	PLINK v1.9beta	GWAS	no filter	≥ 95%	$> 10^{-6}$	719871	57988	RareMetalWorker
OWAB	customized Illumina HumanCoreExome array ("HumanCoreExome_Goncalo_15038949_A")	GeneCall + Zcall	PLINK 1.9	AIMS	no filter	≥ 98%	$> 10^{-6}$	139650	77240	RvTest
Oxford BioBank	Illumina HumanExome-12v1_A	GeneCall + Zcall (Oxford Protocol)	PLINK	ExomeCHIP	no filter	≥ 99%	$> 10^{-6}$	233233	126490	RareMetalWorker
PCOS	Illumina Human Core Exome	GeneCall + Zcall (Oxford Protocol)	MDS/PLINK	GWAS	no filter	≥ 99%	$> 10^{-6}$	524527	80909	RareMetalWorker
PIVUS	Illumina HumanExome-12v1_A	GeneCall + Zcall (Oxford Protocol)	PLINK (MDS)	AIMS	no filter	≥ 99%	$> 10^{-6}$	233149	79997	RareMetalWorker
PROMIS	Customized Illumina ExomeChip V1.1	Opticall + Zcall	R	Other	no filter	≥ 97%	10^{-6} for MAF ≥5% / 10^{-20} for MAF < 5%	233828	121848	RareMetalWorker
PROSPER	Customized Illumina ExomeChip V1.1	Opticall + Zcall	R	Other	no filter	≥ 97%	10^{-6} for MAF ≥5% / 10^{-20} for MAF < 5%	232003	88571	RareMetalWorker
QIMR	Illumina ExomeChip V1.0	GeneCall + Zcall (Oxford Protocol)	MDS	AIMS	no filter	≥ 99%	$> 10^{-6}$	226020	127335	RareMetalWorker
RAINE	Illumina HumanExome-12v1_A	Illumina GenomeStudio GenTrain Clustering algorithm + zCall	EIGENSOFT - smartpca	AIMS	no filter	≥ 95%	$> 10^{-6}$	240806	90819	RvTest
RISC	Illumina Human Exome Beadchip v1	GenCall followed by zCall	PLINK	ExomeCHIP	no filter	≥ 99%	$> 10^{-6}$	236875	69642	RareMetalWorker
RSI	Illumina ExomeChip V1.1	GeneCall + Zcall (CHARGE Protocol)	PLINK	GWAS	no filter	≥ 90%	$> 10^{-6}$	237766	108330	rvtests
SDC	Illumina HumanExome-12v1	GenCall + Zcall	PLINK	AIM SNPs for outlier detection, ExomeCHIP fo adjustment	no filter	≥ 98%	$> 10^{-6}$	227842	98470	RareMetalWorker
SHIP	Illumina ExomeChip V1.0	GenCall + Zcall (Oxford Protocol)	EIGENSTRAT	ExomeCHIP	no filter	≥ 95%	$> 10^{-6}$	247021	156503	RvTest
SHIP-TREND	Illumina ExomeChip V1.0	GenCall + Zcall (Oxford Protocol)	EIGENSTRAT	ExomeCHIP	no filter	≥ 95%	$> 10^{-6}$	247021	156503	RvTest
SOLID-TIMI 52	Affymetrix Axiom Biobank Plus GSKB81	AxiomGT1	GCTA	GWAS	no filter	≥ 95%	$> 10^{-6}$	555033	56159	RareMetalWorker
Sorbs	Illumina HumanExome-12v1_A	GeneCall + Zcall (Oxford Protocol)	plink	ExomeCHIP	no filter	≥ 99%	$> 10^{-6}$	231460	59808	RareMetalWorker
SR	HumanExome-12v1-1_A.bpm	GenomeStudio + Zcall (Oxford Protocol)	GenABEL	ExomeCHIP	no filter	≥ 99%	$> 10^{-6}$	230940	81368	RareMetalWorker
STABILITY	Illumina HumanOmniExpressExome-8 V1.0	Illumina pre-defined EGT clusters (version A) + zCall	SNPRelate	GWAS	no filter	≥ 95%	$> 10^{-20}$	919271	79734	RareMetalWorker
TUDR	Illumina Human ExomeChip V1.2	GenomeStudio with extensive manual review	EIGENSOFT - SmartPCA	ExomeCHIP	no filter	≥ 90%	$> 10^{-6}$	237654	47497	RareMetalWorker
TwinsUK	Illumina HumanExome-12v1_A	GeneCall + Zcall (Oxford Protocol)	PLINK	ExomeCHIP	no filter	≥ 99%	$> 10^{-6}$	233233	87603	RareMetalWorker
UCLA-NL	Illumina ExomeChip V1.0 and OmniExpress (including only ExomeChio variants)	GenCall and Zcall (Exome-chip QC SOP v5.pdf)	PLINK	AIMS	no filter	≥ 99%	$> 10^{-6}$	238206	86752	RvTest
UHP	Illumina ExomeChip V1.1	Genome Studio + Zcall	PLINK	AIMS	no filter	≥ 95%	$> 10^{-5}$	241113	46502	RvTest
UK Biobank	Affymetrix UK Biobank Axiom Affymetrix UK BILEVE Axiom	Algorithms implemented in Affymetrix Power Tools + Customised Algorithms by Affymetrix specifically for UK Biobank See UK Biobank Documentation: http://www.ukbiobank.ac.uk/wp-content/uploads/2014/04/UKBiobank_genotyping_QC_documentation-web.pdf	flashPCA	See UK Biobank Documentation: http://www.ukbiobank.ac.uk/wp-content/uploads/2014/04/UKBiobank_genotyping_QC_documentation-web.pdf	NA	NA	NA	NA	Replication List	BOLT-LMM
ULSAM	Illumina HumanExome-12v1_A	GeneCall + Zcall (Oxford Protocol)	PLINK	AIMS	no filter	≥ 99%	$> 10^{-6}$	233149	81810	RareMetalWorker
Vejle	Illumina HumanExome-12v1	GenCall + Zcall	PLINK	AIM SNPs for outlier detection, ExomeCHIP fo adjustment	no filter	≥ 98%	$> 10^{-6}$	227842	107395 (case) 73630 (control)	RareMetalWorker
WGHS	Illumina Exome Chip v1.1	CHARGE Best Practices (PMID 23874508), GenomeStudio v 2011.1, Zcall, in-house manually valudiated statistical model	EIGENSTRAT	SNPs used from GWAS	no filter	≥ 95%	$> 10^{-6}$	235667	176817	RareMetalWorker
WHI	Illumina ExomeChip V1.0	GenomeStudio v2010.3	PLINK	AIMS	no filter	≥ 90%	$> 10^{-6}$	246470	158669	RvTest
WOSCOPS	Customized Illumina ExomeChip V1.1	Opticall + Zcall	R	Other	no filter	≥ 97%	10^{-6} for MAF ≥5% / 10^{-20} for MAF < 5%	235749	91478	RareMetalWorker
WTCCC/UKT2D	Illumina HumanExome-12v1_A	GeneCall + Zcall (Oxford Protocol)	PLINK	ExomeCHIP	no filter	≥ 99%	$> 10^{-6}$	233233	103735	RareMetalWorker
YFS	Illumina CoreExome v1.0b	GenCall	PLINK	ExomeCHIP	no filter	≥ 95%	$> 10^{-6}$	238194	75794	RvTest

*** Call rate to exclude individuals for whom genotyping success rate is less than a certain percentage (to exclude 'bad' samples/DNA)**

Supplementary Table 3: Study-specific descriptive statistics of ExomeChip cohorts

Study†*	Trait	Men						Women					
		n	mean	SD	median	min	max	n	mean	SD	median	min	max
ADDITION	Age (yrs)	1211	59.5	6.9	60.0	41.0	78.0	1102	59.8	7.2	61.0	37.0	73.0
	BMI (kg/m²)	1211	31.6	5.1	31.0	21.3	57.0	1102	33.4	6.2	33.7	20.1	61.4
	Weight (kg)	1211	98.2	17.3	95.8	58.6	173.8	1102	88.8	17.5	88.7	47.6	158.5
	Height (cm)	1211	176.0	6.7	176.0	153.5	199.0	1102	163.1	6.1	163.0	140.0	185.0
	WC (cm)	1211	109.5	13.2	108.0	61.0	180.0	1102	102.4	13.6	103.0	68.0	162.0
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ADH (AA)	Age (yrs)	822	28.6	1.9	29.0	24.0	34.0	940	28.4	1.8	28.0	24.0	34.0
	BMI (kg/m²)	816	29.1	7.0	27.7	17.9	64.5	938	32.1	9.4	30.4	14.3	75.2
	Weight (kg)	816	91.9	23.3	86.9	43.1	199.3	938	86.7	26.0	82.4	37.7	207.7
	Height (cm)	822	177.6	7.4	177.5	134.0	205.7	940	164.2	7.0	164.0	123.5	193.0
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ADH (EA)	Age (yrs)	1482	28.2	1.7	28.0	24.0	33.0	1510	27.8	1.6	28.0	25.0	33.0
	BMI (kg/m²)	1481	29.0	7.1	27.9	17.0	71.9	1508	28.5	8.2	26.5	14.4	65.7
	Weight (kg)	1481	93.3	23.7	89.3	48.9	232.3	1508	77.4	23.1	71.7	38.7	190.3
	Height (cm)	1482	179.0	7.0	179.0	154.5	204.0	1510	164.5	6.9	165.0	122.5	188.0
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ADH (HA)	Age (yrs)	672	28.9	1.7	29.0	24.0	33.0	677	28.8	1.7	29.0	24.0	33.0
	BMI (kg/m²)	671	30.2	7.0	29.0	17.7	71.7	675	29.3	7.7	28.0	15.6	60.5
	Weight (kg)	671	91.9	22.4	87.3	51.3	227.3	675	76.1	21.2	71.8	40.1	184.6
	Height (cm)	672	174.1	7.5	174.0	129.0	198.1	677	160.7	6.8	161.0	134.0	190.5
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AExoS	Age (yrs)	930	68.9	9.1	69.0	40.0	92.0	433	69.2	9.6	70.0	35.0	93.0
	BMI (kg/m²)	880	26.3	3.3	26.0	17.3	39.9	399	26.2	4.7	25.7	15.2	52.3
	Weight (kg)	884	81.7	11.8	80.0	53.0	130.0	402	71.3	13.1	70.0	43.0	134.0
	Height (cm)	882	176.1	6.9	176.0	158.0	204.0	400	164.8	6.7	165.0	140.0	195.0
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AGES-Reykjavik	Age (yrs)	1260	49.7	5.9	50.0	34.0	75.0	1723	52.0	6.6	52.0	34.0	77.0
	BMI (kg/m²)	1260	25.6	3.1	25.5	16.9	38.6	1713	24.9	3.8	24.3	13.7	50.4
	Weight (kg)	1260	81.4	11.5	80.5	51.0	139.0	1713	67.1	10.4	66.0	32.8	140.6
	Height (cm)	1260	178.1	6.1	178.0	156.0	198.0	1723	164.2	5.4	164.0	145.0	183.0
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AIRWAVE*	Age (yrs)	9340	41.3	8.8	42.0	18.0	74.0	5552	38.8	9.2	39.0	19.0	67.0
	BMI (kg/m²)	9340	28.0	3.7	27.6	16.7	55.7	5552	26.0	4.8	25.1	14.4	64.4
	Weight (kg)	9340	90.5	13.2	89.1	38.4	194.8	5552	71.3	13.5	68.8	40.4	180.6
	Height (cm)	9340	179.8	6.2	179.5	145.0	203.8	5552	165.5	6.2	165.5	132.0	188.3
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	9337	0.9	0.1	0.9	0.5	1.3	5508	0.8	0.1	0.8	0.6	1.4
AMISH	Age (yrs)	793	52.7	17.1	53.0	21.0	99.0	840	53.8	16.3	54.0	20.0	95.0
	BMI (kg/m²)	791	26.7	4.1	26.4	18.3	45.0	839	28.5	5.6	28.2	15.9	47.3
	Weight (kg)	791	78.4	13.0	77.2	49.4	134.4	839	72.5	14.9	70.8	35.6	121.8
	Height (cm)	793	171.3	6.8	171.5	147.0	193.5	840	159.4	6.4	159.8	133.4	175.2
	WC (cm)	786	94.3	11.4	93.7	72.0	136.3	830	88.2	12.4	87.0	62.0	191.6
	Hip (cm)	785	101.9	8.0	101.3	83.0	152.0	829	106.1	11.9	105.0	76.0	152.0
	WHR (cm/cm)	785	0.9	0.1	0.9	0.8	1.2	829	0.8	0.1	0.8	0.6	1.6
ARIC (AA)	Age (yrs)	1276	53.9	6.0	54.0	44.0	66.0	2088	53.5	5.7	53.0	44.0	66.0
	BMI (kg/m²)	1269	27.7	4.9	27.2	15.4	52.4	2085	31.0	6.7	29.8	14.2	65.9
	Weight (kg)	1269	85.9	16.7	84.5	44.1	165.9	2085	82.4	18.3	79.5	37.3	177.3
	Height (cm)	1271	176.1	6.7	176.0	153.0	197.0	2086	163.1	6.1	163.0	125.0	188.0
	WC (cm)	1270	97.2	13.0	97.0	63.0	178.0	2086	101.1	16.6	100.0	57.0	178.0
	Hip (cm)	1271	102.9	10.0	102.0	59.0	192.0	2086	111.0	12.9	109.0	78.0	179.0
	WHR (cm/cm)	1270	0.9	0.1	0.9	0.7	1.1	2086	0.9	0.1	0.9	0.6	1.3
ARIC (EA)	Age (yrs)	5103	54.7	5.7	55.0	44.0	66.0	5775	54.0	5.7	54.0	44.0	66.0
	BMI (kg/m²)	5101	27.4	4.0	26.9	16.1	56.3	5769	26.6	5.5	25.5	14.4	55.2
	Weight (kg)	5101	85.2	13.7	83.6	44.5	182.3	5769	69.9	14.8	67.3	36.4	141.8
	Height (cm)	5102	176.2	6.5	176.0	142.0	199.0	5771	162.0	5.9	162.0	137.0	187.0
	WC (cm)	5099	99.7	10.4	99.0	66.0	171.0	5767	93.2	14.8	91.0	52.0	169.0
	Hip (cm)	5098	102.7	7.6	102.0	61.0	165.0	5768	104.2	10.8	102.0	56.0	173.0
	WHR (cm/cm)	5098	1.0	0.1	1.0	0.6	1.4	5767	0.9	0.1	0.9	0.5	1.3
ASCOT_SC	Age (yrs)	1833	62.5	8.6	63.0	40.0	80.0	629	64.4	8.1	64.0	40.0	80.0
	BMI (kg/m²)	1833	28.7	4.3	28.1	15.0	88.8	629	28.9	5.4	28.3	13.5	92.3
	Height (cm)	1833	174.6	7.1	175.0	100.0	202.0	629	161.2	6.5	161.0	108.0	185.0
ASCOT_UK	Age (yrs)	2656	62.5	8.6	63.0	40.0	80.0	587	64.4	8.1	64.0	40.0	80.0
	BMI (kg/m²)	2656	28.7	4.3	28.1	15.0	88.8	587	28.9	5.4	28.3	13.5	92.3
	Height (cm)	2656	174.6	7.1	175.0	100.0	202.0	587	161.2	6.5	161.0	108.0	185.0
BBMRI-NL	Age (yrs)	2172	57.7	18.8	63.2	18.0	89.4	3064	52.6	19.4	51.8	18.0	94.5
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Height (cm)	2172	178.2	7.1	178.0	139.0	204.0	3070	167.4	7.8	168.0	141.9	193.0
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BC1958	Age (yrs)	3339	44.0	0.0	44.0	44.0	44.0	2606	44.0	0.0	44.0	44.0	44.0
	BMI (kg/m²)	3183	27.8	4.1	27.3	16.5	50.7	2512	26.9	5.4	25.7	15.4	53.8
	Weight (kg)	3233	86.3	14.1	85.0	47.0	148.8	2547	71.3	14.9	68.4	40.0	131.5
	Height (cm)	3257	176.1	6.7	176.0	152.0	202.0	2558	162.8	6.2	163.0	140.0	185.0
	WC (cm)	3323	98.5	11.0	97.4	65.2	154.9	2593	85.6	12.7	83.5	56.2	136.4
	Hip (cm)	3323	105.7	7.4	105.1	80.2	152.4	2593	105.4	11.4	103.3	79.2	170.5
	WHR (cm/cm)	3322	0.9	0.1	0.9	0.7	1.2	2593	0.8	0.1	0.8	0.6	1.1
BioMe (AA)	Age (yrs)	1530	52.8	13.9	53.0	21.0	89.0	2681	54.0	15.5	54.0	20.0	89.0
	BMI (kg/m²)	1530	28.5	6.4	27.6	14.3	66.4	2681	31.6	8.5	30.1	14.6	79.2
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Height (cm)	1527	178.0	7.9	177.8	152.4	205.7	2679	163.9	7.2	162.6	134.6	190.5
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BioMe (EA)	Age (yrs)	1475	66.3	11.2	66.0	28.0	89.0	1134	66.0	10.7	65.0	26.0	89.0
	BMI (kg/m²)	1475	27.7	5.2	26.8	13.9	57.1	1134	26.2	6.0	25.1	15.2	54.2
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Height (cm)	1474	177.2	7.2	177.8	152.4	195.6	1135	162.5	6.9	162.6	139.7	185.4
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BioMe (HA)	Age (yrs)	1980	56.3	15.4	57.0	20.0	89.0	3355	56.2	16.3	57.0	19.0	89.0
	BMI (kg/m²)	1980	28.9	5.8	28.1	15.5	73.2	3355	29.8	6.9	28.6	14.1	72.6
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Height (cm)	1977	172.1	8.0	172.7	142.2	200.7	3351	159.4	7.0	160.0	134.6	185.4
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BioVU (AA)	Age (yrs)	808	52.3	16.7	53.0	18.0	95.0	1086	49.7	19.1	49.0	18.0	95.0
	Height (cm)	808	177.5	8.4	177.8	148.6	207.0	1086	163.5	7.6	163.0	122.0	190.5
	BMI (kg/m²)	807	28.5	7.0	27.8	15.1	88.8	1079	31.0	8.1	29.9	16.4	738.9
BioVU (EA)	Age (yrs)	9594	58.1	16.4	60.0	18.0	96.0	11619	55.3	17.7	56.0	18.0	105.0
	Height (cm)	9594	178.5	7.7	177.8	121.9	222.9	11619	163.3	7.0	162.6	121.9	204.5

	BMI (kg/m²)	9564	28.3	5.7	27.5	15.1	98.7	11568	28.0	7.0	26.5	15.0	138.3
	Age (yrs)	367	66.8	8.8	66.0	49.0	94.0	454	66.6	9.2	66.0	49.0	96.0
	BMI (kg/m²)	367	27.4	4.0	26.9	17.4	44.7	452	27.6	5.1	27.0	16.5	50.7
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BMES	Height (cm)	367	172.0	6.7	172.0	151.5	195.0	454	159.0	6.2	159.0	139.0	180.0
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	2237	51.5	10.3	50.0	18.0	90.0	250	54.1	10.1	55.0	30.0	75.0
	BMI (kg/m²)	2237	22.4	3.5	22.3	12.6	64.1	250	23.4	4.0	23.1	13.9	38.7
BRAVE (CAD cases)	Weight (kg)	2237	60.2	10.3	60.0	31.0	164.2	250	53.3	10.9	52.5	30.0	93.0
	Height (cm)	2237	163.6	6.2	163.0	105.0	185.0	250	150.6	6.0	151.0	130.0	167.0
	WHR (cm/cm)	2236	1.0	0.1	1.0	0.7	1.2	250	0.9	0.1	0.9	0.7	1.2
	Age (yrs)	2462	49.9	10.1	50.0	20.0	85.0	317	52.9	9.6	53.0	26.0	80.0
	BMI (kg/m²)	2462	22.7	3.7	22.5	13.5	35.9	317	23.6	4.5	23.5	13.9	40.1
BRAVE (controls)	Weight (kg)	2462	60.8	10.9	60.2	34.4	99.1	317	53.7	10.9	52.8	28.0	89.5
	Height (cm)	2462	163.6	6.2	164.0	122.0	198.0	317	150.8	5.1	151.0	133.0	166.0
	WHR (cm/cm)	2460	1.0	0.1	1.0	0.7	1.5	317	0.9	0.1	0.9	0.6	1.1
	Age (yrs)	440	57.9	10.6	59.0	22.0	81.0	671	58.7	10.9	59.0	21.0	85.0
	Height (cm)	440	173.5	7.6	173.0	144.0	193.0	671	160.9	6.2	161.0	139.0	181.0
	Weight (kg)	439	83.7	12.2	82.7	54.9	128.9	669	70.9	11.3	70.0	41.7	115.5
BRIGHT	WC (cm)	308	97.8	8.7	98.0	78.0	127.0	480	85.8	10.3	85.0	60.0	122.0
	Hip (cm)	308	103.7	6.4	104.0	84.0	124.0	480	103.9	9.4	104.0	79.0	144.0
	WHR (cm/cm)	308	0.9	0.1	0.9	0.8	1.2	480	0.8	0.1	0.8	0.6	1.1
	Age (yrs)	NA	NA	NA	NA	NA	NA	4348	39.8	7.7	40.0	18.0	90.0
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	4049	23.8	3.7	23.1	15.1	50.8
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Height (cm)	NA	NA	NA	NA	NA	NA	4348	163.3	6.6	163.0	124.0	199.0
CAMCANCER (cases)	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	1359	54.3	6.6	55.0	26.0	69.0	2246	56.7	7.4	57.0	29.0	79.0
	BMI (kg/m²)	1347	27.1	4.0	26.6	14.4	58.6	2238	26.5	5.0	25.7	13.7	53.3
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Height (cm)	1359	177.0	7.1	178.0	127.0	198.0	2243	162.8	6.4	163.0	131.0	201.0
CAMCANCER (controls)	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	2031	0.8	0.1	0.8	0.5	1.1
	Age (yrs)	851	21.2	3.7	24.0	18.0	34.0	1117	24.4	3.9	24.0	18.0	35.0
	Height (cm)	851	177.0	6.9	177.0	150.0	206.5	1117	163.7	7.0	163.5	121.0	188.0
CARDIA (black)	BMI (kg/m²)	850	24.6	4.4	23.9	15.8	51.9	1114	26.0	6.6	24.4	14.5	53.5
	WHR (cm/cm)	849	0.8	0.0	0.8	0.5	1.2	1113	0.7	0.1	0.7	0.5	1.3
	Age (yrs)	1027	25.5	3.3	26.0	18.0	32.0	1146	25.5	3.4	26.0	18.0	31.0
	Height (cm)	1027	178.2	6.8	178.0	157.0	203.0	1146	165.2	6.3	165.0	138.0	185.0
CARDIA (white)	BMI (kg/m²)	1027	24.4	3.7	23.8	16.9	43.3	1142	23.1	4.4	22.0	16.3	46.9
	WHR (cm/cm)	1027	0.8	0.0	0.8	0.7	1.0	1142	0.7	0.1	0.7	0.5	1.3
	Age (yrs)	228	50.0	17.0	52.9	18.1	82.4	345	49.6	16.7	51.7	18.4	90.8
	BMI (kg/m²)	228	27.1	4.1	26.8	18.7	39.5	345	27.6	5.9	27.2	16.6	51.4
	Weight (kg)	228	76.3	12.2	75.0	45.0	125.0	345	65.7	13.5	64.0	39.0	123.0
	Height (cm)	228	167.8	7.4	167.0	148.0	190.0	345	154.7	6.5	154.0	140.0	173.0
CALR	WC (cm)	228	94.9	12.0	95.0	61.0	121.0	345	86.8	14.4	86.0	56.0	129.0
	Hip (cm)	228	102.4	10.3	102.5	50.0	132.0	345	103.6	12.9	102.0	70.0	150.0
	WHR (cm/cm)	228	0.9	0.1	0.9	0.8	1.3	345	0.8	0.1	0.8	0.6	1.2
	Age (yrs)	3590	57.1	15.1	59.0	21.0	93.0	4510	58.5	15.1	61.0	21.0	90.0
	BMI (kg/m²)	3587	26.1	3.9	25.7	15.6	50.4	4495	25.2	4.6	24.4	12.8	50.0
	Weight (kg)	3587	80.3	12.9	79.2	42.2	163.8	4495	66.5	12.3	64.9	30.6	132.9
CCHS	Height (cm)	3590	175.4	7.4	175.1	151.0	208.0	4510	162.6	7.0	162.5	134.0	187.6
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	5636	57.6	13.2	57.0	20.0	90.0	6173	55.7	12.7	55.0	20.0	89.0
	BMI (kg/m²)	5633	26.9	3.8	26.5	15.6	54.3	6172	25.8	4.7	24.9	12.9	64.8
	Weight (kg)	5633	84.9	13.5	83.3	44.8	181.8	6172	70.3	13.4	68.3	33.0	174.7
CGPS	Height (cm)	5636	177.7	7.1	177.5	148.7	212.0	6173	165.1	6.7	165.0	139.0	198.0
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	306	72.7	5.8	71.0	65.0	93.0	505	72.9	5.7	72.0	65.0	93.0
	BMI (kg/m²)	305	26.7	4.3	26.4	16.1	38.2	503	29.5	5.9	28.9	16.3	58.8
	Weight (kg)	305	80.2	14.3	79.2	47.6	139.3	503	75.1	15.7	72.8	43.5	134.0
	Height (cm)	306	173.3	6.6	173.0	153.5	196.0	504	159.6	6.4	159.0	145.0	186.5
CHS-AA	WC (cm)	306	97.0	11.8	96.8	69.0	133.0	501	99.9	15.5	98.5	66.0	167.0
	Hip (cm)	306	100.6	8.6	100.0	80.0	135.5	502	107.1	12.8	105.8	79.0	160.0
	WHR (cm/cm)	306	1.0	0.1	1.0	0.8	1.2	500	0.9	0.1	0.9	0.7	1.2
	Age (yrs)	1845	73.4	5.8	72.0	65.0	95.0	2403	72.4	5.5	71.0	65.0	100.0
	BMI (kg/m²)	1838	26.4	3.7	26.1	15.6	46.2	2397	26.3	5.0	25.7	14.7	48.3
	Weight (kg)	1838	79.1	12.2	78.5	46.3	142.7	2398	66.5	13.2	64.9	32.8	132.9
	Height (cm)	1840	173.1	6.6	173.0	150.0	193.0	2401	158.9	6.2	158.8	124.0	179.9
CHS-EA	WC (cm)	1830	97.7	10.0	97.0	70.5	143.0	2387	90.7	13.7	90.0	54.0	143.0
	Hip (cm)	1833	101.1	7.9	100.5	45.5	155.0	2389	101.8	10.7	100.2	52.0	153.0
	WHR (cm/cm)	1829	1.0	0.1	1.0	0.6	2.3	2387	0.9	0.1	0.9	0.6	2.1
	Age (yrs)	1776	61.8	10.1	62.0	19.0	89.0	679	63.3	11.3	64.0	30.0	91.0
	BMI (kg/m²)	1772	27.4	4.0	26.9	17.3	63.9	679	26.4	5.1	25.7	15.8	70.2
	Weight (kg)	1772	84.5	13.9	83.0	50.0	153.0	679	70.4	13.6	69.0	39.0	125.0
CIHDS	Height (cm)	1776	175.5	6.8	175.0	118.0	206.0	679	163.2	6.3	163.0	112.0	182.0
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	224	71.6	8.0	72.0	50.1	89.5	47	70.2	9.6	69.7	50.6	86.9
	BMI (kg/m²)	224	28.3	4.5	27.4	19.0	48.5	47	27.9	5.3	28.1	18.8	43.9
	Weight (kg)	224	89.4	15.8	86.9	58.3	152.4	47	74.0	14.2	73.5	51.3	119.3
	Height (cm)	224	177.9	6.9	177.8	157.5	193.0	47	163.3	6.9	162.6	149.9	185.4
CLEAR	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	NA	NA	NA	NA	NA	NA	1785	48.5	6.7	47.7	35.7	69.3
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	1778	24.3	4.4	24.1	12.3	42.1
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Height (cm)	NA	NA	NA	NA	NA	NA	1785	150.6	5.0	150.4	130.7	168.8
CLHNS	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	1777	0.9	0.1	0.9	0.7	1.3
	Age (yrs)	304	57.6	13.9	59.0	20.0	90.0	536	55.2	13.8	56.0	18.0	98.0
	BMI (kg/m²)	304	28.8	3.6	28.7	20.5	40.7	536	27.6	4.4	27.3	16.6	53.8
	Weight (kg)	304	89.8	12.5	89.4	58.1	136.2	536	73.4	11.6	72.6	49.9	166.6
	Height (cm)	304	176.6	6.7	177.0	158.3	197.0	536	163.4	6.5	163.7	140.5	186.0
CROATIA-Korcula	WC (cm)	297	100.2	10.2	100.0	62.0	130.0	521	91.1	12.0	91.0	63.0	138.5
	Hip (cm)	296	104.7	6.6	104.5	87.5	127.0	520	103.8	8.6	103.2	74.8	156.3
	WHR (cm/cm)	295	1.0	0.1	1.0	0.6	1.1	519	0.9	0.1	0.9	0.7	1.4
	Age (yrs)	28752	55.1	17.5	54.0	18.1	105.0	47728	48.6	18.2	48.0	18.0	103.0
	BMI (kg/m²)	28752	27.2	4.6	26.5	12.2	72.1	47728	25.7	5.2	24.8	11.2	74.1
	Weight (kg)	28752	87.4	16.0	85.0	35.7	220.0	47728	71.0	14.8	68.9	30.0	197.0
	Height (cm)	28752	179.2	6.7	179.0	130.0	210.0	47728	166.2	6.1	166.0	133.0	199.0
deCODE	WC (cm)	5872	100.5	14.0	100.0	32.0	200.0	7086	94.1	15.7	93.0	30.0	165.0
	Hip (cm)	5872	106.0	9.6	105.0	40.0	195.0	7086	106.9	11.9	105.0	36.5	173.0
	WHR (cm/cm)	5872	0.95	0.09	0.95	0.36	2.25	7086	0.88	0.10	0.88	0.35	1.76
	Age (yrs)	483	63.1	8.9	63.6	35.7	86.0	513	61.9	9.2	61.6	34.2	81.8
	BMI (kg/m²)	483	31.2	5.5	30.5	17.8	56.6	512	33.4	7.3	32.5	17.5	58.0
	Weight (kg)	483	97.1	18.9	94.7	56.7	209.2	512	87.4	20.3	84.1	40.8	164.3
	Height (cm)	483	176.4	6.5	176.1	157.2	202.0	513	161.7	6.0	161.4	144.7	181.7
DHS	WC (cm)	475	108.8	13.6	107.5	76.0	171.0	507	105.4	16.8	104.0	63.5	160.0
	Hip (cm)	474	110.7	11.0	109.0	88.0	177.0	506	116.4	16.0	113.0	84.0	177.5
	WHR (cm/cm)	474	1.0	0.1	1.0	0.8	1.2	506	0.9	0.1	0.9	0.7	1.2
	Age (yrs)	490	54.2	7.4	59.8	29.9	70.3	438	55.3	6.5	59.9	39.6	61.0
	BMI (kg/m²)	490	29.5	4.1	29.1	20.9	55.8	438	30.6	5.4	29.9	18.1	51.7
	Weight (kg)	490	92.7	14.8	91.0	59.0	163.2	438	80.9	14.6	78.5	44.0	145.0
	Height (cm)	490	177.0	6.6	177.0	159.0	198.0	438	162.6	5.4	163.0	143.0	179.0

DIABNORD	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	917	65.7	8.5	67.1	31.2	88.6	606	65.1	9.1	65.8	23.8	88.6
	BMI (kg/m²)	914	31.2	5.2	30.5	19.6	55.2	601	32.1	6.2	31.4	17.9	55.3
	Weight (kg)	914	94.8	17.1	93.3	49.6	161.5	601	82.8	16.9	80.3	48.6	154.1
	Height (cm)	917	174.3	6.4	174.0	154.0	196.0	606	160.5	6.4	161.0	140.0	183.0
Diacore	WC (cm)	909	107.3	13.2	107.0	63.0	147.0	602	99.6	13.9	98.0	62.0	152.0
	Hip (cm)	909	106.3	9.5	105.0	81.0	143.0	602	110.7	12.5	109.0	81.0	155.0
	WHR (cm/cm)	909	1.0	0.1	1.0	0.6	1.2	602	0.9	0.1	0.9	0.7	1.2
	Age (yrs)	137	56.0	7.1	58.7	41.0	65.9	284	55.0	7.0	56.2	39.5	67.9
	BMI (kg/m²)	137	29.8	3.4	29.5	23.5	44.8	284	32.1	4.9	31.5	24.0	50.5
	Weight (kg)	137	91.5	12.4	89.5	62.9	148.1	284	84.3	14.4	82.2	52.9	136.5
	Height (cm)	137	175.1	6.3	175.8	155.5	189.7	284	161.9	5.9	161.9	145.0	177.5
DPS	WC (cm)	137	103.7	9.7	103.0	83.5	139.0	284	100.2	11.5	99.0	75.5	139.0
	Hip (cm)	137	105.2	7.5	105.0	88.0	143.5	284	112.9	10.8	111.8	90.3	161.0
	WHR (cm/cm)	137	1.0	0.0	1.0	0.9	1.1	284	0.9	0.1	0.9	0.7	1.1
	Age (yrs)	221	68.0	6.3	68.2	57.8	78.5	518	66.4	5.3	66.2	57.9	78.7
	BMI (kg/m²)	221	27.6	3.9	26.9	20.3	41.2	518	27.6	4.9	26.8	18.0	48.6
	Weight (kg)	221	83.2	13.7	81.0	52.8	135.9	518	70.6	13.1	69.2	41.9	143.2
	Height (cm)	221	173.4	6.2	173.5	157.2	192.8	518	160.0	5.9	159.8	142.0	178.0
DR's EXTRA	WC (cm)	221	99.0	11.4	97.0	77.0	133.8	518	88.9	12.8	87.4	59.5	132.5
	Hip (cm)	221	100.0	7.9	99.0	79.0	132.3	518	102.1	9.9	101.0	78.5	145.0
	WHR (cm/cm)	221	1.0	0.1	1.0	0.8	1.1	518	0.9	0.1	0.9	0.7	1.1
	Age (yrs)	351	53.2	10.1	51.2	26.8	83.6	205	56.4	9.3	56.0	24.9	81.1
	BMI (kg/m²)	351	29.8	6.0	29.1	18.0	55.6	205	31.1	8.4	29.8	16.9	71.9
DUKE (EA cases)	Weight (kg)	351	94.1	20.9	91.0	49.0	185.0	205	81.9	23.4	79.0	43.0	191.0
	Height (cm)	351	177.4	6.9	178.0	160.0	198.0	205	162.4	7.7	163.0	132.0	183.0
	Age (yrs)	263	68.2	6.4	66.5	55.5	89.7	170	76.5	4.4	76.1	70.1	91.4
	BMI (kg/m²)	263	28.9	6.4	28.1	12.5	60.4	170	27.3	6.1	25.8	17.3	48.2
DUKE (EA controls)	Weight (kg)	263	92.4	20.9	90.0	36.0	185.0	170	71.6	15.8	69.0	46.0	128.0
	Height (cm)	263	178.8	7.6	180.0	147.0	201.0	170	162.1	6.7	163.0	147.0	191.0
	Age (yrs)	313	58.5	10.8	58.7	32.8	93.8	304	61.5	11.3	61.9	31.0	88.0
	BMI (kg/m²)	313	30.5	7.3	29.3	11.6	71.9	304	32.6	8.0	31.6	15.9	62.4
DUKE (AA cases)	Weight (kg)	313	95.6	23.4	92.0	40.0	193.0	304	85.8	21.1	84.0	42.0	168.0
	Height (cm)	313	177.1	7.9	178.0	142.0	205.0	304	162.4	7.0	163.0	138.0	180.0
	Age (yrs)	280	55.0	11.5	54.5	27.0	92.0	425	55.5	11.8	54.9	22.1	86.6
	BMI (kg/m²)	280	31.5	7.9	30.4	17.0	63.3	425	33.4	8.9	32.5	15.1	69.5
DUKE (AA controls)	Weight (kg)	280	99.6	25.9	96.0	48.0	200.0	425	89.1	23.1	87.0	33.0	170.0
	Height (cm)	280	177.9	8.5	178.0	145.0	198.0	425	163.5	7.2	163.0	132.0	196.0
	Age (yrs)	726	32.9	5.9	32.0	17.0	61.0	794	30.4	5.3	31.0	17.0	45.0
	BMI (kg/m²)	723	26.6	3.9	26.0	17.0	48.0	457	25.0	4.6	24.0	17.0	45.0
EFSOCH	Height (cm)	726	1.8	0.1	1.8	1.6	2.0	794	1.7	0.1	1.6	1.5	1.8
	WHR (cm/cm)	719	0.9	0.1	0.9	0.7	1.2	456	0.8	0.1	0.8	0.7	1.1
	Age (yrs)	1645	45.4	16.5	45.0	18.0	87.0	1865	44.9	16.1	44.0	18.0	101.0
	BMI (kg/m²)	1645	27.7	7.3	26.3	15.0	64.2	1865	26.6	9.0	25.1	14.9	60.1
	Weight (kg)	1645	88.5	24.9	85.0	45.0	222.0	1865	75.1	24.7	70.0	37.0	170.0
	Height (cm)	1645	178.6	10.5	178.0	142.0	207.0	1865	165.1	9.8	164.0	135.0	198.0
EGCUT	WC (cm)	1317	96.7	18.5	94.0	59.0	165.0	1511	86.6	19.2	82.0	52.0	167.0
	Hip (cm)	1317	104.2	13.5	102.0	60.0	170.0	1511	106.4	17.1	102.0	64.0	167.0
	WHR (cm/cm)	1317	0.9	0.1	0.9	0.7	1.4	1511	0.8	0.1	0.8	0.5	1.2
	Age (yrs)	1320	29.3	7.4	28.0	20.0	44.0	2567	31.8	7.8	31.0	19.0	73.0
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Height (cm)	1320	180.9	6.2	181.0	147.0	199.0	2567	166.9	5.7	167.0	148.0	195.0
EGCUT CORE	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	7729	56.4	9.8	56.7	21.2	82.9	9626	55.2	10.0	55.4	20.4	81.9
	BMI (kg/m²)	7725	27.1	3.8	26.9	16.3	53.2	9616	26.5	4.8	25.8	15.6	62.0
EPIC-CVD	Weight (kg)	7725	80.8	12.1	80.0	41.8	153.0	9616	68.1	12.2	66.4	39.3	160.8
	Height (cm)	7729	172.7	7.3	173.0	138.0	198.0	9626	160.5	6.9	160.0	136.0	189.0
	WHR (cm/cm)	7629	1.0	0.1	1.0	0.5	1.7	9498	0.8	0.1	0.8	0.5	1.3
	Age (yrs)	953	52.4	8.1	52.9	24.9	69.4	1496	49.0	9.3	48.0	20.2	66.3
	BMI (kg/m²)	953	26.8	3.6	26.5	16.4	55.4	1496	25.7	4.6	24.8	17.2	54.8
	Weight (kg)	953	81.8	11.8	80.9	49.2	162.0	1496	68.3	12.9	66.1	44.9	149.7
	Height (cm)	953	174.8	6.5	174.5	150.5	196.4	1496	163.0	6.1	162.8	142.5	187.0
EPIC-Potsdam	WC (cm)	953	94.1	9.9	93.5	67.0	146.0	1496	80.7	11.7	78.7	56.5	134.0
	Hip (cm)	953	99.9	6.2	99.5	82.5	147.0	1496	101.4	9.2	100.0	78.0	160.0
	WHR (cm/cm)	953	0.9	0.1	0.9	0.7	1.2	1496	0.8	0.1	0.8	0.6	1.1
	Age (yrs)	1187	61.2	8.4	62.7	45.3	75.2	1186	61.4	8.3	63.1	45.3	75.3
	BMI (kg/m²)	1187	26.9	3.4	26.6	18.7	42.3	1185	26.1	4.2	25.6	16.4	50.7
	Weight (kg)	1187	86.3	12.3	85.3	52.4	130.3	1185	71.3	12.3	69.9	39.3	160.6
	Height (cm)	1187	179.0	6.6	179.0	160.0	203.0	1186	165.3	6.1	165.0	144.0	184.5
EpiHealth	WC (cm)	1187	97.6	9.7	97.0	72.0	141.0	1186	87.6	11.5	87.0	61.0	144.0
	Hip (cm)	1187	103.1	6.1	103.0	56.0	131.0	1186	103.0	8.8	102.0	56.0	153.0
	WHR (cm/cm)	1187	0.9	0.1	0.9	0.7	1.4	1186	0.8	0.1	0.8	0.6	1.4
	Age (yrs)	174	76.7	8.8	76.0	60.0	98.0	256	76.6	9.3	75.0	57.0	100.0
	BMI (kg/m²)	174	26.4	4.4	25.7	18.3	65.2	256	25.0	4.0	24.5	16.0	39.8
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Height (cm)	174	174.2	6.6	174.0	153.0	192.0	256	162.5	6.3	163.0	145.0	180.0
EUGENDA_UK (cases)	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	226	69.8	6.6	69.0	53.0	96.0	320	76.6	9.3	75.0	57.0	100.0
	BMI (kg/m²)	226	26.7	3.6	26.0	19.3	42.4	320	25.0	4.0	24.5	16.0	39.8
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Height (cm)	226	176.5	6.3	177.0	160.0	192.0	320	162.5	6.3	163.0	145.0	180.0
EUGENDA_UK (controls)	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	178	74.5	8.2	75.0	53.0	91.0	294	75.4	8.1	76.0	53.0	95.0
	BMI (kg/m²)	178	25.7	3.1	25.3	17.8	36.1	294	26.0	4.7	25.1	17.3	53.1
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Height (cm)	178	176.3	7.2	176.0	156.0	193.0	294	164.1	6.2	164.0	147.0	179.0
EUGENDA_UMCN (cases)	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	145	71.1	6.1	70.0	53.0	91.0	218	70.4	5.4	70.0	51.0	87.0
	BMI (kg/m²)	145	25.8	2.9	25.3	19.6	38.1	218	26.0	3.9	25.4	18.0	43.8
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Height (cm)	145	176.2	6.8	176.0	158.0	200.0	218	165.4	6.1	165.0	148.0	183.0
EUGENDA_UMCN (controls)	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	610	58.4	14.9	61.0	18.0	98.0	971	55.3	14.7	57.0	18.0	94.0
	BMI (kg/m²)	610	28.1	4.5	27.5	14.3	56.8	969	26.8	5.4	25.6	14.4	63.4
EXTEND	Height (cm)	610	1.8	0.1	1.8	1.4	2.0	971	1.6	0.1	1.6	1.2	1.9
	WHR (cm/cm)	609	0.9	0.1	0.9	0.6	1.3	968	0.8	0.1	0.8	0.0	1.3
	Age (yrs)	208	52.4	10.5	52.0	30.0	81.0	400	53.8	10.9	53.0	31.0	83.0
	BMI (kg/m²)	208	30.2	6.2	29.5	16.9	51.1	399	34.0	7.6	32.9	15.7	60.2
	Weight (kg)	208	94.2	20.6	93.0	48.5	152.9	399	90.3	21.4	85.7	44.0	157.9
	Height (cm)	208	176.6	7.3	177.0	140.0	195.0	400	163.1	6.3	163.0	146.0	216.0
FamHS (AA)	WC (cm)	208	103.2	15.7	100.5	68.0	152.0	400	105.8	17.4	104.0	66.0	171.0
	Hip (cm)	208	108.5	12.7	107.0	78.0	157.0	399	117.3	15.3	116.0	76.0	168.0
	WHR (cm/cm)	208	0.9	0.1	1.0	0.8	1.2	399	0.9	0.1	0.9	0.7	1.1
	Age (yrs)	1783	52.0	13.9	53.9	25.2	91.0	1963	52.4	13.4	54.0	25.2	93.6
	BMI (kg/m²)	1783	28.0	4.6	27.3	16.0	63.6	1963	27.5	6.1	26.2	16.1	55.1
	Weight (kg)	1783	87.7	16.1	85.3	45.8	236.8	1963	72.8	16.8	69.4	36.7	152.0
	Height (cm)	1783	176.9	7.0	177.0	155.0	207.0	1963	162.6	6.3	163.0	141.0	196.0
FamHS (EA)	WC (cm)	1783	100.7	12.9	100.0	44.0	188.0	1963	94.8	16.7	93.0	27.0	170.0
	Hip (cm)	1783	104.6	9.1	103.0	53.0	190.0	1963	107.2	12.7	105.0	59.0	196.0

	WHR (cm/cm)	1783	1.0	0.1	1.0	0.4	1.8	1963	0.9	0.1	0.9	0.3	1.6
	Age (yrs)	622	48.5	7.2	48.5	31.3	61.5	719	48.6	7.2	49.1	33.7	61.1
	BMI (kg/m²)	622	27.5	4.0	27.1	18.0	46.6	719	26.6	5.5	25.3	16.6	59.9
	Weight (kg)	622	87.5	13.8	86.2	55.7	152.9	719	71.9	15.3	68.3	43.0	181.0
	Height (cm)	622	178.3	6.6	178.2	159.6	197.3	719	164.4	6.3	164.1	145.8	188.0
FENLAND	WC (cm)	622	97.8	11.2	97.0	73.1	144.3	716	86.2	13.1	84.2	61.1	141.0
	Hip (cm)	622	103.5	6.9	103.0	84.7	139.5	716	104.0	10.8	102.1	81.9	177.6
	WHR (cm/cm)	622	0.9	0.1	0.9	0.8	1.2	716	0.8	0.1	0.8	0.6	1.1
	Age (yrs)	1627	54.9	7.3	59.7	29.8	74.3	711	57.4	7.8	59.9	29.6	74.0
	BMI (kg/m²)	1627	27.2	3.5	26.8	18.0	44.8	711	27.0	4.8	26.2	16.7	47.3
	Weight (kg)	1627	83.9	12.3	82.6	52.0	155.0	711	71.5	13.4	70.0	42.0	124.0
	Height (cm)	1627	175.7	6.5	176.0	140.0	198.0	711	162.7	5.9	163.0	143.0	180.0
FIA3	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	547	53.2	14.0	55.0	18.0	82.0	391	55.6	12.7	57.0	20.0	83.0
	BMI (kg/m²)	547	27.8	4.2	27.0	18.0	42.0	391	27.2	4.9	27.0	17.0	45.0
	Weight (kg)	547	87.8	14.7	85.0	49.0	140.0	391	72.9	13.7	71.0	44.0	120.0
	Height (cm)	547	177.7	6.5	178.0	155.0	198.0	391	163.8	6.2	164.0	148.0	183.0
FINCAVAS	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	1238	60.3	8.4	61.0	45.0	74.0	1336	59.4	8.3	59.0	45.0	74.0
	BMI (kg/m²)	1238	27.5	4.2	26.9	16.5	48.9	1336	27.6	5.4	26.8	17.2	61.3
	Weight (kg)	1238	85.1	14.5	83.4	46.5	160.0	1336	72.9	14.6	71.1	41.9	158.6
	Height (cm)	1238	175.8	6.5	175.5	144.8	198.3	1336	162.5	5.6	162.3	140.9	183.1
FIN-D2D 2007	WC (cm)	1238	100.1	11.8	99.0	63.0	150.0	1336	90.6	13.4	89.0	62.0	150.0
	Hip (cm)	1238	100.6	7.6	99.5	79.0	145.0	1336	103.3	10.0	102.0	79.5	152.0
	WHR (cm/cm)	1238	1.0	0.1	1.0	0.8	1.2	1336	0.9	0.1	0.9	0.7	1.2
	Age (yrs)	316	61.6	9.4	63.0	31.0	74.0	226	62.1	9.7	65.0	27.0	74.0
	BMI (kg/m²)	316	30.3	4.7	29.7	20.0	50.8	226	31.3	6.5	30.0	19.1	53.1
	Weight (kg)	316	91.5	15.9	89.8	53.8	144.3	226	80.5	16.8	78.3	48.6	153.0
	Height (cm)	316	1.7	0.1	1.7	1.5	2.0	226	1.6	0.1	1.6	1.5	1.7
FINRISK 2007 (T2D cases)	WC (cm)	316	104.8	9.3	103.5	86.0	143.0	226	109.9	13.0	108.0	83.0	146.0
	Hip (cm)	316	107.6	12.0	106.5	82.5	145.5	226	99.9	15.1	99.0	62.5	137.5
	WHR (cm/cm)	316	1.0	0.1	1.0	0.8	1.1	226	1.1	0.1	1.1	0.9	1.4
	Age (yrs)	221	65.6	6.5	67.0	43.0	74.0	328	64.0	7.5	66.0	34.0	74.0
	BMI (kg/m²)	221	28.6	3.8	27.7	20.5	48.7	328	30.1	4.9	29.2	21.8	51.1
	Weight (kg)	221	86.8	14.1	85.5	61.1	156.8	328	77.2	14.0	75.9	52.9	138.3
	Height (cm)	221	1.7	0.1	1.7	1.5	2.0	328	1.6	0.1	1.6	1.5	1.8
FINRISK 2007 (T2D controls)	WC (cm)	221	101.9	6.8	101.5	90.0	145.0	328	108.2	10.3	106.8	88.0	146.5
	Hip (cm)	221	102.0	10.3	101.0	80.0	150.0	328	95.1	11.7	94.0	73.0	133.0
	WHR (cm/cm)	221	1.0	0.1	1.0	0.9	1.2	328	1.1	0.1	1.1	1.0	1.4
	Age (yrs)	382	40.6	11.3	39.6	24.4	71.5	392	41.1	12.3	39.8	24.3	74.1
	BMI (kg/m²)	382	28.6	8.2	26.7	16.2	53.4	392	29.0	10.2	26.3	15.4	53.1
	Weight (kg)	382	90.5	27.6	90.1	40.0	174.0	392	76.9	27.2	71.2	36.0	153.0
	Height (cm)	382	177.7	13.6	178.6	134.4	218.0	392	163.3	12.5	164.5	110.0	196.0
FINRISKEXTREMES	WC (cm)	382	74.3	46.4	86.0	6.5	150.0	392	68.7	43.2	73.0	5.8	140.0
	Hip (cm)	382	77.7	46.0	94.5	8.5	153.0	392	81.0	48.1	92.8	8.3	162.0
	WHR (cm/cm)	382	0.95	0.10	0.94	0.68	1.18	392	0.83	0.09	0.82	0.63	1.20
	Age (yrs)	3437	38.0	9.0	38.0	18.0	72.0	4168	37.7	9.0	37.0	18.0	70.0
	BMI (kg/m²)	3437	27.1	4.2	26.6	16.4	56.5	4163	24.8	5.3	23.5	15.0	60.6
	Weight (kg)	3437	84.6	14.6	83.0	30.4	177.4	4163	65.8	14.7	62.6	38.1	170.1
	Height (cm)	3437	176.7	6.9	176.5	123.2	200.0	4168	162.8	6.3	162.6	132.7	185.4
FRAM	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	625	42.0	17.5	36.3	21.3	91.2	1167	51.6	19.8	55.9	21.0	93.3
	BMI (kg/m²)	625	25.5	4.1	24.9	18.1	57.5	1167	25.6	4.8	24.8	16.3	50.9
	Weight (kg)	625	81.2	14.3	79.5	52.0	180.0	1167	67.8	12.4	66.0	39.1	137.0
	Height (cm)	625	178.4	6.4	178.0	157.0	198.0	1167	163.1	6.6	163.0	142.0	187.6
FTCS	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	1248	60.1	8.4	61.0	28.0	80.0	888	62.2	8.1	62.8	34.4	85.0
	BMI (kg/m²)	1248	29.9	4.6	29.5	18.2	53.0	888	31.5	5.6	30.9	16.0	53.5
	Weight (kg)	1248	90.7	15.7	89.3	46.2	167.0	888	80.3	15.3	77.9	35.0	143.5
	Height (cm)	1248	174.1	6.5	174.0	139.0	197.0	888	159.9	5.7	160.0	140.0	179.0
FUSION (T2D cases)	WC (cm)	1248	105.2	12.1	104.0	70.5	160.0	888	99.0	13.3	98.5	59.0	140.0
	Hip (cm)	1248	105.7	8.9	105.0	74.0	164.0	888	110.5	11.5	109.0	79.0	147.5
	WHR (cm/cm)	1248	1.0	0.1	1.0	0.7	1.2	888	0.9	0.1	0.9	0.6	1.2
	Age (yrs)	1199	59.6	8.3	60.0	41.7	90.9	938	62.4	7.5	63.0	41.4	89.1
	BMI (kg/m²)	1199	26.9	3.5	26.6	19.2	51.1	938	27.1	4.3	26.6	17.3	57.2
	Weight (kg)	1199	81.6	12.0	80.6	52.1	151.1	938	69.6	11.5	68.3	43.2	153.8
	Height (cm)	1199	174.3	6.3	174.0	153.0	195.3	938	160.4	6.1	160.0	140.0	179.0
FUSION (T2D controls)	WC (cm)	1199	95.9	9.9	95.0	72.0	147.0	938	85.7	10.7	84.5	58.0	132.0
	Hip (cm)	1199	100.4	6.8	100.0	81.0	145.0	938	102.4	8.5	102.0	83.0	144.0
	WHR (cm/cm)	1199	1.0	0.1	1.0	0.8	1.1	938	0.8	0.1	0.8	0.7	1.1
	Age (yrs)	321	49.6	14.9	50.0	18.0	84.0	445	48.5	15.1	49.0	18.0	91.0
	BMI (kg/m²)	320	26.4	3.8	25.7	18.7	40.8	445	24.2	4.7	23.4	15.9	46.5
	Weight (kg)	320	82.2	13.0	80.0	51.0	126.0	445	64.8	12.9	63.0	40.0	125.0
	Height (cm)	321	176.5	6.5	176.0	140.0	196.0	445	163.9	6.5	164.0	140.0	180.0
FVG	WC (cm)	321	96.2	12.2	95.0	58.0	140.0	445	82.8	12.9	81.0	60.0	129.0
	Hip (cm)	321	104.7	11.3	104.0	78.0	163.0	445	99.8	12.4	99.0	68.0	148.0
	WHR (cm/cm)	321	0.9	0.1	0.9	0.5	1.1	445	0.8	0.1	0.8	0.7	1.2
	Age (yrs)	387	51.7	8.7	52.0	39.0	95.0	437	52.4	8.1	52.0	40.0	78.0
	BMI (kg/m²)	387	23.6	3.2	23.4	16.5	33.1	437	24.3	3.6	23.9	16.0	47.1
	Weight (kg)	387	63.9	10.5	62.7	39.1	97.9	437	56.8	9.2	55.8	36.3	95.0
	Height (cm)	387	164.3	5.9	164.2	139.3	179.8	437	152.7	5.7	153.0	136.5	170.2
GBTDS (controls)	WC (cm)	387	82.6	10.1	82.0	60.0	107.0	436	82.6	9.8	82.4	47.7	120.0
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	433	53.5	9.8	53.0	31.0	81.0	405	56.5	8.7	56.0	33.0	83.0
	BMI (kg/m²)	433	24.3	3.0	24.6	15.1	34.0	405	24.6	3.0	24.7	13.8	35.2
	Weight (kg)	433	66.3	9.8	67.2	36.5	104.6	405	57.3	7.8	57.5	30.1	80.1
	Height (cm)	433	165.0	6.1	165.0	145.7	180.0	405	152.7	5.6	152.8	134.6	168.0
GBTDS (T2D cases)	WC (cm)	433	87.5	9.4	88.6	37.0	110.1	404	85.9	8.7	87.0	56.0	112.3
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	3372	64.3	9.3	66	20	95	4077	62.9	8.7	64	29	97
	BMI (kg/m²)	2311	27	4	26.5	16.3	46.9	3312	26.5	5.4	25.5	15	60
GECCO*	Weight (kg)	2311	85.9	14.1	84	44	172	3312	70.8	15.2	68	38	183.8
	Height (cm)	3372	175.9	7.6	175.3	148	215	4077	162.7	6.6	162.6	135	200.7
	Age (yrs)	189	41.9	12.0	42.0	19.0	68.0	279	42.6	11.3	44.0	20.0	69.0
	BMI (kg/m²)	188	26.0	3.9	25.6	16.4	40.0	276	24.8	5.2	23.9	15.4	55.5
GENDEP	Weight (kg)	188	83.0	12.8	83.0	53.0	125.0	276	67.7	14.2	65.0	39.0	134.0
	Height (cm)	189	178.6	6.5	179.0	158.0	197.0	279	165.1	6.2	165.0	149.0	183.0
	Age (yrs)	353	57.0	10.8	56.3	32.6	86.6	773	55.4	11.4	54.7	23.3	91.2
	BMI (kg/m²)	353	28.3	4.8	28.0	15.2	50.3	773	32.2	7.1	31.6	17.5	61.4
	Weight (kg)	353	89.7	16.9	88.1	50.2	174.1	773	87.3	19.9	85.2	45.0	167.3
	Height (cm)	353	178.0	6.9	178.2	149.9	201.1	773	164.7	6.3	164.8	147.8	187.2
GENOA (AA)	WC (cm)	353	99.3	12.0	98.5	66.3	150.9	773	103.6	18.3	101.5	61.0	170.0
	Hip (cm)	353	105.0	10.2	104.0	76.7	151.5	773	116.5	15.1	115.0	83.0	190.0
	WHR (cm/cm)	353	0.9	0.1	1.0	0.8	1.1	773	0.9	0.1	0.9	0.7	1.1
	Age (yrs)	672	55.6	10.7	56.4	26.9	89.9	840	55.1	10.9	55.4	24.9	81.8
	BMI (kg/m²)	672	30.1	5.0	29.5	16.9	58.3	840	30.6	7.3	29.4	15.8	67.9
	Weight (kg)	672	93.7	17.1	91.6	50.0	185.0	840	81.0	20.1	78.0	42.4	184.8
	Height (cm)	672	176.3	6.3	176.3	158.4	197.1	840	162.7	6.1	162.5	142.0	182.6
GENOA (EA)	WC (cm)	672	104.6	11.9	103.8	75.4	159.9	840	96.4	17.5	94.7	61.0	168.2
	Hip (cm)	672	107.7	9.2	106.6	86.9	169.0	840	111.3	14.6	109.8	81.3	191.6
	WHR (cm/cm)	672	1.0	0.1	1.0	0.7	1.2	840	0.9	0.1	0.9	0.6	1.3
	Age (yrs)	3833	67.5	13.6	69.0	22.0	90.0	3573	61.6	15.9	62.0	20.0	90.0
	BMI (kg/m²)	3833	31.6	8.3	29.8	14.7	87.4	3573	36.2	11.0	34.4	14.5	82.5

	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Height (cm)	3833	176.1	6.8	176.0	152.4	200.7	3573	161.7	6.5	161.9	138.4	186.7
GHS	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	418	49.7	8.5	50.0	30.0	60.0	509	50.6	7.7	50.0	30.0	64.0
	BMI (kg/m²)	418	26.3	3.8	25.9	18.8	59.0	507	25.8	4.0	25.2	16.0	40.3
	Weight (kg)	418	82.1	11.2	81	53	120	507	69.2	11.4	68	40	107
	Height (cm)	418	176.8	6.8	177	120	193	509	163.7	5.9	164	117	181
GLACIER	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	965	39.4	15.1	43.0	18.0	61.0	945	39.1	13.9	43.0	18.0	60.0
	BMI (kg/m²)	965	26.4	4.3	26.4	17.2	48.0	945	25.8	4.9	24.9	15.1	46.6
	Weight (kg)	961	83.5	14.3	81.6	53.0	147.0	939	69.5	13.8	67.0	41.7	150.9
	Height (cm)	961	177.9	6.6	178.0	153.0	200.0	939	164.1	6.4	164.0	143.0	190.0
GRAPHIC	WC (cm)	956	92.6	12.1	92.0	67.0	139.0	928	82.0	11.7	81.0	60.0	130.0
	Hip (cm)	957	103.5	8.2	103.0	72.0	145.0	936	102.8	10.8	102.0	65.0	154.0
	WHR (cm/cm)	953	0.9	0.1	0.9	0.7	1.1	926	0.8	0.1	0.8	0.7	1.1
	Age (yrs)	4100	52.6	13.8	55.0	18.0	99.0	5815	51.9	13.5	54.0	18.0	95.0
	BMI (kg/m²)	4091	27.2	4.3	26.7	16.1	49.5	5790	26.8	5.7	25.8	13.2	71.4
	Weight (kg)	4091	84.1	14.5	82.4	48.0	156.6	5790	70.3	15.3	67.6	31.2	173.4
	Height (cm)	4100	175.7	7.0	175.5	138.5	202.5	5815	161.9	6.5	162.0	125.5	185.2
GS:SFHS	WC (cm)	4050	95.8	11.9	95.0	62.0	186.5	5721	86.0	13.8	84.0	51.0	176.0
	Hip (cm)	4047	103.5	8.5	103.0	69.0	188.0	5722	103.7	11.9	102.0	30.8	180.9
	WHR (cm/cm)	4046	0.9	0.1	0.9	0.5	1.4	5718	0.8	0.1	0.8	0.5	2.8
	Age (yrs)	868	73.9	2.9	74.0	69.0	80.0	780	73.6	2.8	73.0	69.0	80.0
	BMI (kg/m²)	868	27.1	3.7	26.7	17.6	44.2	780	26.1	4.5	25.6	15.6	44.7
HABC (EA)	Height (cm)	868	173.6	6.4	173.4	154.7	194.8	780	159.4	5.8	159.6	141.6	175.6
	Age (yrs)	1639	49.6	12.2	50.0	19.0	72.0	2036	48.3	12.3	49.0	19.0	72.0
	BMI (kg/m²)	1639	26.6	4.1	26.1	16.5	53.5	2036	25.3	4.9	24.3	16.2	52.1
	Weight (kg)	1639	85.6	14.4	84.1	48.4	167.3	2036	69.9	14.0	67.3	40.2	142.6
	Height (cm)	1639	179.3	6.7	179.5	156.0	203.0	2036	166.2	6.3	166.0	145.5	188.7
Health	WC (cm)	1639	95.2	11.7	94.0	62.0	154.0	2036	83.5	12.3	82.0	61.0	144.0
	Hip (cm)	1639	101.6	7.5	101.0	78.0	170.0	2036	102.0	9.9	101.0	78.0	154.0
	WHR (cm/cm)	1639	0.9	0.1	0.9	0.8	1.3	2036	0.8	0.1	0.8	0.7	1.2
	Age (yrs)	423	58.1	20.8	62.0	18.0	96.0	552	62.0	18.9	67.0	18.0	97.0
	BMI (kg/m²)	411	29.3	4.5	28.8	17.0	46.8	543	29.5	5.6	29.2	17.3	50.1
	Weight (kg)	411	84.7	14.5	83.5	50.0	147.4	543	72.3	13.9	71.0	38.7	133.1
	Height (cm)	423	170.1	7.7	170.0	149.0	192.0	552	156.8	7.2	156.0	135.0	175.0
HELIC MANOLIS	WC (cm)	408	102.4	12.1	102.0	58.3	137.0	541	95.2	13.8	96.8	60.0	132.0
	Hip (cm)	408	106.2	8.7	105.5	73.3	143.0	538	109.0	11.2	107.5	80.0	159.0
	WHR (cm/cm)	407	1.0	0.1	1.0	0.6	1.2	538	0.9	0.1	0.9	0.6	1.2
	Age (yrs)	259	47.8	13.9	48.0	18.0	87.0	645	41.6	13.4	41.0	18.0	78.0
	BMI (kg/m²)	259	26.7	4.1	26.5	18.8	38.6	644	28.3	5.7	28.2	16.0	47.5
	Weight (kg)	259	79.5	13.4	79.0	51.0	122.0	644	70.8	14.1	70.0	36.0	126.0
	Height (cm)	259	172.5	7.6	172.0	152.0	196.0	645	158.3	7.0	158.0	120.0	181.0
HELIC Pomak	WC (cm)	243	94.9	12.4	95.0	52.0	126.0	604	88.6	14.8	88.0	58.0	147.0
	Hip (cm)	240	102.1	7.5	102.0	85.0	122.0	603	107.2	11.2	107.0	75.0	150.0
	WHR (cm/cm)	240	0.9	0.1	0.9	0.6	1.1	602	0.8	0.1	0.8	0.6	1.2
	Age (yrs)	821	63.3	10.1	62.0	33.0	96.0	1409	63.0	10.7	61.0	28.0	99.0
	BMI (kg/m²)	775	28.7	5.2	28.5	15.1	51.5	1328	31.9	7.2	31.2	15.1	59.8
	Weight (kg)	775	87.8	17.3	86.6	46.0	137.2	1328	83.1	19.0	81.6	35.2	135.4
	Height (cm)	821	174.8	7.4	175.3	143.5	200.7	1328	161.5	6.6	161.3	137.2	181.6
HRS (AA)	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	4407	67.6	10.4	68.0	34.0	107.0	5966	67.0	11.3	67.0	30.0	101.0
	BMI (kg/m²)	4245	29.3	5.0	28.6	14.8	53.5	5680	28.7	6.3	27.7	15.3	64.1
	Weight (kg)	4245	89.4	16.2	87.5	39.2	137.7	5680	74.0	16.9	71.4	32.2	138.1
	Height (cm)	4245	174.8	7.1	174.8	142.2	198.1	5680	160.5	6.6	160.8	137.2	187.5
HRS (EA)	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	8346	55.5	13.5	55.0	0.0	95.0	6768	56.0	14.7	55.0	20.0	93.0
	BMI (kg/m²)	8322	26.6	3.5	26.3	15.0	47.8	6717	26.8	4.6	26.2	14.8	52.8
	Weight (kg)	8322	83.2	12.2	82.0	43.5	150.0	6718	71.4	12.8	69.5	36.5	144.5
	Height (cm)	8328	176.6	6.5	176.0	149.0	202.0	6726	163.1	6.1	163.0	136.0	189.0
HUNT	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	8314	0.9	0.1	0.9	0.6	1.2	6688	0.8	0.1	0.8	0.6	1.3
	Age (yrs)	2900	46.7	7.8	45.2	29.9	61.1	3091	45.8	8.0	45.1	29.7	61.4
	BMI (kg/m²)	2900	26.9	4.1	26.4	16.7	56.9	3091	25.8	5.1	24.7	15.2	55.8
	Weight (kg)	2900	86.0	14.1	84.4	53.0	183.0	3091	71.1	14.6	68.5	40.5	152.2
	Height (cm)	2900	178.9	6.8	179.0	157.5	207.0	3091	166.0	6.3	166.0	129.0	188.0
Inter99	WC (cm)	2900	93.4	11.1	92.0	53.0	180.0	3091	80.4	12.4	78.0	53.0	146.0
	Hip (cm)	2900	101.5	8.0	101.0	76.0	165.0	3091	100.6	11.3	99.0	68.0	174.0
	WHR (cm/cm)	2900	0.9	0.1	0.9	0.6	1.6	3091	0.8	0.1	0.8	0.6	1.1
	Age (yrs)	1289	55.0	8.2	55.4	29.9	76.9	1352	55.8	8.1	56.4	26.2	77.0
	BMI (kg/m²)	1284	29.3	4.0	28.9	13.6	61.4	1348	30.3	5.3	29.6	17.0	67.9
	Weight (kg)	1284	88.3	13.8	86.8	45.0	181.0	1348	77.7	14.3	76.0	44.8	187.0
	Height (cm)	1289	173.5	7.2	173.0	140.0	196.0	1352	160.3	6.8	160.0	136.0	185.0
InterAct	WC (cm)	1124	102.6	10.3	102.0	65.0	143.0	1210	93.0	12.3	93.0	57.0	158.0
	Hip (cm)	1124	104.8	7.9	104.0	84.0	143.0	1210	108.8	11.2	108.0	79.8	171.0
	WHR (cm/cm)	1124	1.0	0.1	1.0	0.8	1.2	1210	0.9	0.1	0.9	0.7	1.1
	Age (yrs)	232	43.2	14.4	41.3	18.1	79.3	341	42.4	13.6	41.4	18.4	80.3
	BMI (kg/m²)	231	28.8	5.3	28.4	18.6	47.1	339	30.8	7.6	29.4	15.4	54.6
IRASFS (AA)	Height (cm)	232	178.7	6.5	178.5	161.3	199.6	341	164.0	5.7	163.6	150.3	179.0
	WHR (cm/cm)	231	0.9	0.1	0.9	0.7	1.1	339	0.8	0.1	0.8	0.6	1.0
	Age (yrs)	518	41.8	15.0	38.9	18.0	79.9	742	43.3	14.2	42.5	18.0	81.2
	BMI (kg/m²)	516	28.4	5.4	28.0	17.6	45.7	737	29.2	6.6	28.1	16.5	58.1
IRASFS (HA)	Height (cm)	518	171.4	6.9	171.4	142.5	203.5	742	158.4	5.9	158.5	142.0	177.7
	WHR (cm/cm)	516	0.9	0.1	0.9	0.8	1.2	737	0.8	0.1	0.8	0.7	1.0
	Age (yrs)	868	51.8	12.8	51.0	21.0	81.0	1449	53.7	12.6	53.0	21.0	91.0
	BMI (kg/m²)	868	30.4	6.7	29.2	16.3	66.1	1446	31.9	6.0	31.5	16.0	54.2
	Weight (kg)	868	96.2	23.0	92.0	49.1	232.4	1447	86.1	17.4	84.8	41.0	185.1
	Height (cm)	868	177.8	7.0	178.0	158.0	200.0	1449	164.3	6.5	164.0	142.0	185.0
JHS	WC (cm)	678	104.5	15.9	101.6	66.0	188.0	1182	100.0	14.8	99.1	58.4	177.8
	Hip (cm)	678	111.4	13.4	109.2	83.8	188.0	1182	115.2	13.5	114.3	78.7	191.8
	WHR (cm/cm)	678	0.9	0.1	0.9	0.7	1.2	1182	0.9	0.1	0.9	0.6	1.5
	Age (yrs)	1369	56.6	13.4	57.0	32.0	81.0	1478	55.3	13.1	55.0	32.0	81.0
	BMI (kg/m²)	1365	27.8	4.0	27.2	16.3	47.6	1468	27.2	5.2	26.2	16.1	50.4
	Weight (kg)	1365	85.8	13.3	84.3	53.0	160.1	1468	71.6	13.7	69.2	41.5	131.3
	Height (cm)	1365	175.6	7.2	175.6	154.4	197.1	1468	162.3	6.8	162.1	140.0	185.2
KORA-F4	WC (cm)	1367	99.7	11.6	98.8	63.0	170.0	1469	87.8	13.1	87.1	61.3	139.2
	Hip (cm)	1367	106.1	7.5	105.4	76.9	175.2	1468	106.3	10.2	104.6	84.5	162.0
	WHR (cm/cm)	1367	0.9	0.1	0.9	0.7	1.2	1468	0.8	0.1	0.8	0.7	1.1
	Age (yrs)	199	79.1	0.6	79.1	77.7	80.6	291	79.1	0.6	79.1	77.8	80.4
	BMI (kg/m²)	199	26.1	3.4	25.8	18.1	42.1	291	26.1	4.5	25.5	16.4	50.6
	Weight (kg)	199	77.0	10.8	76.0	47.0	124.0	291	64.7	11.2	64.0	37.5	118.0
	Height (cm)	199	171.6	6.9	172.0	148.4	197.0	291	157.4	5.8	157.0	141.5	175.1
LBC 1921	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	500	69.5	0.8	69.5	67.6	71.3	488	69.6	0.8	69.6	67.6	71.3
	BMI (kg/m²)	499	28.0	3.8	27.6	19.0	45.2	488	27.6	4.8	27.3	16.0	48.5
	Weight (kg)	499	83.6	12.2	82.5	57.0	133.8	488	70.7	13.0	69.0	40.0	120.0
	Height (cm)	500	172.8	6.4	172.9	152.5	195.5	488	159.9	6.0	160.0	143.0	174.0
LBC 1936	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Age (yrs)	361	42.4	17.1	40.0	18.0	99.0	541	43.6	15.9	43.0	18.0	91.0

Leipzig-adults	BMI (kg/m²)	351	34.8	11.5	32.1	18.8	79.1	515	37.8	12.1	37.6	14.8	73.9
	Weight (kg)	361	113.6	37.9	105.8	48.0	250.0	541	104.6	35.0	103.0	40.0	209.0
	Height (cm)	361	180.0	6.7	180.0	158.0	198.0	541	166.5	7.0	165.0	142.0	191.0
	WC (cm)	335	119.6	28.0	118.0	60.0	189.0	479	115.0	29.0	118.0	52.0	186.0
	Hip (cm)	335	119.8	24.6	115.0	71.0	192.0	479	126.0	26.0	126.0	63.0	192.0
	WHR (cm/cm)	335	1.0	0.1	1.0	0.8	1.3	479	0.9	0.1	0.9	0.7	1.3
LOLIPOP-Exome	Age (yrs)	1241	52.3	10.2	51.4	31.1	74.8	423	52.1	9.5	51.8	35.1	75.0
	BMI (kg/m²)	1241	27.2	3.8	26.8	16.5	49.2	423	28.4	5.1	27.9	18.7	49.6
	Weight (kg)	1241	79.3	12.6	77.9	48.0	154.0	423	69.4	12.4	68.1	42.4	114.8
	Height (cm)	1241	170.6	6.4	170.4	151.0	192.0	423	156.6	6.1	157.0	132.0	172.0
	WC (cm)	1239	98.4	10.2	98.0	37.0	138.0	421	95.2	12.3	95.0	64.0	146.0
	Hip (cm)	1239	100.9	7.6	101.0	36.0	148.0	421	103.7	9.8	103.0	82.0	152.0
	WHR (cm/cm)	1239	1.0	0.1	1.0	0.8	1.4	421	0.9	0.1	0.9	0.7	1.2
LOLIPOP-OmniEE	Age (yrs)	560	50.3	10.2	48.9	35.1	76.4	417	50.9	9.9	49.7	31.4	74.4
	BMI (kg/m²)	560	27.1	4.1	26.6	15.9	45.2	417	28.4	4.7	27.8	18.8	52.1
	Weight (kg)	560	78.8	13.6	77.2	46.0	140.4	417	69.6	12.9	67.9	43.1	140.0
	Height (cm)	560	170.5	6.7	170.0	150.0	191.1	417	156.5	5.7	156.0	140.5	173.0
	WC (cm)	560	97.6	10.4	97.0	73.0	140.0	417	95.7	12.1	95.0	64.2	134.0
	Hip (cm)	560	101.0	7.8	100.0	80.0	138.0	417	103.3	9.0	102.0	80.0	146.0
	WHR (cm/cm)	560	1.0	0.1	1.0	0.8	1.2	417	0.9	0.1	0.9	0.6	1.3
Marshfield PMRP Exomechip	Age (yrs)	3326	54.6	14.5	55.0	19.0	79.0	5244	51.7	14.7	51.0	19.0	79.0
	BMI (kg/m²)	3326	30.3	5.6	29.5	16.3	57.6	5244	29.9	7.2	28.5	15.8	66.6
	Weight (kg)	3326	94.4	18.9	91.6	44.9	191.6	5244	79.4	19.8	75.8	40.4	192.8
	Height (cm)	3326	176.4	7.0	175.3	137.2	200.7	5244	163.0	6.4	162.6	124.5	195.6
MESA (AA)	Age (yrs)	762	62.3	10.2	62.5	45.0	84.0	893	62.2	10.0	63.0	45.0	84.0
	BMI (kg/m²)	762	28.8	4.7	28.5	15.9	46.9	893	31.3	6.3	30.4	15.9	51.1
	Weight (kg)	762	89.2	16.3	87.8	45.5	142.6	893	82.3	17.4	79.6	39.5	141.7
	Height (cm)	762	175.9	6.9	176.0	152.5	196.7	893	162.2	6.6	162.0	136.9	184.8
	WC (cm)	762	100.7	12.7	99.7	63.0	152.5	893	101.5	15.9	99.8	63.0	156.0
	Hip (cm)	762	106.1	9.7	105.0	83.1	149.5	893	112.8	12.9	111.0	83.0	159.0
	WHR (cm/cm)	762	1.0	0.1	1.0	0.7	1.1	893	0.9	0.1	0.9	0.7	1.2
MESA (EA)	Age (yrs)	1195	62.7	10.1	63.0	45.0	84.0	1302	62.6	10.3	63.0	44.0	84.0
	BMI (kg/m²)	1195	28.0	4.1	27.5	17.4	44.3	1302	27.4	5.6	26.5	16.4	48.0
	Weight (kg)	1195	87.0	14.3	85.3	44.5	136.5	1302	72.2	15.5	69.4	39.0	134.4
	Height (cm)	1195	176.3	6.9	176.2	155.4	202.5	1302	162.2	6.5	162.1	138.0	185.8
	WC (cm)	1195	101.1	11.0	100.0	67.5	143.5	1302	94.9	16.0	93.9	58.5	152.0
	Hip (cm)	1195	105.2	8.1	104.0	83.0	138.0	1302	106.9	11.9	104.7	79.9	160.2
	WHR (cm/cm)	1195	1.0	0.1	1.0	0.7	1.2	1302	0.9	0.1	0.9	0.7	1.3
MESA (EAS)	Age (yrs)	379	62.4	10.3	63.0	44.0	84.0	390	62.3	10.5	62.0	44.0	84.0
	BMI (kg/m²)	379	24.1	3.2	23.7	15.4	33.5	390	23.8	3.3	23.8	16.6	35.4
	Weight (kg)	379	68.1	10.4	67.5	42.6	104.3	390	57.7	8.8	57.6	35.9	82.6
	Height (cm)	379	168.0	6.0	168.0	150.8	188.0	390	155.5	5.7	155.2	137.8	171.9
	WC (cm)	379	87.9	9.1	87.7	58.6	112.7	390	86.3	10.0	85.4	61.0	120.5
	Hip (cm)	379	94.6	5.8	94.7	77.1	113.5	390	95.0	6.8	94.7	77.0	119.0
	WHR (cm/cm)	379	0.9	0.1	0.9	0.7	1.1	390	0.9	0.1	0.9	0.7	1.1
MESA (HA)	Age (yrs)	697	61.2	10.3	61.0	44.0	84.0	738	61.7	10.3	61.0	44.0	84.0
	BMI (kg/m²)	697	28.8	4.3	28.5	17.6	46.3	738	30.0	5.5	29.2	18.3	49.8
	Weight (kg)	697	82.1	14.1	80.8	45.7	146.0	738	72.3	14.3	70.2	32.5	127.0
	Height (cm)	697	168.9	6.6	169.0	148.9	188.7	738	155.2	6.2	155.3	123.8	178.8
	WC (cm)	697	100.8	11.4	99.5	68.2	147.4	738	100.3	14.2	99.2	61.8	159.9
	Hip (cm)	697	102.6	8.8	101.4	83.8	151.9	738	107.6	11.3	106.1	76.9	160.6
	WHR (cm/cm)	697	1.0	0.1	1.0	0.8	1.1	738	0.9	0.1	0.9	0.7	1.2
METSIM	Age (yrs)	8390	57.7	7.2	57.0	45.0	74.0	NA	NA	NA	NA	NA	NA
	BMI (kg/m²)	8390	27.3	4.2	26.7	16.9	52.1	NA	NA	NA	NA	NA	NA
	Weight (kg)	8390	84.6	14.2	83.0	45.0	165.5	NA	NA	NA	NA	NA	NA
	Height (cm)	8390	175.9	6.3	176.0	147.0	203.0	NA	NA	NA	NA	NA	NA
	WC (cm)	8390	98.9	11.6	97.5	68.5	157.5	NA	NA	NA	NA	NA	NA
	Hip (cm)	8390	101.3	7.1	100.0	72.0	160.0	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	8390	1.0	0.1	1.0	0.8	1.4	NA	NA	NA	NA	NA	NA
MGH-CAMP	Age (yrs)	1958	62.6	10.9	65.0	31.0	81.0	1284	61.2	11.8	64.0	32.0	80.0
	BMI (kg/m²)	1958	29.4	5.2	28.5	15.8	59.7	1284	28.1	6.7	26.8	15.5	58.5
	Weight (kg)	1958	92.7	17.2	90.4	49.9	210.9	1284	74.7	18.4	70.9	36.8	161.9
	Height (cm)	1958	177.5	7.4	177.8	121.9	210.8	1284	163.0	6.9	162.6	127.0	190.5
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MHIBB	Age (yrs)	5626	64.37	10.50	66.00	18.00	90.00	3957	62.82	11.41	64.00	19.00	92.00
	BMI (kg/m²)	5625	28.92	4.75	28.40	15.90	71.00	3955	27.99	5.90	27.10	14.50	60.70
	Weight (kg)	5625	86.03	15.46	84.00	47.00	217.50	3955	70.93	15.20	68.00	37.00	146.06
	Height (cm)	5626	172.0	7.0	172.0	145.0	198.0	3957	159.0	7.0	159.0	125.0	187.0
	WC (cm)	5585	102.87	12.34	102.00	64.00	184.00	3912	90.90	14.17	90.00	51.00	160.00
	Hip (cm)	5579	104.94	8.99	104.00	38.00	210.00	3914	104.86	12.06	103.00	68.00	170.00
	WHR (cm/cm)	5579	0.98	0.07	0.98	0.50	2.39	3911	0.87	0.08	0.86	0.62	1.21
MORGAM	Age (yrs)	5155	59.1	8.1	59.2	24.9	77.0	965	57.4	9.6	58.9	24.8	75.3
	BMI (kg/m²)	5154	27.1	4.0	26.7	15.8	51.9	965	27.8	5.3	27.0	16.3	52.2
	Weight (kg)	5154	80.8	13.2	80.0	43.6	154.0	965	70.5	14.0	68.7	37.1	137.0
	Height (cm)	5155	172.7	6.5	173.0	136.0	200.0	965	159.1	6.5	159.0	138.0	178.0
	WHR (cm/cm)	2880	1.0	0.1	1.0	0.7	1.2	845	0.8	0.1	0.8	0.6	1.2
NEO Study	Age (yrs)	2941	56.2	6.0	57.0	44.0	66.0	3186	55.8	5.9	56.0	44.0	66.0
	BMI (kg/m²)	2941	29.8	3.9	29.3	19.3	54.4	3186	30.3	5.5	29.8	17.2	61.2
	Weight (kg)	2941	97.6	14.4	96.0	58.2	198.6	3186	84.3	16.0	82.8	45.8	168.6
	Height (cm)	2941	181.0	6.8	181.0	158.0	208.0	3186	166.8	6.2	167.0	147.0	192.0
	WC (cm)	2938	106.4	11.1	106.0	74.0	165.0	3183	98.1	13.7	98.0	57.0	162.0
	Hip (cm)	2938	108.6	7.3	108.0	87.0	155.0	3183	111.9	11.7	111.0	74.0	177.0
	WHR (cm/cm)	2938	1.0	0.1	1.0	0.8	1.3	3183	0.9	0.1	0.9	0.6	1.2
NHAPC	Age (yrs)	1388	58.8	5.9	58.0	50.0	70.0	1750	58.5	6.1	58.0	50.0	70.0
	BMI (kg/m²)	1388	24.1	3.4	24.0	14.1	35.7	1750	24.7	3.8	24.5	15.0	40.9
	Weight (kg)	1388	66.9	11.0	66.2	39.6	109.0	1750	59.6	10.2	59.1	30.9	95.8
	Height (cm)	1388	166.3	6.1	166.4	139.7	184.1	1750	155.1	5.8	155.0	133.9	173.3
	WC (cm)	1388	85.6	10.5	85.6	55.2	119.0	1750	82.2	10.4	81.7	54.3	122.2
	Hip (cm)	1388	92.9	6.4	92.6	76.1	119.0	1750	94.1	7.2	93.6	62.1	130.0
	WHR (cm/cm)	1388	0.9	0.1	0.9	0.7	1.2	1750	0.9	0.1	0.9	0.6	1.2
Nijmegen	Age (yrs)	2262	67.0	19.4	68.0	29.0	87.0	1247	58.4	11.4	59.0	27.0	96.0
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Height (cm)	2262	177.3	7.8	177.0	126.0	203.0	1247	166.3	6.3	167.0	138.0	186.0
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NMCCS*	Age (yrs)	930	31.8	4.9	32.0	17.0	54.0	936	29.4	4.4	29.0	17.0	44.0
	BMI (kg/m²)	910	25.9	3.2	25.6	18.4	40.1	925	23.9	4.0	23.1	14.8	45.4
	Weight (kg)	910	85.6	11.9	85.0	59.0	130.0	925	67.6	11.7	66.0	37.0	122.0
	Height (cm)	930	181.6	6.4	181.0	160.0	203.0	936	168.2	5.9	168.0	150.0	183.0
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NWIGM	Age (yrs)	247	54.2	4.1	55.0	45.0	65.0	1067	43.2	5.0	43.2	27.0	64.0
	BMI (kg/m²)	247	28.0	5.1	26.8	19.9	53.3	1067	25.2	5.8	25.2	15.4	59.1
	Weight (kg)	247	90.4	16.7	87.1	60.1	178.6	1067	59.4	16.7	64.4	38.1	161.0
	Height (cm)	247	179.7	6.8	179.1	149.9	198.1	1067	165.8	6.4	165.1	147.3	195.6
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
OMICS-EPICNorfolk*	Age (yrs)	9793	59.6	9.2	59.6	39.5	79.1	11251	58.8	9.3	58.3	39.8	78.2
	BMI (kg/m²)	9781	26.5	3.2	26.2	16.1	49.1	11233	26.1	4.2	25.5	15.2	58.7
	Weight (kg)	9784	174.0	6.6	174.0	139.4	200.2	11239	161.1	6.2	161.0	125.4	185.3
	Height (cm)	9788	80.3	11.3	79.4	42.8	160.0	11241	67.8	11.6	66.2	36.0	139.2
	WC (cm)	9780	95.7	9.6	95.0	65.9	145.6	11248	81.9	10.7	80.3	56.0	141.3
	Hip (cm)	9776	102.7	6.3	102.2	80.0	165.0	11236	103.3	9.0	102.0	72.5	164.2
	WHR (cm/cm)	9774	0.9	0.1	0.9	0.6	1.2	11236	0.8	0.1	0.8	0.6	1.2
	Age (yrs)	3685	48.9	7.4	49.1	30.9	63.7	4079	48.9	7.3	49.1	30.5	64.0
	BMI (kg/m²)	3685	27.4	4.2	26.9	15.3	50.6	4079	26.6	5.3	25.5	14.5	58.7

OMICS-Fenland*	Weight (kg)	3685	86.4	14.3	84.7	42.9	177.6	4079	71.5	14.7	68.7	38.2	152.5
	Height (cm)	3685	177.6	6.8	177.6	129.5	199.8	4079	164.1	6.4	164.0	140.4	188.6
	WC (cm)	3681	97.1	11.6	96.1	65.6	149.0	4067	85.4	12.6	83.4	59.0	154.2
	Hip (cm)	3681	103.1	7.1	102.4	76.2	156.4	4067	103.6	10.4	102.1	78.5	168.0
	WHR (cm/cm)	3681	0.9	0.1	0.9	0.7	1.2	4067	0.8	0.1	0.8	0.6	1.2
OWAB	Age (yrs)	290	77.7	7.7	78.4	54.2	95.5	388	79.1	7.7	79.9	54.0	98.4
	BMI (kg/m²)	281	26.6	3.7	25.2	16.3	40.8	367	26.0	4.8	25.2	16.7	47.6
	Weight (kg)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Height (cm)	290	175.3	7.7	175.0	140.0	198.0	388	161.5	7.4	162.0	130.0	187.0
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Oxford BioBank	Age (yrs)	2039	42.1	5.6	43.0	29.0	54.0	2476	41.6	6.0	42.0	29.0	53.0
	BMI (kg/m²)	2039	26.6	4.0	26.1	15.3	48.4	2476	25.4	4.8	24.4	16.5	53.0
	Weight (kg)	2039	85.1	14.1	83.5	44.7	172.1	2476	69.4	13.5	66.8	43.5	139.3
	Height (cm)	2039	178.7	6.7	179.0	157.0	205.0	2476	165.3	6.1	165.0	144.0	190.0
	WC (cm)	2031	93.1	11.0	92.0	61.0	157.0	2476	82.1	11.9	80.0	59.0	150.0
	Hip (cm)	2031	101.5	7.5	101.0	69.0	142.0	2476	101.1	10.0	100.0	64.0	177.0
	WHR (cm/cm)	2031	0.9	0.1	0.9	0.7	1.2	2476	0.8	0.1	0.8	0.6	1.3
PCOS	Age (yrs)	NA	NA	NA	NA	NA	NA	582	32.1	6.8	31.9	18.4	61.4
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	582	28.0	7.9	25.1	18.4	61.4
	Weight (kg)	NA	NA	NA	NA	NA	NA	582	76.1	21.6	68.2	18.4	61.4
	Height (cm)	NA	NA	NA	NA	NA	NA	582	165.0	6.8	165.0	18.4	61.4
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	582	0.8	0.1	0.8	18.4	61.4
PIVUS	Age (yrs)	487	70.1	0.2	70.1	69.8	72.3	474	70.3	0.1	70.3	69.9	70.8
	BMI (kg/m²)	487	27.0	3.7	26.8	17.7	43.4	474	27.1	4.9	26.5	16.6	49.8
	Weight (kg)	487	83.6	13.0	82.0	53.0	138.0	474	71.4	13.2	71.0	42.0	126.0
	Height (cm)	487	175.9	6.5	175.0	155.0	198.0	474	162.3	5.6	162.0	148.0	184.0
	WC (cm)	482	94.8	10.4	94.0	64.0	134.0	468	87.7	11.7	87.5	60.0	134.0
	Hip (cm)	482	100.2	6.7	100.0	86.0	130.0	468	101.4	9.2	101.0	71.0	143.0
	WHR (cm/cm)	482	0.9	0.1	0.9	0.7	1.2	468	0.9	0.1	0.9	0.6	1.1
PROMIS (CAD cases)	Age (yrs)	7851	53.0	10.2	52.0	1.0	88.0	1482	56.5	9.9	55.0	30.0	82.0
	BMI (kg/m²)	7739	25.8	3.9	25.4	13.8	64.7	1463	26.4	4.5	25.9	15.6	54.0
	Weight (kg)	7739	72.7	10.7	72.0	38.0	189.0	1463	67.2	11.2	66.0	36.0	120.0
	Height (cm)	7851	167.9	6.6	168.0	101.0	208.0	1482	159.7	8.6	160.0	128.0	183.0
	WHR (cm/cm)	7835	1.0	0.1	1.0	0.5	2.0	1478	1.0	0.1	1.0	0.6	1.3
PROMIS (controls)	Age (yrs)	8994	55.6	8.9	55.0	27.0	93.0	2861	58.2	9.5	58.0	28.0	100.0
	BMI (kg/m²)	8946	25.8	4.5	25.4	11.9	98.0	2848	27.1	5.4	26.4	13.3	84.6
	Weight (kg)	8946	73.4	13.3	72.0	35.0	174.0	2848	67.0	12.5	66.5	30.0	170.0
	Height (cm)	8994	168.9	7.4	169.0	101.0	198.0	2861	157.6	8.8	158.0	104.0	187.0
	WHR (cm/cm)	8961	1.0	0.1	1.0	0.5	1.8	2834	0.9	0.1	0.9	0.7	1.5
PROSPER	Age (yrs)	708	75.6	3.5	75.3	70.2	83.3	571	76.5	3.6	76.5	70.3	83.3
	BMI (kg/m²)	708	26.5	3.5	26.3	15.2	40.2	571	27.1	4.7	26.7	16.2	43.5
	Weight (kg)	708	78.4	11.4	78.0	40.0	124.0	571	68.7	13.0	67.0	39.0	115.0
	Height (cm)	708	171.9	6.5	172.0	152.0	192.0	571	159.0	6.7	159.0	138.0	176.0
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
QIMR*	Age (yrs)	2028	47.3	16.2	48.6	16.0	87.5	3693	46.7	14.8	46.3	16.0	87.0
	BMI (kg/m²)	2013	26.4	4.6	25.9	14.8	67.6	3672	25.7	5.5	24.6	14.2	72.6
	Weight (kg)	2013	83.2	15.4	82.0	39.8	190.0	3672	69.2	15.1	66.2	37.0	180.0
	Height (cm)	2028	177.5	7.3	177.8	147.3	203.2	3693	164.1	6.9	164.0	134.6	200.0
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
RAINE*	Age (yrs)	561	20.0	0.4	19.9	19.3	22.1	517	20.0	0.4	19.9	19.2	21.8
	BMI (kg/m²)	561	24.7	4.7	23.8	16.7	48.9	517	24.6	5.5	23.2	15.4	51.7
	Weight (kg)	561	79.9	16.5	77.2	51.7	176.5	517	67.9	15.3	65.1	41.9	144.0
	Height (cm)	561	179.8	7.1	180.0	158.1	199.0	517	166.3	6.3	166.4	150.0	190.0
	WC (cm)	554	83.5	12.2	81.2	43.8	145.5	514	77.7	12.9	74.7	44.9	136.2
	Hip (cm)	554	99.5	9.1	98.6	78.8	144.5	514	98.9	11.7	98.0	40.3	153.8
	WHR (cm/cm)	553	0.84	0.06	0.83	0.55	1.08	514	0.79	0.09	0.78	0.46	1.74
RISC	Age (yrs)	156	44.7	8.3	45.0	30.0	60.0	157	45.8	7.9	46.0	30.0	60.0
	BMI (kg/m²)	156	26.0	3.5	26.0	17.9	39.3	157	25.2	4.5	24.3	16.9	42.9
	Height (cm)	156	178.6	7.3	178.0	164.0	203.0	157	164.9	6.7	166.0	148.0	187.0
	WHR (cm/cm)	155	0.9	0.1	0.9	0.8	1.2	156	0.8	0.1	0.8	0.6	1.7
RSI	Age (yrs)	1425	68.1	7.8	67.3	55.1	97.8	1610	70.9	9.0	70.8	55.0	99.1
	BMI (kg/m²)	1425	25.7	3.0	25.6	14.2	38.2	1609	26.7	4.1	26.3	15.4	59.5
	Weight (kg)	1425	78.6	10.8	77.8	41.0	122.3	1609	69.4	11.2	68.5	40.1	130.8
	Height (cm)	1425	174.8	6.7	174.5	151.0	198.0	1610	161.1	6.6	161.0	101.0	180.0
	WC (cm)	1343	94.2	9.7	94.0	58.0	150.0	1472	88.0	11.4	87.0	59.0	138.0
	Hip (cm)	1343	98.5	6.4	98.0	70.0	150.0	1470	101.0	8.6	100.0	72.0	160.0
	WHR (cm/cm)	1343	1.0	0.1	1.0	0.7	1.3	1470	0.9	0.1	0.9	0.7	1.3
SDC	Age (yrs)	807	62.6	10.3	62.9	32.7	91.7	484	65.8	11.0	66.7	28.5	90.9
	BMI (kg/m²)	807	30.1	5.1	29.3	20.1	54.8	484	30.9	6.1	29.9	20.1	59.3
	Weight (kg)	807	94.9	17.5	92.3	54.8	174.0	484	81.2	16.5	79.0	49.5	159.5
	Height (cm)	807	177.5	7.0	177.0	157.0	206.0	484	162.2	6.2	162.0	144.0	183.0
	WC (cm)	807	107.9	13.7	106.0	67.0	162.0	484	100.2	15.0	100.0	62.0	180.0
	Hip (cm)	807	106.7	9.9	106.0	80.0	158.0	484	109.4	13.0	108.0	83.0	180.0
	WHR (cm/cm)	807	1.0	0.1	1.0	0.7	1.3	484	0.9	0.1	0.9	0.7	1.3
SHIP	Age (yrs)	1961	50.7	16.4	51.0	20.0	80.0	1917	47.7	15.4	47.0	20.0	81.0
	BMI (kg/m²)	1961	27.7	4.0	27.4	18.1	48.1	1917	26.9	5.3	26.1	16.1	52.4
	Weight (kg)	1961	85.1	13.5	83.8	49.9	156.4	1917	71.3	13.9	69.1	41.3	133.3
	Height (cm)	1961	175.3	7.1	175.0	148.0	198.0	1917	163.0	6.9	163.0	142.0	186.0
	WC (cm)	1961	95.8	11.7	95.3	67.9	143.5	1917	82.9	12.9	81.2	50.5	129.3
	Hip (cm)	1961	102.8	7.9	102.0	76.8	146.5	1917	103.0	11.4	101.7	57.4	148.0
	WHR (cm/cm)	1961	0.9	0.1	0.9	0.7	1.2	1917	0.8	0.1	0.8	0.6	1.4
SHIP-TREND	Age (yrs)	2064	52.7	15.6	53.0	21.0	83.0	2187	51.4	15.2	52.0	20.0	83.0
	BMI (kg/m²)	2064	28.7	4.6	28.2	17.7	52.8	2187	27.6	5.7	26.7	15.6	54.4
	Weight (kg)	2064	89.1	15.2	87.3	48.7	169.2	2187	74.0	15.1	71.7	43.6	153.6
	Height (cm)	2064	176.3	7.1	176.0	154.0	203.0	2187	163.8	6.8	164.0	137.0	189.0
	WC (cm)	2064	97.6	12.8	96.9	66.4	159.0	2187	85.4	13.6	83.5	48.0	145.6
	Hip (cm)	2064	102.3	9.1	101.3	78.2	159.0	2187	103.0	12.1	101.4	70.0	165.0
	WHR (cm/cm)	2064	1.0	0.1	1.0	0.7	1.2	2187	0.8	0.1	0.8	0.5	1.3
SOLID-TIMI 52 (AA)	Age (yrs)	133	59.4	9.9	60.0	35.0	82.0	69	62.5	10.3	62.0	36.0	83.0
	BMI (kg/m²)	133	29.9	6.8	29.0	14.0	51.4	69	32.0	7.2	31.6	17.9	49.4
	Weight (kg)	133	92.1	24.8	88.0	48.9	168.1	69	82.8	20.2	80.7	47.5	137.0
	Height (cm)	133	174.9	8.9	175.0	147.0	198.0	69	160.6	6.4	162.0	144.0	172.0
	WC (cm)	131	103.6	17.7	102.0	58.0	165.0	67	103.3	17.4	104.0	69.0	146.0
	Hip (cm)	131	106.2	15.0	105.0	70.0	152.0	67	112.0	16.2	112.0	80.0	150.0
	WHR (cm/cm)	131	1.0	0.1	1.0	0.6	1.4	67	0.9	0.1	0.9	0.8	1.2
SOLID-TIMI 52 (EA)	Age (yrs)	6018	63.8	9.0	64.0	30.0	94.0	2089	66.8	9.5	66.0	29.0	93.0
	BMI (kg/m²)	5997	28.8	4.7	28.1	16.5	67.4	2084	29.0	5.7	28.2	15.6	65.5
	Weight (kg)	6013	87.9	15.9	85.2	43.9	183.6	2087	75.2	15.4	73.4	39.0	187.0
	Height (cm)	6000	174.7	7.0	175.0	132.0	213.0	2085	161.1	6.7	161.0	125.0	186.0
	WC (cm)	5948	103.5	12.2	102.0	55.0	168.0	2062	97.8	13.8	97.0	56.0	159.0
	Hip (cm)	5931	104.1	10.1	103.0	66.0	162.0	2059	106.3	13.8	105.0	60.0	210.0
	WHR (cm/cm)	5930	1.0	0.1	1.0	0.6	1.8	2059	0.9	0.1	0.9	0.6	1.8
SOLID-TIMI 52 (EAS)	Age (yrs)	205	62.1	10.0	63.0	34.0	90.0	51	69.6	9.6	70.0	43.0	86.0
	BMI (kg/m²)	205	24.6	4.3	24.0	14.2	55.6	51	22.8	5.5	22.2	14.4	43.5
	Weight (kg)	205	67.7	12.6	66.5	40.0	117.0	51	51.9	13.4	51.6	29.0	104.5
	Height (cm)	205	165.9	6.8	166.0	120.0	181.0	51	150.8	7.0	150.0	135.0	164.0
	WC (cm)	205	90.3	9.6	90.0	66.0	119.0	51	83.5	15.0	82.0	55.0	123.0
	Hip (cm)	205	95.1	9.5	95.0	61.0	119.0	51	92.4	12.8	94.0	58.0	134.0
	WHR (cm/cm)	205	1.0	0.1	0.9	0.8	1.3	51	0.9	0.1	0.9	0.7	1.4
SOLID-TIMI 52 (HA)	Age (yrs)	641	62.4	9.1	63.0	33.0	92.0	253	65.6	10.9	67.0	33.0	89.0
	BMI (kg/m²)	639	28.0	4.9	27.4	13.1	69.0	252	28.7	6.1	27.4	18.7	51.0
	Weight (kg)	639	79.9	16.0	78.0	37.1	206.4	253	68.7	15.8	65.5	40.1	126.0
	Height (cm)	640	168.9	7.2	169.0	146.0	189.0	252	154.5	7.6	154.0	122.0	173.0
	WC (cm)	638	99.9	11.1	99.0	61.0	160.0	251	97.0	13.8	96.0	63.0	145.0
	Hip (cm)	633	100.8	9.3	100.0	63.0	165.0	250	103.3	12.5	102.0	79.0	148.0
	WHR (cm/cm)	633	1.0	0.1	1.0	0.7	1.2	250	0.9	0.1	0.9	0.7	1.4

SOLID-TIMI 52 (SA)	Age (yrs)	100	57.4	9.5	58.5	32.0	75.0	18	62.4	10.0	62.5	31.0	75.0
	BMI (kg/m²)	99	25.4	4.9	25.4	15.1	38.6	18	26.6	3.7	26.7	17.7	32.9
	Weight (kg)	99	70.5	14.9	71.0	40.0	111.8	18	63.4	9.6	63.0	41.0	82.0
	Height (cm)	100	166.5	7.6	166.0	140.0	200.0	18	154.3	6.8	152.0	144.0	168.0
	WC (cm)	100	95.2	11.6	94.0	66.0	129.0	18	97.6	8.9	98.5	84.0	115.0
	Hip (cm)	100	97.5	10.7	98.0	75.0	129.0	18	103.8	6.6	105.5	92.0	114.0
	WHR (cm/cm)	100	1.0	0.1	1.0	0.7	1.2	18	0.9	0.1	0.9	0.8	1.1
Sorbs	Age (yrs)	386	48.2	16.8	48.5	18.1	82.3	556	48.2	16.0	48.6	18.0	88.4
	BMI (kg/m²)	384	27.1	4.0	26.7	17.2	43.9	555	26.9	5.6	26.0	15.4	50.3
	Weight (kg)	384	85.0	12.7	84.0	55.0	139.0	555	72.1	14.1	70.0	43.0	126.0
	Height (cm)	384	177.2	7.0	177.5	158.0	195.0	555	163.9	6.8	164.0	144.0	182.0
	WC (cm)	385	96.5	12.1	97.0	72.0	137.0	555	87.2	14.2	86.0	59.0	139.0
	Hip (cm)	385	102.1	6.8	101.0	70.0	139.0	555	105.2	10.4	103.0	85.0	146.0
	WHR (cm/cm)	385	0.9	0.1	1.0	0.7	1.3	555	0.8	0.1	0.8	0.6	1.1
SR	Age (yrs)	247	40.2	16.6	41.0	18.0	86.0	382	38.9	14.7	39.0	18.0	80.0
	BMI (kg/m²)	246	24.9	3.9	24.3	17.6	37.0	382	24.3	4.9	23.5	14.7	41.0
	Weight (kg)	246	75.3	12.7	73.0	50.0	120.0	382	64.3	13.7	61.0	38.0	105.0
	Height (cm)	247	173.8	7.1	174.0	150.0	198.0	382	162.6	6.7	163.0	140.0	181.0
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
STABILITY (AA)	Age (yrs)	91	62.1	10.6	62.0	36.0	87.0	32	65.1	8.9	65.0	47.0	82.0
	BMI (kg/m²)	90	30.8	7.1	29.4	20.0	61.5	32	30.8	5.5	31.6	20.4	40.2
	Weight (kg)	90	95.1	20.9	91.5	59.0	159.4	32	78.9	15.2	82.1	50.9	106.8
	Height (cm)	91	176.0	8.4	175.0	152.0	198.0	32	160.1	6.3	162.0	141.0	170.0
	WC (cm)	89	105.0	14.6	101.6	77.0	162.0	31	99.9	13.4	101.6	71.1	128.0
	Hip (cm)	89	107.4	13.0	105.0	83.8	165.0	31	105.7	14.9	108.5	72.0	132.5
	WHR (cm/cm)	89	1.0	0.1	1.0	0.8	1.2	31	1.0	0.1	1.0	0.8	1.3
STABILITY (EA)	Age (yrs)	7221	64.5	9.1	65.0	29.0	92.0	1568	66.1	8.6	67.0	31.0	87.0
	BMI (kg/m²)	7211	29.8	4.8	29.1	16.5	57.8	1565	30.3	5.7	29.8	17.6	60.4
	Weight (kg)	7214	90.4	16.2	88.6	46.0	180.9	1565	77.9	15.6	76.3	39.6	149.0
	Height (cm)	7216	174.0	7.0	174.0	142.0	203.0	1565	160.4	6.3	160.0	135.0	185.0
	WC (cm)	7145	105.0	12.4	104.0	51.0	186.5	1556	99.0	14.3	99.0	63.0	147.0
	Hip (cm)	7125	106.1	10.4	105.0	61.0	190.5	1553	108.7	13.3	108.0	70.0	160.0
	WHR (cm/cm)	7123	1.0	0.1	1.0	0.6	1.4	1553	0.9	0.1	0.9	0.7	1.3
STABILITY (EAS)	Age (yrs)	562	62.4	9.7	63.0	36.0	86.0	162	66.8	7.7	67.0	48.0	88.0
	BMI (kg/m²)	562	25.4	3.1	25.2	12.9	36.2	162	25.3	3.7	25.3	16.6	39.6
	Weight (kg)	562	70.7	10.7	70.0	35.0	113.0	162	59.0	9.0	58.5	35.0	87.9
	Height (cm)	562	166.6	6.1	167.0	148.0	190.0	162	152.6	5.4	152.0	136.0	169.0
	WC (cm)	562	92.3	8.3	92.0	61.0	126.0	162	87.8	9.3	87.0	62.2	120.0
	Hip (cm)	562	99.1	7.3	99.0	73.0	127.0	162	97.4	8.1	97.8	78.0	135.0
	WHR (cm/cm)	562	0.9	0.1	0.9	0.8	1.3	162	0.9	0.1	0.9	0.7	1.3
STABILITY (HA)	Age (yrs)	427	64.6	9.1	65.0	36.0	84.0	91	66.2	8.8	67.0	40.0	86.0
	BMI (kg/m²)	426	28.8	4.0	28.4	18.2	42.7	90	29.7	5.3	29.5	20.0	50.1
	Weight (kg)	427	81.3	14.1	79.4	45.5	143.0	90	71.8	14.7	70.9	42.3	123.6
	Height (cm)	426	167.7	7.4	167.0	149.0	198.0	90	155.3	7.0	156.0	138.0	178.0
	WC (cm)	422	101.3	10.9	100.8	69.0	152.0	89	98.6	14.1	100.0	69.0	142.2
	Hip (cm)	422	103.1	9.4	102.0	80.0	150.0	89	105.3	12.4	104.0	70.0	144.0
	WHR (cm/cm)	422	1.0	0.1	1.0	0.7	1.2	89	0.9	0.1	0.9	0.8	1.4
STABILITY (SA)	Age (yrs)	331	56.9	10.3	57.0	26.0	81.0	49	59.1	10.1	60.0	36.0	78.0
	BMI (kg/m²)	331	25.1	3.8	25.0	15.9	40.1	49	28.0	4.9	27.4	17.6	38.8
	Weight (kg)	331	70.8	12.3	70.0	44.0	130.0	49	64.1	10.4	63.5	40.0	85.0
	Height (cm)	331	167.7	7.3	167.0	147.0	200.0	49	151.8	7.3	152.0	129.0	170.0
	WC (cm)	331	95.4	10.4	94.1	69.0	132.0	49	97.8	10.9	98.0	78.0	125.0
	Hip (cm)	331	99.8	9.7	99.0	63.0	150.0	49	105.3	10.3	105.0	80.0	130.0
	WHR (cm/cm)	331	1.0	0.1	1.0	0.7	1.2	49	0.9	0.1	0.9	0.8	1.2
TUDR	Age (yrs)	259	64.9	11.1	65.0	35.0	88.0	289	63.2	10.7	63.0	35.6	86.0
	BMI (kg/m²)	257	24.2	3.3	24.0	15.6	36.2	287	25.2	4.3	25.0	15.6	37.2
	Weight (kg)	259	66.6	10.6	67.0	40.5	105.0	289	60.7	11.3	61.0	36.0	95.0
	Height (cm)	215	165.6	6.2	165.0	146.5	181.0	247	154.7	5.9	155.0	139.5	170.0
	WC (cm)	111	90.7	8.2	90.0	74.0	130.0	139	89.5	10.7	89.0	68.0	130.0
	Hip (cm)	58	97.7	6.9	97.0	85.0	121.0	86	98.2	9.8	98.0	76.0	121.5
	WHR (cm/cm)	58	0.9	0.0	0.9	0.9	1.1	86	0.9	0.1	0.9	0.8	1.1
TwinsUK	Age (yrs)	173	49.9	12.9	50.1	19.6	79.7	826	48.2	13.1	49.2	18.0	80.7
	BMI (kg/m²)	173	26.2	3.7	26.0	17.4	41.2	826	26.1	5.2	25.0	16.2	52.7
	Weight (kg)	173	80.6	11.5	80.5	52.7	118.8	826	69.1	13.9	66.9	41.0	126.6
	Height (cm)	173	175.5	6.9	174.0	162.0	206.0	826	162.8	6.3	163.0	144.0	180.5
	WC (cm)	79	93.0	9.6	93.0	71.0	118.0	600	81.3	11.5	79.0	58.0	122.0
	Hip (cm)	79	101.0	7.0	100.0	81.0	120.0	600	103.2	10.7	102.0	70.0	146.0
	WHR (cm/cm)	79	0.9	0.1	0.9	0.8	1.1	600	0.8	0.1	0.8	0.6	1.4
UCLA-NL	Age (yrs)	760	40.0	13.4	39.0	18.4	80.0	496	45.2	12.5	47.0	18.0	79.0
	BMI (kg/m²)	760	26.1	3.9	25.6	17.1	47.5	495	26.1	4.9	25.1	14.8	53.1
	Weight (kg)	760	87.2	14.0	85.0	57.0	160.0	495	74.8	14.3	72.0	47.0	150.0
	Height (cm)	760	182.1	6.9	183.0	162.0	204.0	495	169.4	169.0	6.5	147.0	188.0
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UHP	Age (yrs)	974	41.1	13.7	36.0	18.0	83.0	1121	39.9	14.2	35.0	18.0	91.0
	BMI (kg/m²)	974	25.5	3.6	25.2	16.5	46.7	1121	24.6	4.1	23.8	16.4	44.1
	Weight (kg)	974	84.7	12.4	84.0	47.0	133.0	1121	69.9	12.2	68.0	43.0	130.0
	Height (cm)	974	182.1	7.6	182.0	123.3	202.4	1121	168.5	6.5	168.6	144.5	192.5
	WC (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Hip (cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ULSAM	Age (yrs)	1102	71.0	0.6	71.0	69.4	74.1	NA	NA	NA	NA	NA	NA
	BMI (kg/m²)	1098	26.2	3.4	25.9	16.7	46.3	NA	NA	NA	NA	NA	NA
	Weight (kg)	1102	80.3	11.4	79.5	46.0	138.7	NA	NA	NA	NA	NA	NA
	Height (cm)	1098	174.9	6.0	175.0	156.0	200.0	NA	NA	NA	NA	NA	NA
	WC (cm)	1081	94.6	9.6	94.0	51.0	137.0	NA	NA	NA	NA	NA	NA
	Hip (cm)	1081	100.1	7.1	100.0	51.0	141.0	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	1081	0.9	0.1	0.9	0.8	1.1	NA	NA	NA	NA	NA	NA
UK Biobank	Age (yrs)	56936	57.3	8.0	59.0	40.0	73.0	63350	56.6	7.9	58.0	40.0	70.0
	BMI (kg/m²)	56668	28.0	4.3	27.4	15.3	63.4	62945	27.2	5.2	26.2	15.0	74.7
	Height (cm)	56832	175.7	6.7	176.0	133.0	205.0	63252	162.6	6.2	162.3	126.0	190.0
	WHR (cm/cm)	56849	0.9	0.1	0.9	0.6	1.3	63175	0.8	0.1	0.8	0.5	1.3
Vejle (cases)	Age (yrs)	1253	63.6	8.5	64.5	33.6	83.5	773	62.8	9.1	63.8	31.8	81.5
	BMI (kg/m²)	1253	30.2	4.9	29.7	17.6	52.6	773	31.0	6.3	30.3	17.8	65.4
	Weight (kg)	1253	92.4	16.9	90.1	55.3	168.2	773	81.9	17.7	80.0	42.1	186.8
	Height (cm)	1253	174.8	6.3	175.0	148.0	203.0	773	162.3	6.4	162.0	140.0	182.0
	WC (cm)	1253	106.3	12.5	105.0	73.0	159.0	773	101.4	14.3	101.0	65.0	160.0
	Hip (cm)	1253	106.8	9.2	105.0	85.0	155.0	773	110.6	13.2	109.0	65.0	189.0
	WHR (cm/cm)	1253	1.0	0.1	1.0	0.8	1.3	773	0.9	0.1	0.9	0.7	1.2
Vejle (controls)	Age (yrs)	147	62.4	10.2	64.2	31.0	77.9	288	55.1	12.5	55.6	26.9	77.8
	BMI (kg/m²)	147	23.1	1.5	23.3	16.5	25.0	288	21.8	1.9	21.8	15.7	25.0
	Weight (kg)	147	72.0	7.5	72.1	47.2	90.6	288	59.5	6.2	59.4	42.4	74.1
	Height (cm)	147	176.6	6.6	177.0	160.0	191.0	288	165.3	5.7	165.0	148.0	180.0
	WC (cm)	147	87.3	6.3	87.0	64.0	103.0	288	77.1	6.6	77.0	59.0	99.0
	Hip (cm)	147	95.1	5.3	95.8	80.0	108.0	288	91.9	6.3	92.0	71.0	113.0
	WHR (cm/cm)	147	0.9	0.1	0.9	0.7	1.0	288	0.8	0.1	0.8	0.6	1.0
WGHS	Age (yrs)	NA	NA	NA	NA	NA	NA	22426	54.7	7.1	52.9	38.7	89.9
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	22223	25.9	5.0	24.9	14.2	59.6
	Weight (kg)	NA	NA	NA	NA	NA	NA	22223	70.0	14.1	68.0	38.6	175.1
	Height (cm)	NA	NA	NA	NA	NA	NA	22426	164.4	6.3	165.1	129.5	200.7
	WC (cm)	NA	NA	NA	NA	NA	NA	19800	88.9	14.3	86.4	38.1	167.6
	Hip (cm)	NA	NA	NA	NA	NA	NA	19775	106.3	12.1	104.1	50.8	193.0
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	19766	0.8	0.1	0.8	0.3	1.9
WHI (AA)	Age (yrs)	NA	NA	NA	NA	NA	NA	3519	64.9	6.6	65.0	50.0	79.0
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	3519	30.6	6.2	29.8	15.8	141.0
	Weight (kg)	NA	NA	NA	NA	NA	NA	3515	80.6	17.1	78.2	42.6	171.5
	Height (cm)	NA	NA	NA	NA	NA	NA	3502	162.0	6.6	162.0	101.2	194.1
	WC (cm)	NA	NA	NA	NA	NA	NA	3513	90.9	13.0	90.0	35.5	161.7
	Hip (cm)	NA	NA	NA	NA	NA	NA	3512	110.2	12.5	109.0	43.5	170.5

	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	3510	0.8	0.1	0.8	0.3	1.4
WHI (EA)	Age (yrs)	NA	NA	NA	NA	NA	NA	21858	66.2	6.7	67.0	50.0	81.0
	BMI (kg/m²)	NA	NA	NA	NA	NA	NA	21857	28.2	5.9	27.3	13.8	159.7
	Weight (kg)	NA	NA	NA	NA	NA	NA	21820	73.9	16.2	71.2	32.0	197.5
	Height (cm)	NA	NA	NA	NA	NA	NA	21777	161.5	6.4	161.5	96.0	193.7
	WC (cm)	NA	NA	NA	NA	NA	NA	21791	87.9	13.9	86.0	35.5	191.8
	Hip (cm)	NA	NA	NA	NA	NA	NA	21780	107.0	12.2	105.0	42.0	196.5
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	21773	0.8	0.1	0.8	0.3	2.5
WOSCOPS	Age (yrs)	1337	55.6	5.6	55.8	45.2	65.7	NA	NA	NA	NA	NA	NA
	BMI (kg/m²)	1337	25.9	3.2	25.6	17.5	41.2	NA	NA	NA	NA	NA	NA
	Weight (kg)	1337	76.6	10.9	75.5	50.0	135.0	NA	NA	NA	NA	NA	NA
	Height (cm)	1337	172.0	7.0	172.0	145.0	196.0	NA	NA	NA	NA	NA	NA
	WHR (cm/cm)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
WTCCC/UKT2D	Age (yrs)	1165	52.5	10.1	53.0	20.9	87.0	851	53.0	11.0	54.0	23.4	83.4
	BMI (kg/m²)	1165	30.5	5.6	29.7	16.8	60.3	850	32.9	7.2	32.0	17.9	65.2
	Weight (kg)	1165	94.2	18.7	92.1	47.6	190.5	850	85.8	20.5	82.6	43.0	171.0
	Height (cm)	1165	175.7	7.2	175.3	150.0	220.0	851	161.3	6.6	161.0	139.0	180.3
	WC (cm)	1144	106.8	14.1	105.0	71.1	200.7	835	102.5	15.7	101.0	66.0	172.0
	Hip (cm)	1144	109.2	11.5	108.0	78.7	215.9	835	115.2	15.3	114.0	71.0	177.0
	WHR (cm/cm)	1144	1.0	0.1	1.0	0.8	1.3	835	0.9	0.1	0.9	0.7	1.2
YFS	Age (yrs)	851	41.9	5.0	43.0	34.0	49.0	1042	42.1	4.9	43.0	34.0	49.0
	BMI (kg/m²)	851	27.0	4.3	26.3	16.2	51.0	1042	26.1	5.5	25.0	16.5	58.5
	Weight (kg)	851	87.3	15.8	85.0	54.0	186.0	1042	72.0	15.3	69.0	43.0	167.0
	Height (cm)	851	179.7	6.7	180.0	156.0	203.0	1042	166.1	6.0	166.0	148.0	191.0
	WC (cm)	851	96.8	12.5	95.3	69.0	160.4	1042	87.6	14.0	85.3	61.1	145.7
	Hip (cm)	851	101.1	7.5	100.5	85.0	149.7	1042	102.0	10.2	100.5	79.4	167.3
	WHR (cm/cm)	851	1.0	0.1	1.0	0.7	1.2	1042	0.86	0.07	0.85	0.66	1.11

†Studies that included more than one ancestry are indicated with abbreviations next to the study name including: EA-European Ancestry; AA-African Ancestry; HA-Hispanic Ancestry; EAS-East Asian Ancestry; SAS-South Asian Ancestry.

***Indicates that study was used for validation meta-anlayses**

Supplementary Table 4. Number of variants and genes from the ExomeChip that were tested in each ancestry. [1]Variants analyzed include all single nucleotide polymorphic sites with valid association results. [2] We created two lists (masks) of variant (minor allele frequency <5%) for gene-based analyses. The "broad" mask includes nonsense, stop-loss, splice site variants, and missense defined as damaging by at least one of prediction algorithms (PolyPhen2 HumDiv and HumVar, LRT, MutationTaster and SIFT). The "strict" mask included the same variants as the "broad" mask, except for missense variants. Only missense variants predicted to be damaging by all five algorithms were included in the "strict" list.

Ancestry	Variants, Additive model[1]	Variants, Recessive model[1]	Genes/variants strict definition[2]	Genes/variants broad definition[2]
All Ancestry	243511	139740	9268/23572	16222/135166
European Ancestry	241419	104623	9310/23812	16263/138902
African Ancestry	208257	72764	9299/23741	16261/137576
Hispanic Ancestry	195122	59049	9314/23840	16262/138774
East Asian Ancestry	97831	37322	9316/23837	16272/139137
South Asian Ancestry	158674	48362	9313/23820	16264/138856

Supplementary Table 5. ExomeChip variants with Pdiscovery <2e-07 in the All-ancestries meta-analysis (N=458,927). For the functional annotation, we provide the most severe consequence based on the ENSEMBL's Variant Effect Predictor (VEP) tool. The direction of the effect (Beta) and effect allele frequency (EAF) is given for the alternate (Alt) allele.

Chr	Pos (hg19)	rsID	Gene	VEP annotation	Ref	Alt	N	EAF	Beta	SE	P-value
1	2069172	rs425277	*PRKCZ*	intron_variant	C	T	458253	0.2697	0.018	0.002	3.26E-13
1	7877488	rs4908482	*RP3-467L1.4*	intron_variant	A	G	457404	0.6142	-0.012	0.002	1.33E-07
1	7897133	rs10462021	*PER3*	missense_variant	A	G	448549	0.1820	-0.016	0.003	6.49E-08
1	7913029	rs34305100	*UTS2*	missense_variant	A	G	458927	0.1694	0.020	0.003	2.47E-11
1	7913445	rs13306061	*UTS2*	missense_variant	C	T	458927	0.1697	0.020	0.003	5.33E-11
1	8046672	rs12727642	*PARK7*	upstream_gene_variant	C	A	457648	0.1618	0.018	0.003	6.96E-09
1	9304731	rs2239560	*H6PD*	intron_variant	G	A	452883	0.1655	0.018	0.003	7.92E-10
1	9305445	rs34603401	*H6PD*	missense_variant	A	C	458927	0.1378	-0.017	0.003	1.69E-07
1	10285709	rs6541085	*MIR1273D*	intron_variant	A	G	447196	0.4847	0.012	0.002	1.19E-07
1	17306675	rs2284746	*MFAP2*	intron_variant	C	G	450341	0.4855	0.039	0.002	2.94E-65
1	17312743	rs3170740	*ATP13A2*	missense_variant	C	T	321329	0.4711	0.039	0.003	3.21E-47
1	17331676	rs3738814	*ATP13A2*	intron_variant	A	G	455011	0.4679	-0.036	0.002	2.81E-57
1	17395480	rs2076599	*PADI2*	3_prime_UTR_variant	G	A	456974	0.5808	0.022	0.002	1.02E-23
1	19765518	rs12045440	*CAPZB*	intron_variant	T	G	437065	0.3315	-0.016	0.002	1.46E-11
1	21031983	rs6702859	*KIF17*	intron_variant	A	G	432300	0.5489	0.014	0.002	4.64E-09
1	21629447	rs213060	*RP5-1071N3.1*	intron_variant	A	C	447196	0.4349	0.012	0.002	1.07E-07
1	22368342	rs2501279	-	regulatory_region_variant	C	T	447196	0.5837	-0.014	0.002	6.84E-10
1	23536891	rs1738475	-	regulatory_region_variant	C	G	430838	0.4292	-0.016	0.002	5.12E-12
1	23537555	rs627304	-	intergenic_variant	T	C	422795	0.4304	-0.015	0.002	4.84E-11
1	25044111	rs4601530	-	intergenic_variant	C	T	457648	0.2859	-0.014	0.002	1.65E-08
1	26450009	rs17163588	*PDIK1L*	3_prime_UTR_variant	C	T	457648	0.1723	0.025	0.003	1.48E-16
1	26517267	rs41284333	*CNKSR1*	missense_variant	A	G	437739	0.1817	0.021	0.003	3.45E-11
1	26517794	rs11247866	*CNKSR1*	missense_variant	A	G	434240	0.1809	0.021	0.003	3.61E-11
1	26521140	rs11809207	*CNKSR1*	intron_variant	G	A	409854	0.1810	0.022	0.003	6.01E-12
1	26526439	rs17257155	*CATSPER4*	missense_variant	A	G	437739	0.1780	0.021	0.003	2.93E-11
1	26741544	rs7532866	*LIN28A*	intron_variant	A	G	457648	0.3429	-0.020	0.002	2.01E-17
1	26883511	rs2229712	*RPS6KA1*	missense_variant	A	C	348119	0.2123	-0.024	0.003	7.33E-15
1	27138393	rs12748152	*RN7SL165P*	upstream_gene_variant	C	T	458927	0.0732	0.022	0.004	1.92E-07
1	32092525	rs2271933	*PEF1*	missense_variant	A	G	458927	0.5870	0.013	0.002	2.09E-08
1	32673514	rs150341307	*RP4-622L5.7*	missense_variant	G	C	408014	0.0018	-0.140	0.026	5.17E-08
1	32842319	rs34885668	*BSDC1*	missense_variant	T	C	458927	0.0298	0.034	0.006	4.87E-08
1	38289383	rs12751325	*MTF1*	splice_region_variant	T	C	456554	0.2824	-0.017	0.002	1.84E-12
1	38338795	rs11488569	*INPP5B*	missense_variant	A	G	433069	0.6811	-0.017	0.002	5.34E-12
1	40773149	rs2228564	*COL9A2*	missense_variant	T	C	455446	0.2462	-0.021	0.003	5.22E-17
1	41485902	rs3738368	*SLFNL1*	missense_variant	C	G	213947	0.2856	0.030	0.004	1.02E-16
1	41486245	rs1138293	*SLFNL1*	missense_variant	C	T	458927	0.1762	0.027	0.003	5.26E-21
1	41530871	rs6686842	*SCMH1*	intron_variant	T	C	422450	0.5891	-0.025	0.002	1.87E-26
1	41540902	rs143365597	*SCMH1*	missense_variant	G	A	442153	0.0036	0.181	0.018	1.95E-24
1	41618297	rs114233776	*SCMH1*	missense_variant	G	A	415391	0.0055	-0.116	0.015	3.75E-15
1	41745770	rs2154319	*RP11-399E6.1*	intron_variant	T	C	422256	0.1926	0.038	0.003	1.49E-38
1	51873967	rs41292521	*EPS15*	missense_variant	G	A	455040	0.0170	0.046	0.008	1.81E-08
1	67390468	rs1886686	*MIER1*	missense_variant	C	G	434787	0.7500	0.015	0.003	2.69E-08
1	78623626	rs17391694	-	regulatory_region_variant	C	T	452406	0.1046	0.033	0.004	6.89E-20
1	89123443	rs6699417	*PKN2-AS1*	intron_variant	C	T	458927	0.6138	0.020	0.002	1.92E-18
1	89271574	rs786906	*PKN2*	splice_region_variant	T	C	458927	0.5535	0.020	0.002	1.74E-18
1	89388944	rs7532151	*RP11-82K18.2*	upstream_gene_variant	A	C	400168	0.4813	-0.016	0.002	1.12E-11
1	93009438	rs7515577	*EVI5*	intron_variant	C	A	446591	0.8139	0.017	0.003	5.98E-09
1	93160902	rs2391199	*EVI5*	missense_variant	T	C	458927	0.9052	0.022	0.004	2.16E-09
1	93323971	rs10874746	*FAM69A*	intron_variant	T	C	455040	0.6504	0.017	0.002	1.05E-12
1	93401837	rs12745968	*RP11-386I23.1*	intron_variant	A	G	458927	0.3537	-0.015	0.002	4.06E-10
1	103216881	rs713162	-	intergenic_variant	G	A	456730	0.3943	0.016	0.002	3.54E-13
1	103379918	rs3753841	*COL11A1*	missense_variant	G	A	432257	0.5866	-0.017	0.002	1.51E-12
1	103432657	rs12755987	*COL11A1*	intron_variant	A	G	433823	0.6786	-0.023	0.003	7.30E-20
1	103483514	rs945748	*COL11A1*	intron_variant	C	T	433823	0.6797	-0.022	0.003	9.51E-19
1	113098534	rs6658555	*ST7L*	missense_variant	C	T	437065	0.2368	0.015	0.003	8.27E-09
1	113190807	rs17030613	*CAPZA1*	intron_variant	A	C	458253	0.2137	-0.017	0.003	5.72E-10
1	118868405	rs17038182	-	regulatory_region_variant	G	C	452126	0.2517	-0.041	0.003	3.52E-58
1	118883973	rs12735613	-	intergenic_variant	G	A	458253	0.2360	-0.040	0.003	1.06E-54
1	119427467	rs61730011	*TBX15*	missense_variant	A	C	427531	0.0402	-0.057	0.006	1.98E-25
1	119503843	rs984222	*TBX15*	intron_variant	C	G	450033	0.5996	0.016	0.002	2.82E-13
1	149892872	rs11205277	*SF3B4*	upstream_gene_variant	A	G	437485	0.3985	0.040	0.002	9.32E-67
1	149906413	rs11205303	*MTMR11*	missense_variant	T	C	458253	0.3707	0.045	0.002	2.69E-85
1	149998494	rs12027024	-	intergenic_variant	T	C	454504	0.6421	0.013	0.002	5.22E-09
1	150551327	rs11580946	*MCL1*	missense_variant	G	A	432977	0.0117	0.057	0.010	9.89E-09
1	151259543	rs3748545	*PI4KB*	missense_variant	G	A	458253	0.1144	-0.021	0.003	9.08E-10
1	154987704	rs141845046	*ZBTB7B*	missense_variant	C	T	458253	0.0240	0.053	0.007	5.17E-15
1	171753039	rs2232816	*METTL13*	missense_variant	A	G	455880	0.2716	-0.017	0.002	1.41E-11
1	172053287	rs17346452	*DNM3*	intron_variant	T	C	427061	0.2512	0.033	0.003	4.72E-36
1	172189889	rs678962	*DNM3*	intron_variant	T	G	456974	0.2197	0.043	0.003	3.92E-60
1	172410967	rs1063412	*PIGC*	missense_variant	G	A	408083	0.5510	-0.016	0.002	1.41E-11
1	172434812	rs2901656	*C1orf105*	3_prime_UTR_variant	C	T	447196	0.4862	-0.012	0.002	9.30E-08
1	172437592	rs1129942	*C1orf105*	missense_variant	G	A	415622	0.7901	-0.024	0.003	7.15E-18
1	176219438	rs1553770	-	intergenic_variant	C	T	443697	0.5357	-0.014	0.002	5.71E-10
1	176792249	rs1325598	*PAPPA2*	intron_variant	A	G	453732	0.5725	0.028	0.002	6.80E-36
1	176863867	rs2228956	*ASTN1*	missense_variant	T	C	437065	0.8347	0.019	0.003	2.37E-10
1	182973491	rs10752881	-	intergenic_variant	A	G	447196	0.5324	-0.017	0.002	1.08E-13
1	183085755	rs20563	*LAMC1*	missense_variant	A	G	448719	0.5541	-0.018	0.002	2.85E-14
1	183094547	rs20558	*LAMC1*	missense_variant	T	C	458253	0.5541	-0.018	0.002	7.93E-15
1	183106739	rs10797854	*LAMC1*	intron_variant	G	A	398880	0.5469	-0.018	0.002	7.44E-14
1	183495812	rs144712473	*SMG7*	missense_variant	A	G	452987	0.0055	-0.097	0.014	4.09E-12
1	184020945	rs2274432	*TSEN15*	missense_variant	G	A	438119	0.3368	0.039	0.002	7.31E-61
1	184023529	rs1046934	*TSEN15*	missense_variant	A	C	457315	0.3393	0.039	0.002	1.81E-61
1	218950403	rs2889809	-	intergenic_variant	A	G	447196	0.4656	-0.019	0.002	3.23E-17
1	219009835	rs2647116	-	intergenic_variant	G	A	453488	0.3772	-0.019	0.002	5.32E-17
1	219743719	rs11118346	-	intergenic_variant	C	T	456974	0.4567	-0.015	0.002	9.11E-11
1	219750717	rs4846567	-	intergenic_variant	G	T	444831	0.2706	0.014	0.003	7.55E-08
1	223178026	rs144673025	*DISP1*	missense_variant	T	C	434709	0.0072	-0.077	0.013	9.42E-10
1	227935444	rs2236359	*SNAP47*	missense_variant	A	G	452399	0.4098	-0.016	0.002	4.90E-13
2	1756908	rs6726313	-	intergenic_variant	C	T	440437	0.3265	0.014	0.002	1.02E-08
2	9662210	rs10495563	*ADAM17*	3_prime_UTR_variant	G	A	457648	0.6399	0.021	0.002	2.14E-19
2	11323276	rs978906	*PQLC3*	3_prime_UTR_variant	T	C	454601	0.4632	-0.016	0.002	3.88E-13

2	11359120	rs2230774	*ROCK2*	missense_variant	G	T	456974	0.5171	-0.015	0.002	1.31E-11
2	11500314	rs6739310	*AC099344.2*	intron_variant	C	A	447196	0.5470	-0.014	0.002	2.42E-10
2	20205541	rs52826764	*AC079145.4*	missense_variant	C	T	458253	0.0253	-0.065	0.007	3.37E-23
2	20396122	rs6749689	*SDC1*	downstream_gene_variant	T	C	454357	0.5669	0.016	0.002	5.16E-13
2	23898317	rs4665630	*KLHL29*	intron_variant	C	T	422309	0.8759	0.021	0.004	6.12E-09
2	24244603	rs115334231	*MFSD2B*	missense_variant	G	A	437739	0.0556	-0.031	0.005	1.27E-10
2	24247514	rs7561273	*MFSD2B*	intron_variant	A	G	457648	0.5398	0.023	0.002	3.78E-26
2	24692639	rs2119997	-	intergenic_variant	G	A	442019	0.8146	0.016	0.003	6.18E-08
2	24692809	rs2165738	-	intergenic_variant	C	G	443182	0.7008	0.015	0.003	2.31E-09
2	25022598	rs1550116	*CENPO*	missense_variant	A	G	427180	0.1392	-0.019	0.003	3.22E-09
2	25116977	rs7586879	*ADCY3*	intron_variant	C	T	457404	0.3800	-0.025	0.002	3.77E-26
2	25141538	rs11676272	*ADCY3*	missense_variant	A	G	429062	0.4904	-0.030	0.002	2.01E-35
2	25158008	rs713586	-	intergenic_variant	T	C	420229	0.4888	-0.029	0.002	8.70E-33
2	25187599	rs4665736	*AC013267.1*	intron_variant	C	T	440727	0.5149	0.031	0.002	3.73E-40
2	25276284	rs6733301	*EFR3B*	intron_variant	G	A	458927	0.1243	-0.025	0.003	8.69E-14
2	25328703	rs12233132	*EFR3B*	intron_variant	C	T	456125	0.3150	0.020	0.002	1.27E-17
2	25482883	rs7594432	*DNMT3A*	intron_variant	T	C	447870	0.4389	0.034	0.002	6.91E-53
2	27730940	rs1260326	*GCKR*	missense_variant	T	C	458927	0.6287	0.018	0.002	3.97E-13
2	27741237	rs780094	*GCKR*	intron_variant	T	C	439951	0.6311	0.018	0.003	2.16E-12
2	27742603	rs780093	*GCKR*	intron_variant	T	C	429677	0.6370	0.017	0.003	8.15E-12
2	33361425	rs6714546	*LTBP1*	intron_variant	A	G	448114	0.7414	0.032	0.003	8.32E-37
2	33405151	rs6751657	*LTBP1*	intron_variant	T	C	456125	0.5146	0.023	0.002	5.14E-26
2	33527299	rs41464348	*LTBP1*	intron_variant	G	A	454406	0.5225	-0.014	0.002	1.93E-10
2	33567971	rs61751742	*LTBP1*	missense_variant	C	T	433789	0.0093	-0.059	0.011	1.37E-07
2	36673555	rs7562790	*CRIM1*	intron_variant	T	G	458927	0.4373	-0.014	0.002	4.31E-11
2	36690242	rs848534	*CRIM1*	intron_variant	C	T	454162	0.3036	-0.015	0.002	2.03E-10
2	36771309	rs12712508	*FEZ2*	intron_variant	A	G	445497	0.3652	0.016	0.002	1.27E-12
2	36782886	rs848642	*FEZ2*	missense_variant	G	A	458927	0.3549	-0.019	0.002	2.08E-16
2	36810586	rs14291	*FEZ2*	synonymous_variant	T	C	448709	0.3823	0.015	0.002	6.72E-11
2	37995727	rs12615742	-	regulatory_region_variant	C	T	453655	0.4662	0.025	0.002	1.27E-30
2	38298139	rs1800440	*RMDN2*	missense_variant	T	C	458927	0.1712	-0.016	0.003	3.49E-08
2	43519977	rs35720761	*THADA*	missense_variant	C	T	457404	0.1089	0.019	0.004	1.37E-07
2	43732823	rs7578597	*THADA*	missense_variant	T	C	413411	0.1095	0.020	0.004	8.04E-08
2	43806918	rs10495903	*THADA*	intron_variant	C	T	402624	0.1272	0.020	0.004	1.32E-08
2	44547574	rs698761	*SLC3A1*	missense_variant	G	A	445265	0.6404	-0.014	0.002	1.46E-08
2	44768202	rs2341459	*CAMKMT*	intron_variant	T	C	457648	0.7237	-0.018	0.002	5.65E-13
2	45640374	rs3755073	*SRBD1*	missense_variant	C	A	428205	0.1094	-0.020	0.004	5.78E-08
2	46921285	rs12474201	*SOCS5*	upstream_gene_variant	G	A	438159	0.3314	0.027	0.002	1.41E-29
2	54120025	rs805408	*PSME4*	missense_variant	A	T	452026	0.3076	-0.013	0.002	1.60E-07
2	56008904	rs7577894	-	regulatory_region_variant	T	C	447020	0.4601	-0.019	0.002	1.11E-16
2	56096892	rs3791679	*EFEMP1*	intron_variant	A	G	454406	0.2414	-0.065	0.003	3.87E-133
2	56111309	rs3791675	*EFEMP1*	intron_variant	C	T	453312	0.2492	-0.060	0.003	2.15E-117
2	71627539	rs3771371	*ZNF638*	intron_variant	C	T	433122	0.5371	-0.028	0.002	2.96E-31
2	71633389	rs6714975	*ZNF638*	synonymous_variant	C	T	458927	0.5440	-0.026	0.002	5.89E-31
2	71654175	rs1804020	*ZNF638*	missense_variant	G	A	442892	0.2534	0.022	0.003	1.98E-16
2	71958480	rs2900976	-	intergenic_variant	C	T	457648	0.3241	0.016	0.002	1.44E-11
2	88874891	rs1805165	*EIF2AK3*	missense_variant	C	A	415780	0.7114	-0.029	0.003	1.04E-27
2	88895123	rs13045	*EIF2AK3*	missense_variant	T	C	447889	0.6559	-0.027	0.002	5.08E-30
2	88895351	rs7571971	*EIF2AK3*	5_prime_UTR_variant	T	C	370399	0.7157	-0.030	0.003	8.80E-27
2	88913273	rs867529	*EIF2AK3*	missense_variant	G	C	412435	0.2805	0.029	0.003	2.07E-26
2	89130009	rs17838437	*AC096579.13*	intron_variant	G	T	453517	0.4261	-0.014	0.002	2.05E-10
2	121612659	rs2166898	*GLI2*	intron_variant	G	A	456974	0.1562	-0.029	0.003	3.48E-22
2	128944424	rs744265	*UGGT1*	intron_variant	T	C	458253	0.5955	0.012	0.002	8.78E-08
2	135988127	rs59900519	*ZRANB3*	missense_variant	T	A	427642	0.1286	-0.021	0.004	2.29E-09
2	135988416	rs935615	*ZRANB3*	missense_variant	C	T	424235	0.1256	-0.021	0.004	1.07E-08
2	169707428	rs540652	*NOSTRIN*	missense_variant	C	T	190718	0.4460	0.019	0.003	1.24E-08
2	171822466	rs4668356	*GORASP2*	synonymous_variant	C	T	453732	0.9128	0.022	0.004	5.83E-08
2	178545566	rs75127279	*PDE11A*	missense_variant	C	T	457682	0.0234	0.039	0.007	1.58E-08
2	178565913	rs17400325	*AC012499.1*	missense_variant	T	C	458253	0.0334	0.033	0.006	2.56E-08
2	178684720	rs7567851	*PDE11A*	intron_variant	G	C	417738	0.0897	0.026	0.004	3.39E-11
2	183703336	rs288326	*FRZB*	missense_variant	G	A	454366	0.1033	0.023	0.004	2.22E-10
2	200142847	rs1813849	*SATB2*	intron_variant	T	C	441345	0.8575	0.019	0.003	7.83E-09
2	216577567	rs13022398	*AC012668.2*	intron_variant	C	A	423533	0.6455	0.014	0.002	1.39E-08
2	217878209	rs6435957	-	intergenic_variant	T	C	456974	0.3510	0.017	0.002	6.67E-13
2	217905832	rs13387042	-	intergenic_variant	A	G	442458	0.4809	0.014	0.002	7.98E-10
2	218271898	rs1351164	*DIRC3*	intron_variant	T	C	458253	0.2293	-0.022	0.003	1.67E-17
2	218283303	rs13395110	*DIRC3*	intron_variant	T	G	456730	0.3618	-0.018	0.002	1.31E-15
2	219195799	rs10932775	*CATIP-AS2*	intron_variant	G	A	456730	0.5026	0.015	0.002	2.03E-12
2	219508372	rs3770213	*ZNF142*	missense_variant	A	T	452126	0.3519	-0.017	0.002	9.26E-12
2	219508988	rs3770214	*ZNF142*	missense_variant	T	C	458253	0.6387	0.017	0.002	6.08E-13
2	219509618	rs2230115	*ZNF142*	missense_variant	C	A	458253	0.5589	0.021	0.002	4.38E-19
2	219555262	rs1344642	*STK36*	missense_variant	G	A	458253	0.4413	-0.021	0.002	9.23E-20
2	219562675	rs1863704	*STK36*	missense_variant	G	A	456605	0.3516	-0.016	0.002	2.45E-11
2	219895548	rs56411706	*CCDC108*	missense_variant	C	A	378491	0.1124	-0.028	0.004	3.37E-12
2	219900068	rs17852959	*CCDC108*	missense_variant	C	T	458253	0.0939	-0.033	0.004	2.11E-16
2	219908369	rs12470505	*CCDC108*	upstream_gene_variant	T	G	458253	0.1154	-0.034	0.004	8.35E-20
2	219924961	rs142036701	*IHH*	missense_variant	G	T	448787	0.0007	-0.301	0.039	1.28E-14
2	219934348	rs1052483	*RP11-33O4.1*	non_coding_transcript_exon_variant	G	T	404860	0.0999	-0.038	0.004	2.78E-21
2	219943846	rs6724465	*NHEJ1*	intron_variant	G	A	458253	0.0963	-0.037	0.004	2.76E-21
2	219949184	rs16859517	*NHEJ1*	intron_variant	C	T	458253	0.0483	0.051	0.005	4.29E-23
2	220046840	rs3210652	*FAM134A*	missense_variant	G	A	458253	0.1300	-0.021	0.003	1.85E-09
2	220078652	rs147445258	*ABCB6*	missense_variant	C	T	445220	0.0083	-0.083	0.012	5.56E-13
2	225047744	rs2629046	-	regulatory_region_variant	T	C	456974	0.4690	-0.020	0.002	2.34E-19
2	232263127	rs2290130	*AC017104.6*	missense_variant	G	A	450521	0.2466	-0.014	0.002	3.65E-08
2	232349636	rs4973417	*NCL*	upstream_gene_variant	G	T	424331	0.5572	-0.018	0.002	5.53E-15
2	232796610	rs749052	-	intergenic_variant	T	C	440571	0.0651	-0.048	0.004	2.84E-26
2	232797966	rs2580816	-	intergenic_variant	C	T	457648	0.2227	-0.035	0.003	2.67E-38
2	232944860	rs3100583	*DIS3L2*	intron_variant	G	A	406284	0.5987	0.017	0.002	6.26E-12
2	232982257	rs11677466	*DIS3L2*	intron_variant	A	T	443266	0.0758	0.050	0.004	2.11E-33
2	233077064	rs7571816	*DIS3L2*	intron_variant	A	G	446784	0.0430	-0.050	0.006	1.68E-19
2	233155110	rs6717918	*DIS3L2*	intron_variant	T	C	443542	0.2818	-0.028	0.003	6.85E-28
2	233349588	rs1529874	*ECEL1*	missense_variant	G	A	458927	0.9816	0.043	0.008	6.20E-08
2	233633460	rs1801251	*KCNJ13*	missense_variant	G	A	458927	0.3498	-0.016	0.002	7.87E-12
2	233699415	rs10211596	*GIGYF2*	intron_variant	G	A	455031	0.5358	0.012	0.002	9.40E-08
2	242163359	rs7590653	*ANO7*	missense_variant	G	A	447870	0.2034	-0.016	0.003	1.72E-08

2	242192848	rs7578199	*HDLBP*	missense_variant	T	C	449393	0.2222	-0.016	0.003	8.73E-09
2	242262986	rs12694997	*42615*	intron_variant	G	A	447020	0.2110	-0.015	0.003	1.74E-07
2	242493511	rs4675801	*BOK-AS1*	intron_variant	C	T	457404	0.4717	-0.018	0.002	1.34E-16
3	11641535	rs6772112	*VGLL4*	intron_variant	C	T	407221	0.9343	0.029	0.005	4.22E-10
3	11643465	rs2276749	*VGLL4*	missense_variant	T	C	458253	0.9451	0.029	0.005	7.49E-10
3	14214524	rs2229089	*XPC*	missense_variant	G	A	457349	0.0272	-0.037	0.006	7.51E-09
3	33194990	rs6810039	*SUSD5*	missense_variant	C	A	436091	0.4354	-0.013	0.002	1.82E-08
3	38047954	rs9816693	*PLCD1*	missense_variant	G	C	452800	0.1901	0.017	0.003	3.48E-09
3	41123735	rs10490823	-	intergenic_variant	C	T	455685	0.4966	0.014	0.002	2.07E-09
3	41137672	rs87938	-	intergenic_variant	A	G	458927	0.5500	0.012	0.002	1.42E-07
3	43097765	rs3732858	*FAM198A*	missense_variant	G	A	454696	0.1782	-0.018	0.003	2.38E-10
3	46939587	rs121434601	*PTH1R*	missense_variant	C	T	442763	0.0023	0.155	0.022	8.83E-13
3	47036565	rs17079425	*NBEAL2*	missense_variant	G	A	375565	0.0256	0.045	0.007	2.75E-09
3	47162886	rs76208147	*SETD2*	missense_variant	C	T	442897	0.0236	0.048	0.007	1.60E-11
3	48623124	rs35761247	*COL7A1*	missense_variant	G	A	437685	0.0492	0.041	0.005	6.28E-15
3	49162284	rs34759087	*LAMB2*	missense_variant	C	T	455040	0.1172	0.024	0.004	1.19E-11
3	49162583	rs35713889	*LAMB2*	missense_variant	C	T	429764	0.0375	0.044	0.006	2.83E-14
3	50597092	rs1034405	*C3orf18*	missense_variant	G	A	437739	0.8579	-0.025	0.003	1.54E-14
3	51071713	rs13088462	*DOCK3*	intron_variant	T	C	411014	0.0463	0.057	0.005	2.66E-25
3	52551010	rs79979130	*STAB1*	synonymous_variant	C	T	441034	0.0766	0.027	0.004	5.64E-10
3	52719398	rs1866268	*GNL3*	intron_variant	C	A	457404	0.4238	-0.014	0.002	3.66E-08
3	52721305	rs11177	*GNL3*	missense_variant	G	A	458927	0.3773	-0.014	0.003	3.07E-08
3	52727257	rs2289247	*GNL3*	missense_variant	G	A	458927	0.4238	-0.014	0.002	2.65E-08
3	52740182	rs6617	*SPCS1*	missense_variant	C	G	452800	0.4241	-0.014	0.002	2.67E-08
3	52797634	rs1029871	*NEK4*	missense_variant	G	C	452026	0.3759	-0.014	0.003	7.90E-08
3	52833219	rs2535629	*ITIH3*	intron_variant	G	A	455685	0.3704	-0.018	0.003	1.17E-12
3	52852538	rs4687657	*ITIH4*	missense_variant	G	T	395382	0.2525	-0.019	0.003	6.76E-11
3	52861211	rs13072536	*ITIH4*	missense_variant	A	T	251614	0.2263	-0.023	0.004	4.67E-10
3	52874288	rs6445538	*TMEM110*	3_prime_UTR_variant	T	C	458927	0.2376	-0.020	0.003	1.52E-13
3	53118739	rs2336725	*RP11-894J14.5*	intron_variant	C	T	458927	0.5435	-0.028	0.002	8.30E-38
3	55474073	rs1392224	-	intergenic_variant	A	G	457404	0.4781	0.013	0.002	6.77E-09
3	56533016	rs978979	-	intergenic_variant	A	G	454162	0.6130	0.017	0.002	3.40E-13
3	56628031	rs7637449	*CCDC66*	missense_variant	G	A	437739	0.4929	0.026	0.002	9.81E-27
3	56650054	rs111934125	*CCDC66*	missense_variant	T	C	437739	0.1424	-0.022	0.003	2.38E-11
3	56658871	rs2291498	*CCDC66*	missense_variant	T	C	447020	0.1377	-0.022	0.003	8.88E-11
3	56667682	rs9835332	*FAM208A*	missense_variant	G	C	452800	0.5174	-0.023	0.002	2.58E-22
3	67416322	rs17806888	*SUCLG2*	intron_variant	T	C	458927	0.1048	-0.027	0.004	2.12E-13
3	67426281	rs35494829	*SUCLG2*	missense_variant	T	C	445265	0.0997	-0.027	0.004	3.07E-13
3	72437413	rs9863706	*RYBP*	intron_variant	C	T	458927	0.2152	-0.033	0.003	9.36E-36
3	98503792	rs112115496	*ST3GAL6*	missense_variant	A	G	438159	0.0440	0.028	0.005	9.61E-08
3	98600385	rs9838238	*DCBLD2*	missense_variant	T	C	458927	0.0442	0.028	0.005	5.55E-08
3	99266337	rs13070584	-	intergenic_variant	C	T	409265	0.0496	0.031	0.005	2.40E-09
3	114511356	rs12490319	*ZBTB20*	intron_variant	T	C	441345	0.8047	-0.023	0.003	3.16E-15
3	128976451	rs62266876	*COPG1*	missense_variant	C	G	451352	0.0866	0.021	0.004	6.07E-08
3	129050756	rs6439167	*RP13-685P2.8*	upstream_gene_variant	T	C	458253	0.7960	0.036	0.003	5.23E-41
3	129284818	rs2625973	*PLXND1*	missense_variant	A	C	458253	0.2568	0.016	0.003	1.28E-09
3	129293256	rs2255703	*PLXND1*	missense_variant	T	C	447875	0.4033	0.016	0.002	1.82E-12
3	134233092	rs10935120	*CEP63*	intron_variant	A	G	435786	0.6686	0.025	0.002	2.32E-25
3	135720540	rs9814557	*PPP2R3A*	missense_variant	A	G	437065	0.2957	-0.019	0.003	3.46E-14
3	135720851	rs6779903	*PPP2R3A*	missense_variant	G	T	458253	0.2886	0.014	0.002	1.40E-08
3	135722264	rs17197552	*PPP2R3A*	missense_variant	A	G	458253	0.3044	-0.018	0.002	8.72E-13
3	135926622	rs645040	*RP11-463H24.1*	upstream_gene_variant	G	T	454366	0.7811	-0.014	0.003	5.48E-08
3	135974216	rs9844666	*PCCB*	5_prime_UTR_variant	G	A	437065	0.2211	-0.031	0.003	4.57E-30
3	136574501	rs1052618	*SLC35G2*	missense_variant	A	G	458253	0.6949	-0.019	0.002	4.20E-15
3	141105570	rs724016	*ZBTB38*	5_prime_UTR_variant	A	G	417793	0.4512	0.074	0.002	1.26E-221
3	141134818	rs16851397	*ZBTB38*	intron_variant	A	G	445917	0.0475	0.058	0.005	4.96E-29
3	141137035	rs9825379	*ZBTB38*	intron_variant	G	A	445502	0.0753	0.042	0.004	5.73E-23
3	141143430	rs10513137	*ZBTB38*	intron_variant	G	A	455011	0.1031	0.034	0.004	1.45E-20
3	156862145	rs6809394	*CCNL1*	downstream_gene_variant	C	T	447196	0.3667	-0.013	0.002	1.35E-08
3	157081324	rs11918974	*RP11-550I24.2*	missense_variant	A	G	417879	0.2413	-0.016	0.003	8.97E-10
3	157682536	rs9845687	-	intergenic_variant	T	C	451564	0.7437	-0.017	0.003	2.66E-11
3	157992814	rs7643792	*RSRC1*	intron_variant	A	G	437065	0.4429	0.016	0.002	1.82E-12
3	158104706	rs7648196	*RSRC1*	intron_variant	A	G	224798	0.4644	-0.019	0.003	1.25E-08
3	171780763	rs4894796	*FNDC3B*	intron_variant	A	G	456730	0.5632	0.012	0.002	5.20E-08
3	171969077	rs7652177	*FNDC3B*	missense_variant	C	G	436371	0.5352	0.040	0.002	1.86E-72
3	172165727	rs572169	*GHSR*	synonymous_variant	C	T	433823	0.2989	0.026	0.002	1.67E-26
3	172236440	rs231983	*TNFSF10*	intron_variant	T	G	451115	0.4355	0.016	0.002	5.79E-13
3	183476685	rs262993	*YEATS2*	missense_variant	G	A	458253	0.4263	0.012	0.002	5.52E-08
3	183976103	rs11546878	*CAMK2N2*	missense_variant	C	T	425612	0.1617	-0.020	0.003	6.34E-11
3	183995341	rs1001817	*ECE2*	intron_variant	C	T	458253	0.4935	-0.013	0.002	3.22E-09
3	184020542	rs11545169	*PSMD2*	missense_variant	G	T	351460	0.1485	-0.023	0.003	3.42E-11
3	185548683	rs720390	-	intergenic_variant	G	A	458253	0.3715	0.029	0.002	2.96E-36
3	191093175	rs2028574	*CCDC50*	missense_variant	T	A	436711	0.4125	0.012	0.002	1.64E-07
3	191093310	rs4677728	*CCDC50*	missense_variant	A	G	458253	0.4140	0.012	0.002	1.83E-07
3	191114266	rs2293377	*CCDC50*	3_prime_UTR_variant	T	C	458253	0.3897	0.013	0.002	5.17E-09
4	1701317	rs2247341	*SLBP*	synonymous_variant	G	A	441349	0.3494	0.024	0.002	1.33E-24
4	1729556	rs34205238	*TACC3*	missense_variant	G	A	443722	0.1535	-0.021	0.003	2.11E-11
4	1729988	rs1063743	*TACC3*	missense_variant	G	A	389306	0.2384	-0.018	0.003	2.39E-10
4	1732978	rs17680881	*TACC3*	missense_variant	G	A	453256	0.2382	-0.017	0.003	1.56E-10
4	5016883	rs11722554	*CYTL1*	missense_variant	G	A	458927	0.0373	-0.047	0.005	2.17E-17
4	5023112	rs10937615	*CYTL1*	upstream_gene_variant	G	A	416743	0.7291	-0.017	0.003	5.39E-11
4	5035587	rs6446315	-	regulatory_region_variant	G	A	456125	0.8257	-0.021	0.003	2.69E-13
4	8454639	rs1880024	*TRMT44*	missense_variant	A	G	457648	0.6751	0.012	0.002	1.82E-07
4	8503359	rs1949733	*RP11-689P11.2*	intron_variant	A	G	455275	0.7152	0.016	0.002	5.40E-11
4	12963574	rs763318	-	intergenic_variant	G	A	449836	0.4805	-0.024	0.002	2.29E-28
4	13606576	rs1971278	*BOD1L1*	missense_variant	A	T	424240	0.7963	-0.016	0.003	1.43E-08
4	17707449	rs61741460	*FAM184B*	missense_variant	C	T	444832	0.0465	-0.032	0.005	1.14E-09
4	17797966	rs7678436	*DCAF16*	downstream_gene_variant	G	A	458253	0.1842	-0.047	0.003	1.00E-55
4	17805379	rs7690457	*DCAF16*	missense_variant	G	A	458253	0.0454	-0.034	0.005	4.36E-11
4	17829990	rs3795243	*NCAPG*	missense_variant	G	C	451352	0.1221	-0.047	0.003	5.45E-41
4	17944840	rs16896068	*LCORL*	intron_variant	G	A	458253	0.1786	-0.056	0.003	4.70E-75
4	17972372	rs2320299	*LCORL*	intron_variant	G	A	458253	0.7208	-0.045	0.002	6.19E-75
4	18017730	rs6830062	*LCORL*	intron_variant	T	C	439425	0.1793	-0.056	0.003	1.59E-73
4	18033488	rs6449353	-	intergenic_variant	T	C	458253	0.1779	-0.056	0.003	9.47E-77
4	25408838	rs34811474	*ANAPC4*	missense_variant	G	A	455178	0.1964	0.021	0.003	2.27E-14

4	40121562	rs794001	*N4BP2*	missense_variant	G	A	400838	0.7702	0.017	0.003	3.00E-10
4	48493237	rs79858408	*ZAR1*	missense_variant	G	A	334783	0.4616	-0.014	0.003	4.00E-08
4	48498290	rs10031777	*FRYL*	downstream_gene_variant	T	C	344435	0.4687	0.017	0.003	1.25E-10
4	48988450	rs3747690	*CWH43*	missense_variant	C	A	430539	0.4471	-0.012	0.002	1.43E-07
4	57797414	rs3796529	*REST*	missense_variant	C	T	153772	0.1836	0.036	0.005	1.78E-13
4	57823476	rs17081935	*RP11-738E22.3*	downstream_gene_variant	C	T	446591	0.1982	0.033	0.003	1.29E-33
4	73178175	rs150270324	*ADAMTS3*	missense_variant	T	C	454469	0.0115	-0.056	0.010	7.37E-09
4	73179445	rs141374503	*ADAMTS3*	missense_variant	C	T	458356	0.0024	-0.128	0.021	4.01E-10
4	73470972	rs1518485	-	intergenic_variant	C	T	447870	0.5291	-0.029	0.002	1.37E-36
4	73472941	rs1589163	-	intergenic_variant	C	T	395343	0.4736	-0.033	0.002	1.63E-40
4	73515313	rs7697556	-	intergenic_variant	T	C	436460	0.4988	-0.033	0.002	2.44E-46
4	81952637	rs74764079	*BMP3*	missense_variant	T	A	436912	0.0215	-0.039	0.007	8.05E-08
4	82149831	rs710841	-	intergenic_variant	C	T	455685	0.2760	0.043	0.002	2.60E-66
4	82318524	rs10028610	-	intergenic_variant	G	A	447870	0.3830	0.025	0.002	1.08E-27
4	87730980	rs61730641	*PTPN13*	missense_variant	C	T	454469	0.0129	-0.086	0.009	1.65E-20
4	103188709	rs13107325	*SLC39A8*	missense_variant	C	T	458253	0.0541	-0.033	0.005	3.99E-12
4	106081636	rs9884482	*TET2*	intron_variant	T	C	431698	0.3738	0.024	0.002	9.31E-24
4	106106353	rs10010325	*TET2*	intron_variant	C	A	421338	0.4860	0.025	0.002	2.36E-27
4	106196951	rs2454206	*TET2*	missense_variant	A	G	455880	0.3399	-0.023	0.002	5.88E-23
4	106317429	rs13787	*PPA2*	missense_variant	C	G	421404	0.4423	-0.014	0.002	1.70E-09
4	109408608	rs1562975	-	intergenic_variant	G	A	433169	0.2811	0.026	0.002	4.65E-26
4	120422407	rs149385790	*PDE5A*	missense_variant	T	G	435705	0.0012	0.252	0.031	2.16E-16
4	120716967	rs7699214	*LINC01365*	downstream_gene_variant	A	G	430886	0.5227	0.012	0.002	1.53E-07
4	122664323	rs28532673	-	intergenic_variant	G	A	444823	0.4315	0.016	0.002	3.65E-13
4	122665514	rs7659604	-	intergenic_variant	C	T	265996	0.4353	0.017	0.003	1.19E-08
4	122748308	rs1507995	*BBS7*	intron_variant	G	A	186322	0.3054	0.021	0.004	1.08E-08
4	123838758	rs12648093	*NUDT6*	missense_variant	A	G	445477	0.7115	-0.015	0.003	2.15E-09
4	135121721	rs116807401	*PABPC4L*	missense_variant	T	C	458253	0.0146	0.065	0.009	5.24E-14
4	144359490	rs28925904	*GAB1*	missense_variant	C	T	458253	0.0163	-0.047	0.008	9.50E-09
4	145460230	rs13147758	-	intergenic_variant	A	G	444831	0.4090	0.013	0.002	6.41E-08
4	145485738	rs1980057	-	intergenic_variant	C	T	446110	0.4096	0.013	0.002	5.92E-08
4	145486389	rs13118928	-	regulatory_region_variant	A	G	456974	0.4074	0.013	0.002	2.20E-08
4	145568352	rs7689420	*HHIP-AS1*	non_coding_transcript_exon_variant	T	C	447440	0.8250	0.063	0.003	7.74E-101
4	145574844	rs1812175	*HHIP*	intron_variant	A	G	455011	0.8252	0.063	0.003	7.00E-100
4	145643079	rs6854783	*HHIP*	intron_variant	G	A	456974	0.5925	0.030	0.002	1.13E-38
4	145650021	rs1492820	*HHIP*	intron_variant	G	A	451359	0.5470	0.037	0.002	1.19E-57
4	145658429	rs2639576	*HHIP*	intron_variant	T	C	456730	0.4489	-0.024	0.002	1.98E-26
4	154557616	rs34343821	*KIAA0922*	missense_variant	C	T	435057	0.0101	0.055	0.011	1.96E-07
4	184236868	rs4862155	*WWC2*	missense_variant	G	A	456730	0.0629	-0.036	0.004	3.63E-16
5	31515657	rs55656741	*DROSHA*	missense_variant	G	A	458927	0.4598	0.015	0.002	2.53E-11
5	32784907	rs146301345	*AC026703.1*	missense_variant	G	A	456488	0.0022	0.133	0.022	7.57E-10
5	32830521	rs1173727	-	intergenic_variant	T	C	454406	0.6067	-0.031	0.002	1.17E-44
5	32888818	rs10472828	*CTD-2218G20.1*	upstream_gene_variant	C	T	458927	0.4448	-0.012	0.002	7.33E-08
5	32941161	rs10067052	*CTD-2066L21.3*	intron_variant	G	A	426682	0.4310	-0.014	0.002	2.17E-09
5	33176567	rs11744729	*CTD-2066L21.3*	intron_variant	G	A	431546	0.5448	0.018	0.002	2.34E-16
5	33230034	rs11745439	*CTD-2066L21.3*	intron_variant	A	G	454162	0.6923	0.024	0.002	7.32E-24
5	36954812	rs292182	*NIPBL*	intron_variant	G	A	456125	0.4660	-0.024	0.002	7.25E-27
5	37239240	rs7735138	*C5orf42*	intron_variant	A	C	431835	0.3783	-0.015	0.002	4.41E-10
5	39397132	rs11959928	*DAB2*	intron_variant	T	A	432577	0.4146	0.013	0.002	2.26E-08
5	41574561	rs668732	-	intergenic_variant	C	A	447870	0.4856	-0.012	0.002	1.55E-08
5	42473555	rs13188386	*GHR*	intron_variant	G	A	455275	0.2580	-0.019	0.002	2.17E-14
5	42719239	rs6180	*GHR*	missense_variant	A	C	433069	0.4488	-0.022	0.002	3.36E-21
5	42782492	rs2973011	*CCDC152*	intron_variant	T	C	447870	0.4528	-0.021	0.002	5.39E-20
5	54410099	rs444527	*CDC20B*	missense_variant	G	A	456554	0.1967	0.015	0.003	7.93E-08
5	54439466	rs1021580	*CDC20B*	missense_variant	G	A	444411	0.8162	-0.015	0.003	1.50E-07
5	54960609	rs4865614	*SLC38A9*	synonymous_variant	A	G	450208	0.6544	-0.024	0.002	1.23E-23
5	54960673	rs4865615	*SLC38A9*	missense_variant	C	G	408811	0.6527	-0.026	0.003	1.37E-24
5	55001899	rs11958779	*SLC38A9*	intron_variant	G	A	457648	0.6801	-0.023	0.002	1.20E-20
5	56031884	rs889312	-	intergenic_variant	C	A	457648	0.7040	0.018	0.002	4.98E-14
5	56177443	rs702689	*MAP3K1*	missense_variant	G	A	456554	0.6728	0.018	0.002	6.20E-14
5	56177743	rs832582	*MAP3K1*	missense_variant	G	A	456554	0.8045	0.018	0.003	2.71E-10
5	56207123	rs2257505	*SETD9*	missense_variant	T	A	449933	0.7113	0.019	0.003	9.00E-14
5	64565261	rs10057851	*ADAMTS6*	intron_variant	G	A	442255	0.5166	0.012	0.002	4.03E-08
5	64766798	rs61736454	*ADAMTS6*	missense_variant	G	A	435249	0.0018	-0.139	0.025	2.71E-08
5	67596088	rs3756668	*PIK3R1*	3_prime_UTR_variant	G	A	453312	0.4743	-0.013	0.002	2.55E-09
5	88354675	rs10037512	*MEF2C-AS1*	intron_variant	T	C	458927	0.4827	-0.027	0.002	1.26E-32
5	88376061	rs1366594	*MEF2C-AS1*	intron_variant	A	C	454406	0.4839	-0.026	0.002	1.33E-30
5	88416354	rs9293511	*MEF2C-AS1*	intron_variant	C	T	457279	0.3813	-0.026	0.002	6.86E-31
5	90151589	rs2247870	*ADGRV1*	missense_variant	G	A	458927	0.5266	0.014	0.002	1.06E-09
5	95539448	rs4869272	*CTD-2337A12.1*	intron_variant	C	T	458927	0.6890	-0.013	0.002	9.73E-08
5	95728898	rs6235	*PCSK1*	missense_variant	C	G	423723	0.2680	0.017	0.003	7.50E-11
5	95728974	rs6234	*PCSK1*	missense_variant	G	C	452800	0.2711	0.017	0.003	5.17E-11
5	108113344	rs13177718	*FER*	intron_variant	C	T	429104	0.0673	-0.027	0.004	8.56E-10
5	122685727	rs1047437	*CEP120*	missense_variant	C	G	452126	0.1678	-0.015	0.003	1.05E-07
5	122718736	rs6595440	*CEP120*	missense_variant	G	C	181242	0.4217	-0.024	0.003	8.04E-12
5	126250812	rs34821177	*MARCH3*	missense_variant	C	T	444591	0.0310	0.033	0.006	8.22E-08
5	127371588	rs10063647	*LINC01184*	intron_variant	A	G	453078	0.4895	0.014	0.002	1.02E-09
5	127668685	rs78727187	*FBN2*	missense_variant	G	T	431369	0.0052	0.180	0.015	1.40E-33
5	127685135	rs154001	*FBN2*	missense_variant	C	T	458253	0.6905	0.019	0.002	1.12E-16
5	127699375	rs374748	*FBN2*	intron_variant	G	A	447440	0.8922	0.020	0.004	3.29E-08
5	131396478	rs40401	*IL3*	missense_variant	C	T	454366	0.2617	-0.015	0.003	6.90E-09
5	131447104	rs247008	-	regulatory_region_variant	A	G	443309	0.6430	0.021	0.002	1.18E-18
5	131607721	rs10479001	*P4HA2*	missense_variant	C	T	425069	0.0471	0.034	0.005	1.45E-10
5	131663062	rs272893	*SLC22A4*	missense_variant	T	C	444832	0.5993	0.029	0.002	3.50E-32
5	131676320	rs1050152	*SLC22A4*	missense_variant	C	T	373364	0.3429	0.021	0.003	5.31E-13
5	131699867	rs274546	*MIR3936*	intron_variant	A	G	451124	0.5976	0.028	0.002	9.69E-31
5	131723288	rs2073643	*SLC22A5*	intron_variant	T	C	454366	0.4967	0.020	0.002	1.86E-18
5	131744574	rs1016988	*C5orf56*	upstream_gene_variant	T	C	454366	0.2156	-0.018	0.003	6.11E-11
5	131770805	rs2188962	*C5orf56*	intron_variant	C	T	441934	0.3587	0.022	0.003	4.18E-17
5	131784393	rs12521868	*C5orf56*	intron_variant	G	T	448856	0.3607	0.023	0.003	4.93E-19
5	131801726	rs2522056	*AC116366.6*	intron_variant	G	A	453087	0.2262	-0.020	0.003	6.91E-14
5	134076812	rs12657663	*CAMLG*	missense_variant	G	A	456605	0.1102	-0.021	0.003	8.70E-10
5	134356705	rs526896	-	intergenic_variant	T	G	456974	0.2799	-0.020	0.002	1.61E-16
5	134364518	rs479632	*C5orf66*	missense_variant	C	G	450274	0.2629	-0.024	0.003	4.46E-21
5	134372685	rs31198	*C5orf66*	intron_variant	T	C	458253	0.2637	-0.024	0.003	1.72E-21

5	140562739	rs61743469	*PCDHB16*	missense_variant	G	A	458253	0.0528	0.027	0.005	8.40E-08
5	141573265	rs3910203	-	intergenic_variant	G	A	456730	0.5837	0.012	0.002	6.32E-08
5	168256240	rs4282339	*SLIT3*	intron_variant	G	A	433413	0.2001	-0.033	0.003	2.12E-33
5	170838791	rs11745536	*NPM1*	downstream_gene_variant	G	A	447196	0.5556	-0.021	0.002	1.48E-22
5	171281875	rs4868125	-	intergenic_variant	C	G	448510	0.5999	0.030	0.002	2.28E-42
5	172196752	rs34471628	*DUSP1*	missense_variant	A	G	431196	0.0315	0.047	0.006	2.79E-14
5	172197790	rs34013988	*DUSP1*	missense_variant	C	T	286303	0.0297	0.053	0.008	1.19E-11
5	172755066	rs148833559	*STC2*	missense_variant	C	A	443140	0.0008	0.287	0.037	3.79E-15
5	172984114	rs889014	-	regulatory_region_variant	C	T	455848	0.3648	-0.024	0.002	3.85E-27
5	173003451	rs1077613	*CTB-33O18.3*	upstream_gene_variant	T	C	454357	0.3525	-0.015	0.002	1.06E-10
5	176516631	rs1966265	*FGFR4*	missense_variant	G	A	437065	0.2270	0.045	0.003	3.08E-63
5	176517326	rs422421	*FGFR4*	intron_variant	T	C	432175	0.7931	0.035	0.003	5.18E-36
5	176517797	rs376618	*FGFR4*	missense_variant	C	T	436818	0.7647	0.021	0.003	6.44E-15
5	176554850	rs11954311	-	intergenic_variant	G	A	422790	0.0286	0.052	0.007	7.35E-15
5	176637471	rs28932177	*NSD1*	missense_variant	G	A	422955	0.0258	0.058	0.007	2.57E-16
5	176637576	rs28932178	*NSD1*	missense_variant	T	C	432977	0.1652	0.020	0.003	1.55E-10
5	176722005	rs78247455	*NSD1*	missense_variant	G	A	454366	0.0251	-0.068	0.007	5.12E-24
5	176734179	rs149685981	*RAB24*	missense_variant	C	T	432977	0.0124	0.052	0.010	7.96E-08
5	176830627	rs17876032	*F12*	non_coding_transcript_exon_variant	G	A	439683	0.5908	-0.021	0.002	5.94E-18
5	176842474	rs2731672	*GRK6*	intron_variant	T	C	455011	0.7110	-0.020	0.002	5.17E-16
5	178507069	rs1445846	*RP11-281O15.7*	missense_variant	T	C	458253	0.6884	-0.019	0.002	1.30E-15
5	178507090	rs1445845	*RP11-281O15.7*	missense_variant	G	A	458253	0.6883	-0.020	0.002	7.62E-16
5	178540975	rs1054480	*ADAMTS2*	missense_variant	G	A	409724	0.2869	-0.015	0.003	1.25E-08
5	179731014	rs6879260	*GFPT2*	intron_variant	T	C	458253	0.6016	0.028	0.002	1.00E-35
6	1901495	rs1570534	*GMDS*	intron_variant	C	T	447196	0.6446	0.015	0.002	6.33E-11
6	7211818	rs1334576	*RREB1*	missense_variant	G	A	433651	0.4319	0.013	0.002	5.27E-09
6	7231843	rs9379084	*RREB1*	missense_variant	G	A	355810	0.1089	-0.051	0.004	6.32E-39
6	7247344	rs35742417	*RREB1*	missense_variant	C	A	458927	0.1737	0.028	0.003	2.17E-21
6	7310259	rs10004	*SSR1*	missense_variant	A	G	458927	0.2751	0.017	0.002	9.30E-12
6	7720059	rs12198986	-	intergenic_variant	G	A	458927	0.4486	0.038	0.002	1.11E-64
6	7725760	rs3812163	*BMP6*	upstream_gene_variant	A	T	437931	0.4433	0.038	0.002	2.12E-62
6	17665479	rs6906499	*NUP153*	missense_variant	G	C	451352	0.2962	0.013	0.002	1.04E-07
6	17675246	rs2228375	*NUP153*	missense_variant	T	C	458253	0.2787	0.016	0.003	1.39E-10
6	17699322	rs12199222	*NUP153*	intron_variant	G	T	456974	0.2950	0.013	0.002	1.41E-07
6	19841493	rs1047014	*ID4*	upstream_gene_variant	T	C	453732	0.2330	0.026	0.003	3.11E-23
6	25776949	rs11754288	*SLC17A4*	missense_variant	G	A	455040	0.4048	0.022	0.002	5.25E-19
6	25813150	rs1165196	*SLC17A1*	missense_variant	G	A	455040	0.5784	-0.022	0.002	4.31E-19
6	25823444	rs1183201	*SLC17A1*	intron_variant	A	T	384098	0.5681	-0.022	0.003	2.51E-17
6	25842951	rs1408272	*SLC17A3*	intron_variant	T	G	442209	0.0531	0.030	0.005	3.62E-08
6	25870542	rs1165205	*SLC17A3*	intron_variant	T	A	445671	0.5582	-0.023	0.002	9.76E-21
6	26056604	rs2230653	*HIST1H1C*	missense_variant	G	A	416421	0.0428	-0.038	0.006	2.24E-10
6	26093141	rs1800562	*HFE*	missense_variant	G	A	445451	0.0507	0.029	0.005	8.88E-08
6	26107790	rs198845	*HIST1H1T*	missense_variant	G	T	431933	0.3558	0.033	0.002	4.32E-39
6	26108168	rs2051542	*HIST1H1T*	missense_variant	G	A	450240	0.0874	-0.025	0.004	2.50E-10
6	26108282	rs198844	*HIST1H1T*	missense_variant	C	G	433158	0.5176	0.018	0.002	9.01E-14
6	26200677	rs806794	*HIST1H2AD*	3_prime_UTR_variant	A	G	387752	0.3235	-0.047	0.003	5.83E-70
6	26233387	rs10946808	*HIST1H1D*	non_coding_transcript_exon_variant	A	G	452667	0.3029	-0.047	0.003	5.37E-76
6	26500563	rs13194984	*BTN1A1*	upstream_gene_variant	G	T	453761	0.1095	0.027	0.004	8.22E-13
6	27037080	rs13194491	-	intergenic_variant	C	T	452113	0.0615	0.027	0.005	1.37E-07
6	27178028	rs858985	*RP11-209A2.1*	upstream_gene_variant	T	C	373991	0.9023	0.023	0.004	5.65E-08
6	28916252	rs4947339	*LINC01556*	downstream_gene_variant	C	T	419797	0.4514	-0.021	0.003	2.29E-14
6	29045632	rs9393941	*SAR1P1*	upstream_gene_variant	G	A	430610	0.4435	-0.021	0.003	7.50E-14
6	29084232	rs3129109	*OR2J3*	downstream_gene_variant	T	C	430610	0.5566	0.021	0.003	7.43E-14
6	29191411	rs714470	*XXbac-BPG308J9.3*	upstream_gene_variant	C	A	437779	0.5508	0.015	0.003	3.64E-09
6	29274486	rs9257694	*OR14J1*	missense_variant	T	C	455040	0.4981	0.016	0.003	3.08E-10
6	29350854	rs1419640	*OR5V1*	intron_variant	G	T	438159	0.5445	0.014	0.003	1.10E-07
6	30861729	rs3132572	*DDR1*	intron_variant	G	A	451798	0.9088	-0.030	0.005	2.89E-09
6	30882689	rs6926224	*GTF2H4*	missense_variant	C	T	455040	0.0373	-0.033	0.006	1.33E-07
6	30882803	rs6926723	*GTF2H4*	missense_variant	G	A	453517	0.0373	-0.033	0.006	1.69E-07
6	30902533	rs2844650	*Y_RNA*	intron_variant	T	C	450519	0.9062	-0.026	0.005	9.66E-08
6	30914751	rs2517451	*DPCR1*	intron_variant	C	T	442264	0.9056	-0.028	0.005	9.71E-09
6	30920086	rs79792575	*DPCR1*	missense_variant	C	T	455040	0.0330	-0.037	0.007	1.58E-08
6	30997824	rs12110785	*MUC22*	missense_variant	T	C	455040	0.1501	-0.022	0.004	3.06E-09
6	30999902	rs4713422	*MUC22*	intron_variant	G	C	447128	0.3949	-0.015	0.003	9.17E-08
6	30999997	rs10947121	*MUC22*	missense_variant	T	C	455040	0.3965	-0.015	0.003	8.78E-08
6	31005726	rs2844670	*MUC22*	downstream_gene_variant	G	A	426522	0.8463	-0.022	0.004	4.83E-08
6	31019562	rs2394427	*HCG22*	upstream_gene_variant	G	A	298146	0.1451	-0.024	0.005	9.74E-08
6	31079994	rs2233976	*PSORS1C1*	missense_variant	C	T	455040	0.0927	-0.033	0.005	2.09E-12
6	31112484	rs130072	*CCHCR1*	missense_variant	C	T	455040	0.0879	-0.038	0.005	1.89E-15
6	31115441	rs3131012	*CCHCR1*	intron_variant	T	C	329605	0.5437	-0.016	0.003	1.90E-07
6	31118898	rs11540822	*CCHCR1*	missense_variant	A	T	439379	0.0845	-0.037	0.005	2.24E-13
6	31122126	rs2073717	*CCHCR1*	intron_variant	G	C	440069	0.5957	-0.015	0.003	7.11E-08
6	31125257	rs72856718	*CCHCR1*	stop_gained	C	A	377375	0.0891	-0.036	0.005	5.36E-13
6	31129707	rs2073724	*POU5F1*	missense_variant	C	T	445506	0.0881	-0.038	0.005	5.75E-15
6	31132085	rs3130933	*POU5F1*	intron_variant	T	C	427323	0.8859	-0.037	0.005	2.77E-13
6	31158689	rs7759909	*XXbac-BPG299F13.17*	downstream_gene_variant	G	T	364982	0.1168	-0.023	0.004	1.15E-07
6	31162963	rs4713447	*HCG27*	upstream_gene_variant	A	G	455040	0.4306	-0.016	0.003	3.92E-09
6	31165566	rs3094609	*HCG27*	missense_variant	T	C	429331	0.8602	-0.029	0.005	1.31E-10
6	31170713	rs9263873	*HCG27*	3_prime_UTR_variant	T	C	452667	0.4304	-0.016	0.003	1.16E-08
6	31174527	rs2894181	*HCG27*	upstream_gene_variant	A	G	453761	0.4798	-0.016	0.003	8.71E-09
6	31177915	rs3130952	-	regulatory_region_variant	G	A	430610	0.8597	-0.029	0.005	9.30E-11
6	31184196	rs3869109	-	regulatory_region_variant	A	G	439462	0.5787	-0.015	0.003	1.19E-07
6	31190850	rs12662501	*XXbac-BPG299F13.15*	non_coding_transcript_exon_variant	C	T	455040	0.1567	-0.024	0.004	1.16E-10
6	31207692	rs3868082	-	regulatory_region_variant	A	G	337693	0.5406	-0.019	0.003	3.10E-08
6	31207920	rs3132499	-	regulatory_region_variant	C	T	427569	0.8567	-0.029	0.005	3.76E-10
6	31237124	rs1130838	*HLA-C*	missense_variant	T	C	425884	0.6942	-0.021	0.003	4.45E-11
6	31244021	rs2524074	*HLA-C*	non_coding_transcript_exon_variant	G	A	428237	0.7105	-0.023	0.003	5.09E-12
6	31247067	rs7382297	*RPL3P2*	upstream_gene_variant	T	G	387514	0.8593	-0.027	0.005	3.42E-09
6	31252396	rs2524054	*WASF5P*	downstream_gene_variant	A	C	392609	0.7578	-0.033	0.004	1.60E-15
6	31254088	rs2853933	*WASF5P*	downstream_gene_variant	T	C	440930	0.6170	-0.019	0.003	2.29E-10
6	31257625	rs2524040	*XXbac-BPG248L24.13*	upstream_gene_variant	T	C	440930	0.6170	-0.019	0.003	3.46E-10
6	31258837	rs9468925	*XXbac-BPG248L24.13*	upstream_gene_variant	G	A	422984	0.3994	-0.016	0.003	4.47E-08
6	31259579	rs2524163	*XXbac-BPG248L24.13*	upstream_gene_variant	C	T	417025	0.6176	-0.019	0.003	1.06E-09
6	31261276	rs2243868	*XXbac-BPG248L24.13*	upstream_gene_variant	A	G	445451	0.6167	-0.019	0.003	1.49E-10
6	31265490	rs2247056	*XXbac-BPG248L24.13*	intron_variant	T	C	412845	0.7559	-0.032	0.004	9.98E-17

6	31265539	rs3905495	*XXbac-BPG248L24.13*	intron_variant	G	A	430610	0.3647	-0.016	0.003	2.27E-08
6	31266190	rs2853922	*XXbac-BPG248L24.13*	intron_variant	A	G	403938	0.6183	-0.021	0.003	2.77E-11
6	31266522	rs2524089	*XXbac-BPG248L24.13*	intron_variant	G	T	442209	0.6164	-0.019	0.003	1.70E-10
6	31272261	rs6457374	*XXbac-BPG248L24.13*	upstream_gene_variant	C	T	208878	0.7551	-0.033	0.006	3.20E-09
6	31273745	rs3873386	*XXbac-BPG248L24.13*	upstream_gene_variant	T	C	450519	0.4178	-0.016	0.003	2.02E-08
6	31321685	rs1058026	*HLA-B*	3_prime_UTR_variant	A	C	437621	0.1930	-0.018	0.003	6.26E-08
6	31328542	rs2523578	*HLA-B*	upstream_gene_variant	G	A	392609	0.7599	-0.030	0.004	6.20E-14
6	31330546	rs2596548	*DHFRP2*	downstream_gene_variant	T	G	453761	0.8422	-0.027	0.004	9.94E-12
6	31331829	rs2523554	*DHFRP2*	downstream_gene_variant	C	T	451798	0.6484	-0.021	0.003	8.05E-13
6	31342484	rs2523644	*FGFR3P1*	upstream_gene_variant	C	T	328052	0.8342	-0.027	0.005	1.57E-08
6	31353593	rs2844529	*ZDHHC20P2*	upstream_gene_variant	G	A	430610	0.3465	-0.017	0.003	1.95E-08
6	31354819	rs4711269	*HLA-S*	upstream_gene_variant	C	T	455040	0.2693	-0.016	0.003	1.31E-07
6	31360255	rs7751505	*XXbac-BPG181B23.7*	downstream_gene_variant	A	C	415474	0.2623	-0.018	0.003	2.99E-08
6	31360341	rs7771971	*XXbac-BPG181B23.7*	downstream_gene_variant	T	C	258587	0.2695	-0.021	0.004	1.52E-07
6	31361897	rs2523473	*XXbac-BPG181B23.7*	downstream_gene_variant	A	C	386200	0.3464	-0.017	0.003	3.77E-08
6	31362930	rs2523467	*XXbac-BPG181B23.7*	non_coding_transcript_exon_variant	C	T	412148	0.3445	-0.017	0.003	1.38E-08
6	31366595	rs2596542	*Y_RNA*	upstream_gene_variant	C	T	429331	0.3422	-0.016	0.003	9.54E-08
6	31379304	rs2853977	*HCP5*	intron_variant	A	T	397594	0.5700	-0.022	0.003	2.00E-13
6	31380529	rs2256183	*HCP5*	intron_variant	A	G	415218	0.5707	-0.024	0.003	3.52E-16
6	31387373	rs2596530	*HCP5*	intron_variant	G	A	389380	0.5701	-0.023	0.003	3.38E-14
6	31388214	rs2844513	*HCP5*	intron_variant	G	A	397390	0.4517	-0.016	0.003	1.11E-07
6	31448976	rs3099844	*HCP5*	downstream_gene_variant	C	A	453761	0.1132	0.026	0.005	5.95E-08
6	31456567	rs3132469	-	intergenic_variant	A	G	391168	0.8821	-0.027	0.005	5.26E-08
6	31488145	rs3130637	*XXbac-BPG16N22.5*	upstream_gene_variant	A	G	436613	0.7737	-0.020	0.003	2.32E-09
6	31491131	rs3093992	*PPIAP9*	upstream_gene_variant	C	A	447020	0.7731	-0.021	0.003	8.12E-10
6	31492025	rs3095226	*PPIAP9*	upstream_gene_variant	C	A	333958	0.7674	-0.022	0.004	1.23E-08
6	31496915	rs2259435	*AL662801.1*	missense_variant	G	A	433460	0.1758	-0.020	0.003	3.80E-09
6	31496925	rs3093983	*AL662801.1*	missense_variant	G	A	455040	0.8287	-0.024	0.004	3.67E-10
6	31497835	rs3115537	*AL662801.1*	3_prime_UTR_variant	G	C	440069	0.8289	-0.024	0.004	4.34E-10
6	31498497	rs3093978	*AL662801.1*	non_coding_transcript_exon_variant	C	A	450519	0.8287	-0.024	0.004	6.30E-10
6	31502767	rs3131628	*AL662801.1*	non_coding_transcript_exon_variant	C	T	451798	0.8287	-0.024	0.004	3.46E-10
6	31506801	rs2523512	*DDX39B*	intron_variant	G	A	442601	0.1773	-0.020	0.003	6.00E-09
6	31511857	rs2251824	*DDX39B*	intron_variant	G	A	447122	0.1647	-0.019	0.003	5.58E-08
6	31538244	rs2009658	*LTA*	upstream_gene_variant	C	G	431080	0.1635	-0.020	0.004	1.17E-08
6	31540556	rs2229094	*LTA*	missense_variant	T	C	455040	0.2711	-0.017	0.003	1.45E-09
6	31542476	rs1800630	*LTA*	upstream_gene_variant	C	A	439752	0.1623	-0.021	0.004	1.33E-09
6	31564821	rs2844480	*NCR3*	upstream_gene_variant	C	T	447020	0.1978	-0.019	0.003	2.47E-09
6	31567422	rs2857596	-	intergenic_variant	G	T	233486	0.7687	-0.027	0.005	4.14E-08
6	31572956	rs2844479	-	intergenic_variant	A	C	440741	0.3437	-0.017	0.003	4.90E-09
6	31578772	rs2844477	*AIF1*	upstream_gene_variant	T	C	442264	0.3627	-0.017	0.003	7.77E-09
6	31582025	rs3132451	*AIF1*	upstream_gene_variant	G	C	440069	0.1842	0.022	0.004	4.37E-09
6	31583827	rs2259571	*AIF1*	5_prime_UTR_variant	T	G	455040	0.3544	-0.017	0.003	4.16E-09
6	31585219	rs2857697	*PRRC2A*	upstream_gene_variant	C	T	451798	0.3885	-0.020	0.003	1.63E-12
6	31587870	rs2857694	*AIF1*	upstream_gene_variant	A	T	446616	0.3893	-0.020	0.003	2.47E-12
6	31589676	rs2844472	*AIF1*	intron_variant	A	G	451798	0.3634	-0.018	0.003	2.70E-09
6	31591808	rs3130070	*PRRC2A*	intron_variant	A	G	455040	0.1772	0.023	0.004	3.90E-09
6	31595487	rs2736171	*PRRC2A*	intron_variant	A	G	451798	0.3895	-0.021	0.003	4.72E-13
6	31603591	rs2261033	*BAG6*	non_coding_transcript_exon_variant	A	G	436857	0.4614	-0.021	0.003	1.00E-13
6	31603770	rs11229	*BAG6*	synonymous_variant	A	G	455040	0.1773	0.022	0.004	6.97E-09
6	31604591	rs10885	*BAG6*	missense_variant	C	T	314938	0.1778	0.026	0.005	6.70E-08
6	31610529	rs1077393	*BAG6*	non_coding_transcript_exon_variant	A	G	438136	0.4810	-0.015	0.003	1.49E-07
6	31610686	rs1052486	*BAG6*	missense_variant	A	G	414036	0.4832	-0.016	0.003	7.14E-08
6	31611777	rs760293	*BAG6*	intron_variant	T	C	408201	0.8274	-0.020	0.004	7.18E-08
6	31618761	rs3130050	*BAG6*	intron_variant	G	A	432573	0.8706	-0.026	0.005	1.58E-08
6	31619576	rs3117583	*BAG6*	5_prime_UTR_variant	A	G	451798	0.1773	0.022	0.004	9.70E-09
6	31632134	rs3130618	*XXbac-BPG32J3.22*	missense_variant	C	A	429182	0.1770	0.023	0.004	5.79E-09
6	31704294	rs3131383	*MSH5*	5_prime_UTR_variant	G	T	430610	0.0986	0.031	0.006	5.84E-08
6	31721033	rs3131379	*MSH5*	intron_variant	G	A	429087	0.0986	0.032	0.006	4.65E-08
6	31725230	rs3117574	*MSH5*	5_prime_UTR_variant	G	A	432573	0.0986	0.031	0.006	1.23E-07
6	31749142	rs915652	*VARS*	non_coding_transcript_exon_variant	G	A	440741	0.0909	0.033	0.006	6.26E-08
6	31812038	rs9267576	*C6orf48*	downstream_gene_variant	T	G	452238	0.8830	-0.031	0.005	1.22E-10
6	31883957	rs644045	*C2*	intron_variant	A	G	419742	0.6789	-0.019	0.003	1.31E-08
6	31888367	rs3130683	*C2*	intron_variant	C	T	443983	0.8815	-0.033	0.005	5.30E-12
6	31912523	rs36221133	*CFB*	missense_variant	T	C	433852	0.0137	-0.068	0.011	6.87E-10
6	31916400	rs537160	*CFB*	intron_variant	A	G	434443	0.6925	-0.023	0.003	1.00E-12
6	31922254	rs630379	*SKIV2L*	intron_variant	A	C	423575	0.7475	-0.023	0.004	2.33E-10
6	31927342	rs440454	*SKIV2L*	non_coding_transcript_exon_variant	A	G	427268	0.7401	-0.024	0.004	1.72E-11
6	31928799	rs419788	*SKIV2L*	intron_variant	T	C	440930	0.7398	-0.023	0.003	1.52E-11
6	31929014	rs437179	*SKIV2L*	missense_variant	A	C	417718	0.7392	-0.023	0.004	2.01E-10
6	31946614	rs6941112	*STK19*	intron_variant	G	A	455040	0.3016	-0.016	0.003	6.95E-08
6	31947460	rs389883	*STK19*	non_coding_transcript_exon_variant	G	T	419783	0.7448	-0.024	0.004	1.18E-11
6	32038700	rs2071295	*TNXB*	intron_variant	C	T	428237	0.3094	-0.016	0.003	1.66E-07
6	32062687	rs2071293	*TNXB*	intron_variant	G	A	429331	0.2999	-0.016	0.003	1.50E-07
6	32071893	rs3134954	*TNXB*	intron_variant	C	T	451798	0.8750	-0.028	0.004	5.86E-10
6	32080146	rs3130342	*ATF6B*	intron_variant	A	C	450519	0.8755	-0.027	0.004	1.63E-09
6	32083175	rs8111	*ATF6B*	3_prime_UTR_variant	C	T	430610	0.2729	-0.017	0.003	1.37E-07
6	32088854	rs2228628	*ATF6B*	synonymous_variant	G	C	418107	0.2817	-0.018	0.003	2.41E-08
6	32105001	rs4713505	-	intergenic_variant	G	T	433852	0.2841	-0.017	0.003	5.61E-08
6	32112626	rs3130279	*PRRT1*	downstream_gene_variant	A	G	453761	0.8732	-0.028	0.004	3.96E-10
6	32113980	rs4713506	*PRRT1*	downstream_gene_variant	G	A	433852	0.2714	-0.019	0.003	3.58E-09
6	32119898	rs3131283	*PPT2-EGFL8*	5_prime_UTR_variant	T	C	450519	0.8854	-0.029	0.005	2.58E-09
6	32122386	rs3134604	*PPT2-EGFL8*	missense_variant	C	G	445187	0.8827	-0.025	0.004	3.39E-08
6	32151222	rs1035798	*PBX2*	splice_region_variant	G	A	442209	0.2368	-0.017	0.003	1.80E-07
6	32151994	rs1800684	*PBX2*	synonymous_variant	A	T	421868	0.8835	-0.031	0.005	5.46E-10
6	32172993	rs3131296	*NOTCH4*	intron_variant	C	T	395901	0.1260	0.028	0.005	2.86E-08
6	32190028	rs3132946	*NOTCH4*	intron_variant	A	G	453761	0.8843	-0.028	0.005	2.20E-09
6	32411307	rs2239806	*HLA-DRA*	intron_variant	C	T	438159	0.1719	0.021	0.004	7.45E-08
6	32411646	rs7192	*HLA-DRA*	missense_variant	T	G	450809	0.6096	-0.017	0.003	1.22E-08
6	32412480	rs7194	*HLA-DRA*	3_prime_UTR_variant	G	A	453761	0.6097	-0.017	0.003	7.26E-09
6	32413459	rs2227139	*HLA-DRA*	downstream_gene_variant	G	A	438136	0.6090	-0.017	0.003	1.25E-08
6	32658310	rs9469220	-	intergenic_variant	G	A	435923	0.4998	-0.018	0.003	5.42E-11
6	32663851	rs6457617	-	intergenic_variant	C	T	431050	0.5051	-0.022	0.003	1.15E-14
6	32663999	rs6457620	-	intergenic_variant	G	C	287809	0.4745	-0.022	0.004	6.31E-10
6	32664458	rs2647012	-	intergenic_variant	T	C	451798	0.6137	-0.023	0.003	6.08E-15
6	32669018	rs1612904	*MTCO3P1*	downstream_gene_variant	C	A	396050	0.6431	-0.024	0.003	1.55E-13

6	32670308	rs2856717	*MTCO3P1*	downstream_gene_variant	A	G	450519	0.6167	-0.022	0.003	2.32E-14
6	32675109	rs9275524	*MTCO3P1*	upstream_gene_variant	T	C	441378	0.5776	-0.020	0.003	5.89E-12
6	32678182	rs6932517	*MTCO3P1*	upstream_gene_variant	C	G	327535	0.5520	-0.020	0.003	2.67E-09
6	32678999	rs9275572	*MTCO3P1*	upstream_gene_variant	A	G	453761	0.5784	-0.021	0.003	1.42E-13
6	32681631	rs9275596	*XXbac-BPG254F23.7*	upstream_gene_variant	C	T	431479	0.6427	-0.024	0.003	7.52E-15
6	33626717	rs2296343	*ITPR3*	intron_variant	T	C	455685	0.2812	0.017	0.003	4.34E-11
6	33638180	rs2229634	*ITPR3*	synonymous_variant	C	T	457648	0.3151	0.013	0.003	9.73E-08
6	33686103	rs549652	*IP6K3*	downstream_gene_variant	G	A	436216	0.1317	-0.021	0.004	2.98E-08
6	33690796	rs4713668	*IP6K3*	missense_variant	C	T	458927	0.4668	0.018	0.002	1.00E-14
6	33719877	rs943463	-	regulatory_region_variant	T	C	456125	0.7947	0.020	0.003	1.27E-10
6	33723383	rs1536500	-	intergenic_variant	T	C	371666	0.7887	0.020	0.003	2.11E-09
6	33728755	rs2395449	-	intergenic_variant	T	A	428771	0.3771	0.016	0.003	1.04E-10
6	33745071	rs2296748	*LEMD2*	intron_variant	C	T	435366	0.3804	0.017	0.002	2.31E-12
6	33751767	rs2182659	*LEMD2*	intron_variant	A	G	444413	0.8228	0.022	0.003	3.03E-11
6	33755711	rs756138	*LEMD2*	intron_variant	G	C	441659	0.7901	0.017	0.003	8.51E-09
6	33764158	rs751727	*MLN*	intron_variant	A	G	452883	0.8228	0.022	0.003	5.95E-12
6	33775446	rs1547668	*MLN*	upstream_gene_variant	A	G	447870	0.8133	0.020	0.003	3.39E-10
6	34165721	rs7742369	-	regulatory_region_variant	A	G	456554	0.1986	0.051	0.003	3.60E-72
6	34199092	rs2780226	-	regulatory_region_variant	C	T	455685	0.8911	-0.076	0.004	1.95E-95
6	34214322	rs1150781	*HMGA1*	missense_variant	C	G	355693	0.8865	-0.072	0.004	5.55E-61
6	34214524	rs143851251	*HMGA1*	missense_variant	A	G	376502	0.0011	0.217	0.035	6.14E-10
6	34498328	rs41312309	*PACSIN1*	missense_variant	C	T	458927	0.0821	0.034	0.004	1.31E-16
6	34546560	rs2814982	*RP3-391O22.3*	upstream_gene_variant	C	T	458927	0.1209	0.024	0.003	2.12E-12
6	34552797	rs2814944	*C6orf106*	downstream_gene_variant	G	A	457648	0.1621	0.046	0.003	1.11E-49
6	34618893	rs2814993	*C6orf106*	intron_variant	G	A	457279	0.1492	0.051	0.003	3.17E-58
6	34730395	rs34427075	*SNRPC*	synonymous_variant	C	T	458927	0.0129	-0.109	0.009	6.82E-31
6	34826921	rs61732793	*UHRF1BP1*	missense_variant	G	C	452026	0.0446	-0.030	0.005	9.26E-09
6	34827085	rs9469913	*UHRF1BP1*	missense_variant	A	T	206280	0.1597	0.032	0.005	1.80E-12
6	34831856	rs13205210	*UHRF1BP1*	missense_variant	T	C	448902	0.1119	-0.027	0.004	5.42E-14
6	34839644	rs34672415	*UHRF1BP1*	missense_variant	G	A	449393	0.0128	-0.107	0.010	3.34E-29
6	34845449	rs4646949	*TAF11*	intron_variant	T	G	420486	0.3162	-0.019	0.003	2.08E-12
6	35088381	rs2234045	*TCP11*	missense_variant	C	G	452800	0.1446	-0.026	0.003	1.43E-15
6	35108553	rs35693439	*TCP11*	missense_variant	T	G	458927	0.1455	-0.026	0.003	4.17E-16
6	35117399	rs1886243	*TCP11*	upstream_gene_variant	A	C	439646	0.6399	0.018	0.003	1.64E-12
6	35285720	rs2395617	*DEF6*	missense_variant	A	C	458927	0.8919	0.023	0.004	9.42E-11
6	35289024	rs9296146	*DEF6*	missense_variant	G	A	398109	0.0067	-0.092	0.015	3.02E-10
6	35402785	rs4713858	-	intergenic_variant	A	G	457648	0.8529	0.022	0.003	1.47E-12
6	35402805	rs6457821	-	regulatory_region_variant	C	A	432372	0.0184	-0.083	0.008	5.37E-24
6	35411091	rs3800378	*MKRNP2*	intron_variant	G	A	447870	0.6033	0.013	0.002	2.52E-08
6	35423886	rs7761870	*FANCE*	missense_variant	C	T	458927	0.0187	-0.078	0.008	7.36E-23
6	35467891	rs41270076	*TULP1*	synonymous_variant	C	T	458927	0.0263	-0.049	0.007	4.99E-14
6	35765043	rs2766597	*CLPS*	missense_variant	A	G	379549	0.0149	-0.087	0.010	3.93E-19
6	36094188	rs6922865	*MAPK13*	upstream_gene_variant	T	G	447020	0.6312	-0.012	0.002	1.63E-07
6	36198577	rs3748045	*BRPF3*	3_prime_UTR_variant	G	C	348732	0.6262	-0.016	0.003	8.31E-10
6	36339143	rs61730656	*ETV7*	missense_variant	C	T	447870	0.0087	-0.077	0.012	2.27E-11
6	41903798	rs33966734	*CCND3*	stop_gained	C	A	164243	0.0120	-0.126	0.016	2.43E-15
6	43270151	rs2270860	*CRIP3*	splice_region_variant	C	T	458927	0.3378	-0.015	0.002	3.62E-10
6	43273604	rs2242416	*CRIP3*	missense_variant	A	G	457279	0.5649	0.015	0.002	1.15E-10
6	44946506	rs9472414	*SUPT3H*	intron_variant	T	A	452026	0.2189	-0.025	0.003	9.48E-21
6	45095163	rs9395066	*SUPT3H*	intron_variant	A	C	424077	0.4109	0.023	0.002	2.72E-22
6	47623292	rs12195173	*ADGRF2*	upstream_gene_variant	G	A	367205	0.6591	0.015	0.003	5.29E-08
6	47649573	rs10807371	*ADGRF2*	synonymous_variant	C	T	458927	0.6185	0.013	0.002	6.45E-08
6	47649574	rs10807372	*ADGRF2*	missense_variant	A	G	458927	0.6186	0.013	0.002	5.19E-08
6	47649694	rs9381594	*ADGRF2*	missense_variant	A	G	458927	0.6210	0.013	0.002	1.21E-07
6	56919443	rs61740375	*KIAA1586*	missense_variant	A	G	445451	0.0872	0.022	0.004	5.03E-08
6	76173832	rs6903448	*RP11-415D17.1*	intron_variant	C	T	457404	0.1663	-0.026	0.003	4.83E-19
6	76174857	rs2951916	*RP11-415D17.1*	non_coding_transcript_exon_variant	A	G	410539	0.5045	0.024	0.002	3.35E-24
6	76265642	rs9360921	-	regulatory_region_variant	T	G	453899	0.1063	0.044	0.004	4.99E-35
6	80956208	rs648831	*BCKDHB*	intron_variant	C	T	432974	0.4969	0.033	0.002	1.06E-47
6	81038921	rs1341278	*BCKDHB*	intron_variant	T	G	389285	0.0601	0.037	0.005	4.70E-14
6	81253073	rs10943716	-	regulatory_region_variant	C	T	447870	0.5301	0.012	0.002	9.55E-08
6	81315597	rs9443804	-	regulatory_region_variant	A	G	457404	0.4472	0.021	0.002	5.29E-21
6	81913895	rs2323150	-	intergenic_variant	G	A	421572	0.5573	-0.023	0.002	3.38E-23
6	83838673	rs4706980	*DOPEY1*	missense_variant	G	A	446176	0.1207	0.018	0.003	1.56E-07
6	105378954	rs7759938	-	intergenic_variant	C	T	458253	0.6663	-0.038	0.002	7.53E-57
6	105400837	rs314280	*LIN28B*	upstream_gene_variant	A	G	455011	0.5331	-0.030	0.002	4.88E-39
6	105407662	rs314277	*LIN28B*	intron_variant	A	C	458253	0.8371	-0.033	0.003	8.91E-29
6	105412932	rs314274	*LIN28B*	intron_variant	A	C	456730	0.6689	-0.037	0.002	1.02E-53
6	105417978	rs314268	*LIN28B*	intron_variant	G	A	443954	0.6601	-0.037	0.002	3.96E-52
6	108988184	rs2153960	*FOXO3*	intron_variant	G	A	394485	0.6604	0.018	0.003	3.10E-12
6	108996963	rs3800229	*FOXO3*	intron_variant	G	T	440066	0.6661	0.020	0.002	4.11E-16
6	109013930	rs9486916	-	intergenic_variant	C	T	441345	0.2362	-0.022	0.003	6.85E-16
6	109742015	rs9487094	*PPIL6*	intron_variant	G	A	454601	0.3778	-0.020	0.002	3.70E-17
6	109764535	rs1476387	*PPIL6*	missense_variant	G	T	432977	0.4426	-0.025	0.002	3.47E-25
6	109767931	rs59056467	*SMPD2*	missense_variant	C	T	447196	0.3295	-0.018	0.003	1.39E-12
6	109783941	rs1046943	*ZBTB24*	3_prime_UTR_variant	A	G	455011	0.4472	-0.024	0.002	2.34E-23
6	109827716	rs2277114	*AK9*	missense_variant	C	T	458253	0.3868	-0.020	0.002	6.03E-17
6	109885475	rs10499052	*AK9*	missense_variant	G	A	458253	0.2599	-0.016	0.003	1.80E-09
6	109894773	rs12175588	*AK9*	missense_variant	T	A	438464	0.2329	0.015	0.003	2.84E-08
6	109906342	rs78047280	*AK9*	missense_variant	C	T	316601	0.3707	-0.022	0.003	6.55E-14
6	116387134	rs1999930	-	intergenic_variant	C	T	432544	0.2478	0.018	0.003	3.34E-11
6	116446576	rs1064583	*COL10A1*	missense_variant	A	G	456605	0.3987	0.013	0.002	5.59E-08
6	116783330	rs1057192	*KRT18P22*	missense_variant	G	A	445344	0.2297	-0.015	0.003	9.75E-09
6	117522156	rs961764	-	intergenic_variant	C	G	256627	0.5565	0.022	0.003	5.53E-14
6	126210395	rs6919947	*NCOA7*	missense_variant	T	G	447196	0.4977	0.012	0.002	3.29E-08
6	126698719	rs9388489	-	intergenic_variant	A	G	444831	0.4726	0.037	0.002	3.23E-54
6	126767600	rs1361108	-	intergenic_variant	C	T	456974	0.4782	0.038	0.002	3.28E-58
6	126835655	rs1490388	-	intergenic_variant	C	T	446110	0.4751	0.038	0.002	2.43E-56
6	126851160	rs1490384	-	intergenic_variant	C	T	444831	0.5151	0.036	0.002	2.18E-51
6	126966308	rs4549631	*PRELID1P1*	downstream_gene_variant	T	C	458253	0.5121	0.035	0.002	5.27E-50
6	127167072	rs13204965	-	intergenic_variant	A	C	391195	0.2162	-0.024	0.003	1.44E-16
6	130322179	rs2876066	-	regulatory_region_variant	C	A	452209	0.1017	-0.027	0.004	3.87E-13
6	130349119	rs6569648	*L3MBTL3*	intron_variant	C	T	444591	0.7931	-0.047	0.003	5.71E-61
6	130354855	rs9388766	*L3MBTL3*	intron_variant	T	C	456730	0.6934	-0.035	0.002	1.30E-45
6	130358428	rs6899976	*L3MBTL3*	intron_variant	G	A	444198	0.6725	-0.035	0.003	4.29E-44

6	130374102	rs9388768	*L3MBTL3*	missense_variant	C	A	455011	0.6406	-0.030	0.002	5.02E-36
6	134013272	rs9493698	*TARID*	intron_variant	A	G	421680	0.2772	0.014	0.003	9.44E-08
6	136227558	rs7752169	*PDE7B*	intron_variant	T	C	456730	0.5404	0.011	0.002	1.16E-07
6	141443540	rs2931796	-	intergenic_variant	C	T	449601	0.5785	-0.012	0.002	8.34E-08
6	142548099	rs225717	*VTA1*	downstream_gene_variant	C	T	458253	0.7786	0.021	0.003	1.25E-15
6	142565531	rs1931983	-	intergenic_variant	C	T	431454	0.6614	0.014	0.002	1.64E-09
6	142679572	rs6570507	*ADGRG6*	intron_variant	G	A	442868	0.3227	-0.050	0.003	9.54E-83
6	142691549	rs11155242	*ADGRG6*	missense_variant	A	C	437065	0.1927	-0.038	0.003	7.04E-38
6	142703877	rs4896582	*ADGRG6*	intron_variant	G	A	432055	0.3474	-0.049	0.003	8.85E-80
6	142750516	rs3817928	*ADGRG6*	intron_variant	A	G	400632	0.1932	-0.038	0.003	1.42E-35
6	142767633	rs3748069	*ADGRG6*	downstream_gene_variant	A	G	456974	0.3161	-0.050	0.003	4.41E-87
6	142797289	rs7763064	-	intergenic_variant	G	A	456974	0.3154	-0.048	0.002	3.38E-82
6	146125793	rs3811102	*RP11-545I5.3*	missense_variant	A	T	452126	0.4070	-0.014	0.002	1.85E-09
6	146126419	rs9373475	*RP11-545I5.3*	missense_variant	C	T	458253	0.4099	-0.013	0.002	4.92E-09
6	146394655	rs969694	*GRM1*	intron_variant	A	G	447196	0.4477	-0.013	0.002	8.19E-09
6	152110943	rs543650	*ESR1*	intron_variant	T	G	421608	0.6084	0.026	0.002	2.59E-28
6	155450779	rs148543891	*TIAM2*	missense_variant	A	G	451151	0.0024	-0.124	0.022	1.45E-08
6	158743188	rs1539312	*TULP4*	intron_variant	G	A	456730	0.5209	-0.016	0.002	3.56E-14
6	158910698	rs12206717	*TULP4*	missense_variant	G	A	454366	0.0501	-0.043	0.005	3.31E-18
6	168810725	rs2147457	-	intergenic_variant	A	G	456730	0.4353	-0.020	0.002	5.93E-20
7	2763102	rs798544	*GNA12*	intron_variant	C	T	455685	0.2768	-0.044	0.003	2.03E-65
7	2789880	rs798502	*GNA12*	intron_variant	A	C	455685	0.2752	-0.047	0.003	1.91E-71
7	2795957	rs798497	*GNA12*	intron_variant	A	G	454406	0.2799	-0.047	0.003	6.34E-74
7	2801803	rs798489	*AMZ1*	splice_donor_variant	C	T	432489	0.2438	-0.047	0.003	2.06E-63
7	2869985	rs1182188	*GNA12*	intron_variant	T	C	454406	0.2830	-0.045	0.003	6.95E-70
7	18891259	rs13245206	*HDAC9*	intron_variant	G	A	435319	0.4090	-0.012	0.002	1.13E-07
7	19616522	rs4470914	*AC007091.1*	intron_variant	C	T	240138	0.1963	0.030	0.004	1.81E-15
7	23502974	rs12534093	*IGF2BP3*	intron_variant	T	A	418382	0.2187	-0.035	0.003	2.00E-36
7	25871109	rs1055144	-	intergenic_variant	C	T	433218	0.1902	0.024	0.003	1.51E-16
7	25901639	rs12700667	-	regulatory_region_variant	G	A	424094	0.6941	-0.015	0.003	2.46E-09
7	28180556	rs864745	*JAZF1*	intron_variant	T	C	455685	0.4602	-0.026	0.002	4.44E-30
7	28185091	rs849141	*JAZF1*	intron_variant	A	G	458927	0.7319	-0.043	0.003	2.80E-64
7	28189411	rs1635852	*JAZF1*	intron_variant	T	C	455275	0.4615	-0.026	0.002	2.47E-30
7	28189946	rs1708299	*JAZF1*	intron_variant	A	G	453844	0.7213	-0.042	0.003	5.82E-62
7	28196222	rs849134	*JAZF1*	intron_variant	A	G	458927	0.4546	-0.027	0.002	1.67E-32
7	37947103	rs1802074	*SFRP4*	missense_variant	C	T	458927	0.2109	0.017	0.003	4.58E-10
7	38128326	rs6959212	-	intergenic_variant	T	C	354404	0.6616	0.018	0.003	1.73E-11
7	38136277	rs1524058	-	intergenic_variant	T	C	458927	0.5880	0.015	0.002	2.03E-11
7	46201355	rs1007358	-	regulatory_region_variant	A	G	454162	0.2217	0.019	0.003	2.64E-13
7	46275728	rs1486139	-	intergenic_variant	A	G	455685	0.5247	0.012	0.002	4.29E-08
7	46437154	rs17172694	-	intergenic_variant	G	T	457404	0.0779	-0.037	0.004	1.91E-20
7	50730452	rs2715094	*GRB10*	intron_variant	G	A	454162	0.7636	-0.016	0.003	3.08E-09
7	50751090	rs10248619	*GRB10*	intron_variant	T	C	455275	0.7637	-0.015	0.003	2.78E-08
7	55855180	rs11982736	*RNU6-1126P*	upstream_gene_variant	G	A	444392	0.2173	-0.020	0.003	6.93E-13
7	92248076	rs42235	*CDK6*	intron_variant	C	T	448114	0.2970	0.051	0.002	4.46E-96
7	92264410	rs2282978	*CDK6*	intron_variant	T	C	457648	0.3346	0.048	0.002	2.37E-94
7	99081730	rs6962772	*ZNF789*	missense_variant	A	G	407927	0.1816	0.018	0.003	3.97E-08
7	99489571	rs17277546	*TRIM4*	3_prime_UTR_variant	G	A	457415	0.0428	0.033	0.005	7.15E-10
7	100490077	rs7636	*ACHE*	synonymous_variant	G	A	429735	0.0557	-0.027	0.005	8.72E-08
7	100490797	rs1799805	*ACHE*	missense_variant	G	T	447071	0.0414	-0.035	0.006	4.12E-10
7	129663496	rs11556924	*RP11-306G20.1*	missense_variant	C	T	458253	0.3390	0.014	0.002	1.49E-09
7	132526350	rs4731907	*CHCHD3*	intron_variant	T	C	423635	0.5422	-0.012	0.002	3.53E-08
7	135048804	rs3812265	*CNOT4*	missense_variant	C	T	458253	0.2441	0.016	0.003	1.21E-09
7	135082953	rs77841106	*CNOT4*	missense_variant	G	C	451352	0.0925	0.022	0.004	8.84E-09
7	135123060	rs17480616	*CNOT4*	missense_variant	G	C	420630	0.0251	0.060	0.007	7.39E-18
7	135293128	rs4294134	*NUP205*	intron_variant	A	G	454601	0.8153	-0.020	0.003	6.61E-12
7	137600690	rs273957	*CREB3L2*	missense_variant	C	T	458253	0.6415	0.020	0.002	2.60E-18
7	140244560	rs2293177	*DENND2A*	missense_variant	C	T	434692	0.3172	0.015	0.002	4.80E-10
7	148650634	rs822552	-	intergenic_variant	C	G	451352	0.2689	0.028	0.002	2.73E-30
7	150667210	rs3807375	*KCNH2*	intron_variant	C	T	452638	0.4033	0.015	0.002	2.02E-10
8	13273477	rs7834383	*DLC1*	intron_variant	G	T	455451	0.3215	0.018	0.002	1.14E-14
8	13356802	rs3816747	*DLC1*	missense_variant	G	A	437065	0.9242	0.027	0.004	1.62E-10
8	13357502	rs34575560	*DLC1*	missense_variant	G	A	458253	0.0286	-0.035	0.006	2.94E-08
8	23148940	rs2272761	*R3HCC1*	missense_variant	G	A	458927	0.5630	0.012	0.002	3.54E-08
8	23150878	rs13530	*R3HCC1*	missense_variant	T	G	458927	0.5643	0.012	0.002	1.25E-07
8	23167353	rs1063582	*LOXL2*	missense_variant	T	G	452085	0.7735	-0.024	0.003	7.29E-20
8	23418444	rs2942202	*SLC25A37*	intron_variant	A	C	408932	0.5030	-0.015	0.002	3.22E-11
8	23423697	rs3736032	*SLC25A37*	missense_variant	G	A	445265	0.0836	0.021	0.004	1.96E-07
8	24116304	rs1013209	-	intergenic_variant	C	T	436460	0.2537	-0.025	0.003	1.35E-23
8	30383013	rs2979531	*RBPMS*	intron_variant	A	G	447870	0.5040	-0.013	0.002	4.23E-09
8	57078933	rs35883156	*PLAG1*	missense_variant	G	T	361294	0.1561	-0.040	0.004	1.96E-30
8	57095808	rs10958476	*PLAG1*	intron_variant	T	C	458927	0.1990	0.043	0.003	1.91E-55
8	57100149	rs7833986	*PLAG1*	intron_variant	G	A	458927	0.1831	-0.035	0.003	6.32E-32
8	57100791	rs13273123	*PLAG1*	intron_variant	A	G	443986	0.1666	-0.038	0.003	1.39E-33
8	57155598	rs9650315	-	intergenic_variant	G	T	435184	0.1486	-0.055	0.003	4.46E-63
8	57179020	rs7815788	-	intergenic_variant	C	T	436460	0.1382	-0.048	0.003	7.27E-48
8	57194163	rs7460090	-	intergenic_variant	T	C	394820	0.1173	-0.060	0.004	4.89E-57
8	57400489	rs2582394	*RP11-17A4.2*	intron_variant	C	T	457404	0.4705	0.014	0.002	1.50E-10
8	76147954	rs16939046	*CASC9*	intron_variant	T	C	398227	0.0858	-0.023	0.004	2.81E-08
8	76776862	rs969826	-	intergenic_variant	G	A	444628	0.4945	0.011	0.002	1.90E-07
8	78093837	rs7821178	-	intergenic_variant	C	A	352631	0.3490	0.028	0.003	4.54E-26
8	78160179	rs7846385	-	intergenic_variant	T	C	457648	0.2717	0.031	0.002	5.28E-36
8	78178485	rs6473015	-	intergenic_variant	A	C	429999	0.2719	0.031	0.003	3.20E-33
8	87568644	rs2304787	*CPNE3*	intron_variant	T	G	453732	0.7072	0.014	0.002	6.64E-09
8	116599199	rs2293889	*TRPS1*	intron_variant	T	G	456974	0.6152	-0.013	0.002	3.77E-09
8	117556270	rs4876662	-	intergenic_variant	A	G	458253	0.7781	-0.015	0.003	2.11E-08
8	120353267	rs2469997	-	intergenic_variant	G	C	449259	0.8287	0.018	0.003	1.16E-09
8	126490972	rs2954029	*RP11-136O12.2*	intron_variant	A	T	442592	0.4499	0.012	0.002	7.20E-08
8	130760850	rs4144738	*GSDMC*	missense_variant	A	G	458253	0.4968	-0.031	0.002	4.60E-44
8	130762291	rs77681114	*GSDMC*	synonymous_variant	G	A	436811	0.0436	-0.037	0.005	4.91E-12
8	135494742	rs3936152	*ZFAT*	intron_variant	C	T	447196	0.5713	0.014	0.002	1.46E-10
8	135614553	rs112892337	*ZFAT*	missense_variant	G	C	433868	0.0033	0.198	0.018	6.84E-27
8	135622851	rs75596750	*ZFAT*	missense_variant	G	A	447874	0.0008	0.255	0.036	7.05E-13
8	135637337	rs12680655	*ZFAT*	intron_variant	C	G	452126	0.4099	-0.029	0.002	2.95E-39
8	135649848	rs12541381	*ZFAT*	missense_variant	G	A	458253	0.2457	-0.026	0.003	1.40E-24

8	135669810	rs17778003	*ZFAT*	missense_variant	C	T	444823	0.0903	0.025	0.004	1.44E-10
8	144997927	rs7002002	*PLEC*	missense_variant	G	A	424515	0.3822	-0.018	0.003	4.82E-13
8	145001031	rs55895668	*PLEC*	missense_variant	T	C	432068	0.4369	-0.018	0.002	1.81E-13
8	145007187	rs11136336	*PLEC*	missense_variant	G	A	237121	0.3364	-0.018	0.003	7.92E-08
8	145011204	rs6993938	*PLEC*	synonymous_variant	A	G	432717	0.3669	-0.016	0.002	9.89E-11
8	145058986	rs11136343	*PARP10*	missense_variant	A	G	452416	0.3823	-0.015	0.002	7.91E-10
8	145059425	rs11136344	*PARP10*	missense_variant	T	C	437065	0.4259	-0.019	0.002	5.79E-15
9	34660864	rs11575580	*IL11RA*	missense_variant	C	T	458927	0.0145	-0.062	0.009	5.79E-13
9	78542286	rs11144688	*PCSK5*	intron_variant	G	A	454203	0.1143	-0.042	0.003	1.24E-34
9	85126163	rs7866939	*RP11-15B24.5*	intron_variant	T	C	441676	0.3477	0.012	0.002	9.33E-08
9	86617265	rs1982151	*RMI1*	missense_variant	A	G	458927	0.7192	-0.022	0.002	4.59E-20
9	89099362	rs353785	-	intergenic_variant	T	C	452209	0.5282	0.021	0.002	7.93E-22
9	90811182	rs2814828	-	regulatory_region_variant	T	C	458927	0.7467	-0.022	0.003	1.63E-18
9	90835726	rs2778031	-	regulatory_region_variant	T	C	437466	0.7158	-0.022	0.003	9.92E-17
9	90883630	rs10746839	-	intergenic_variant	A	G	456125	0.5357	-0.020	0.002	2.74E-19
9	94486321	rs10761129	*ROR2*	missense_variant	C	T	438159	0.6796	-0.015	0.002	3.47E-10
9	95284982	rs10120210	*ECM2*	missense_variant	T	G	357407	0.5532	-0.015	0.003	8.04E-09
9	95429120	rs9969804	*IPPK*	intron_variant	A	C	458927	0.5947	-0.018	0.002	1.82E-15
9	95555939	rs7868651	-	intergenic_variant	T	G	447870	0.5275	-0.015	0.002	8.25E-12
9	96893945	rs1257763	-	intergenic_variant	A	G	458927	0.9615	-0.047	0.005	7.91E-18
9	97369149	rs1769259	*FBP1*	missense_variant	C	T	458927	0.9456	-0.027	0.005	1.10E-08
9	98209594	rs357564	*PTCH1*	missense_variant	G	A	445644	0.3477	-0.036	0.002	6.79E-55
9	98231008	rs16909898	*PTCH1*	intron_variant	A	G	448114	0.0980	0.033	0.004	2.39E-19
9	98259703	rs10512248	*PTCH1*	intron_variant	T	G	453732	0.3404	0.031	0.002	1.56E-40
9	98319969	rs17370391	-	intergenic_variant	T	C	455178	0.1554	0.023	0.003	7.77E-15
9	98410405	rs10990303	*RP11-180I4.1*	upstream_gene_variant	C	T	457404	0.2345	0.031	0.003	2.43E-34
9	99280421	rs7852498	*CDC14B*	intron_variant	A	G	279789	0.3609	0.024	0.003	2.95E-16
9	99581568	rs34763627	*ZNF782*	missense_variant	T	C	424117	0.0909	0.026	0.004	5.59E-11
9	101748356	rs2075663	*COL15A1*	missense_variant	A	G	458253	0.4230	-0.015	0.002	5.11E-11
9	108925389	rs4452860	-	intergenic_variant	A	G	455451	0.2938	-0.022	0.002	1.34E-19
9	108936674	rs7861820	-	intergenic_variant	T	C	423643	0.5131	-0.014	0.002	1.29E-09
9	108967088	rs2090409	-	intergenic_variant	C	A	451124	0.3234	-0.022	0.002	2.11E-20
9	109132446	rs7048618	*RP11-308N19.1*	intron_variant	G	A	447196	0.6286	0.017	0.002	1.62E-13
9	109599046	rs7027110	-	intergenic_variant	G	A	456974	0.2235	0.026	0.003	2.35E-23
9	109632353	rs4743034	*ZNF462*	intron_variant	G	A	458253	0.2404	0.026	0.003	1.80E-23
9	111659483	rs2230793	*IKBKAP*	missense_variant	T	G	445502	0.2103	0.016	0.003	2.54E-08
9	111660851	rs2230792	*IKBKAP*	missense_variant	C	T	447196	0.2078	0.016	0.003	8.04E-09
9	113807082	rs1468758	-	intergenic_variant	C	T	456974	0.2384	-0.020	0.003	1.12E-15
9	119106881	rs7020782	*PAPPA*	missense_variant	C	A	372595	0.6723	0.016	0.003	2.54E-10
9	119122342	rs751543	*PAPPA*	intron_variant	C	T	407018	0.6944	0.024	0.003	6.46E-22
9	119134796	rs7869550	*PAPPA*	intron_variant	A	G	458253	0.1775	-0.033	0.003	4.09E-30
9	119232655	rs10817896	*ASTN2*	intron_variant	C	T	456730	0.2821	-0.017	0.002	5.38E-12
9	124422403	rs7025486	*DAB2IP*	intron_variant	G	A	456974	0.2698	0.016	0.002	9.73E-11
9	133464084	rs7466269	*FUBP3*	intron_variant	A	G	447440	0.3475	-0.029	0.002	1.70E-36
9	136996067	rs28473627	*WDR5*	upstream_gene_variant	A	G	447196	0.5842	-0.013	0.002	3.92E-09
9	139110654	rs12684650	*QSOX2*	splice_region_variant	C	T	458253	0.2794	-0.031	0.002	1.65E-36
9	139111870	rs7849585	*QSOX2*	intron_variant	G	T	192874	0.3191	0.028	0.004	2.26E-14
9	139121740	rs12338076	*QSOX2*	intron_variant	A	C	429735	0.3622	0.027	0.002	3.21E-29
9	139323311	rs8413	*INPP5E*	3_prime_UTR_variant	T	C	416549	0.4054	0.013	0.002	5.11E-08
9	139368953	rs3812594	*SEC16A*	missense_variant	G	A	447189	0.2436	0.020	0.003	1.10E-13
10	4963327	rs12774134	*AKR1C2*	downstream_gene_variant	C	T	369829	0.1230	-0.034	0.004	4.36E-21
10	12918764	rs7909670	-	intergenic_variant	C	T	356961	0.4372	-0.018	0.002	1.49E-13
10	22839628	rs2230469	*PIP4K2A*	missense_variant	T	C	442597	0.2940	0.013	0.002	6.25E-08
10	63723577	rs10821936	*ARID5B*	intron_variant	C	T	457648	0.6709	-0.012	0.002	1.39E-07
10	69926334	rs10823148	*MYPN*	missense_variant	C	G	450707	0.4847	0.016	0.002	2.57E-11
10	69933921	rs10997975	*MYPN*	missense_variant	G	A	458927	0.4666	0.018	0.002	1.94E-14
10	69933969	rs7916821	*MYPN*	missense_variant	G	A	458927	0.4649	0.018	0.002	1.54E-14
10	69959242	rs7079481	*MYPN*	missense_variant	C	A	349595	0.4659	0.015	0.003	1.02E-08
10	69991853	rs7916697	*RP11-153K11.3*	5_prime_UTR_variant	A	G	454406	0.7070	0.015	0.003	3.56E-09
10	70000881	rs1900004	*RP11-153K11.3*	intron_variant	C	T	453732	0.2833	-0.015	0.003	8.42E-09
10	70011838	rs3858145	-	intergenic_variant	A	G	458927	0.2899	-0.015	0.003	1.06E-09
10	70019371	rs12571093	*KRT19P4*	upstream_gene_variant	G	A	457648	0.1635	-0.019	0.003	9.17E-10
10	70044031	rs4142048	*PBLD*	missense_variant	T	C	409992	0.2205	-0.017	0.003	7.30E-09
10	70332580	rs10823229	*TET1*	missense_variant	A	G	458927	0.3548	0.017	0.002	2.57E-13
10	70332672	rs12773594	*TET1*	missense_variant	T	A	452800	0.1702	-0.020	0.003	1.91E-11
10	70332862	rs12221107	*TET1*	missense_variant	C	T	399879	0.0961	-0.032	0.004	3.21E-15
10	70405539	rs16925541	*TET1*	missense_variant	A	G	457415	0.0890	-0.027	0.004	2.59E-12
10	70405855	rs3998860	*TET1*	missense_variant	A	G	455685	0.7918	0.018	0.003	1.58E-10
10	79580976	rs41274586	*DLG5*	missense_variant	G	A	449393	0.0151	-0.061	0.009	7.74E-13
10	89336834	rs7914810	-	intergenic_variant	A	G	457404	0.4818	-0.012	0.002	1.75E-07
10	93032943	rs2631681	*PCGF5*	intron_variant	C	T	457404	0.3338	0.024	0.002	6.43E-25
10	99969568	rs11189513	*R3HCC1L*	missense_variant	A	G	410398	0.3133	0.016	0.003	5.21E-11
10	100017453	rs1983864	*RP11-34A14.3*	missense_variant	T	G	458253	0.3393	0.017	0.002	4.27E-13
10	101805442	rs11599750	*CPN1*	intron_variant	C	T	458253	0.3690	-0.016	0.002	1.48E-11
10	101912064	rs2862954	*ERLIN1*	missense_variant	T	C	455011	0.4167	-0.013	0.002	4.33E-08
10	102744331	rs11591349	*MRPL43*	missense_variant	A	T	408425	0.4245	0.017	0.002	4.97E-13
10	104269217	rs2281880	*SUFU*	intron_variant	G	A	456974	0.5146	0.023	0.002	1.30E-24
10	104500659	rs10786706	*SFXN2*	3_prime_UTR_variant	C	T	434445	0.4679	0.018	0.002	3.10E-15
10	104572963	rs284860	*WBP1L*	missense_variant	T	C	455880	0.5857	-0.012	0.002	7.41E-08
10	104775908	rs7914558	*CNNM2*	intron_variant	G	A	456974	0.4106	0.013	0.002	5.33E-08
10	105659826	rs2487999	*OBFC1*	missense_variant	T	C	458253	0.8954	-0.020	0.004	3.20E-08
10	114169276	rs3736946	*RP11-324O2.3*	missense_variant	A	G	458253	0.1013	-0.019	0.004	1.52E-07
10	121429633	rs2234962	*BAG3*	missense_variant	T	C	458253	0.1989	-0.014	0.003	1.79E-07
10	124165615	rs6585827	*PLEKHA1*	intron_variant	G	A	458253	0.4916	0.016	0.002	1.46E-12
10	124189197	rs1045216	*PLEKHA1*	missense_variant	A	G	361622	0.6352	0.016	0.003	3.26E-09
10	124214448	rs10490924	*ARMS2*	missense_variant	G	T	361294	0.2248	0.017	0.003	2.37E-08
11	1977552	rs12812	*MRPL23*	missense_variant	G	A	437065	0.1471	0.019	0.003	1.98E-09
11	2169014	rs10770125	*IGF2-AS*	missense_variant	A	G	437065	0.4669	0.020	0.002	5.26E-19
11	2766282	rs2237878	*KCNQ1*	intron_variant	G	A	457648	0.1016	0.029	0.004	1.72E-16
11	2810731	rs2237886	*KCNQ1*	intron_variant	C	T	428485	0.1009	0.044	0.004	2.97E-33
11	8252853	rs110419	*LMO1*	intron_variant	A	G	424117	0.4943	-0.016	0.002	3.16E-12
11	9537904	rs10743108	*ZNF143*	missense_variant	G	C	282948	0.9415	0.038	0.007	1.51E-07
11	11986061	rs3206824	*DKK3*	missense_variant	T	C	411207	0.7448	0.016	0.003	1.46E-09
11	12698040	rs7926971	*TEAD1*	intron_variant	A	G	458253	0.4491	0.019	0.002	6.44E-18
11	13293905	rs900145	*ARNTL*	upstream_gene_variant	C	T	338771	0.6771	-0.016	0.003	5.98E-09

11	17316029	rs1330	*NUCB2*	intron_variant	C	T	444198	0.3387	0.014	0.002	9.37E-10
11	17351683	rs757081	*NUCB2*	missense_variant	C	G	420815	0.3171	0.017	0.003	6.00E-12
11	18632984	rs10128711	*SPTY2D1*	intron_variant	T	C	364993	0.6934	-0.021	0.003	5.87E-14
11	18645843	rs11024739	*SPTY2D1*	intron_variant	C	A	441345	0.6873	-0.020	0.002	4.17E-15
11	27016360	rs138273386	*FIBIN*	missense_variant	G	A	455040	0.0037	-0.118	0.017	6.26E-12
11	45935689	rs35214605	*PEX16*	missense_variant	C	G	399739	0.0240	-0.039	0.007	1.91E-07
11	46052575	rs16938437	*PHF21A*	intron_variant	C	T	453761	0.1009	-0.030	0.004	1.68E-16
11	47290984	rs1449627	*MADD*	5_prime_UTR_variant	T	G	443983	0.3518	0.014	0.003	3.24E-08
11	47298360	rs326214	*MADD*	synonymous_variant	G	A	429182	0.6380	-0.014	0.003	4.71E-08
11	47354787	rs1052373	*MADD*	synonymous_variant	C	T	428485	0.3519	0.015	0.003	2.44E-08
11	47370041	rs3729989	*MYBPC3*	missense_variant	T	C	455040	0.1173	0.020	0.004	3.95E-08
11	47454701	rs10742805	*RAPSN*	downstream_gene_variant	A	G	441610	0.6950	-0.019	0.003	7.71E-13
11	47640429	rs1064608	*Y_RNA*	missense_variant	G	C	374444	0.3259	-0.025	0.003	1.91E-19
11	47650993	rs3817334	*MTCH2*	intron_variant	C	T	418369	0.3900	-0.020	0.003	6.97E-15
11	47663049	rs10838738	*MTCH2*	intron_variant	A	G	455040	0.3309	-0.024	0.003	3.08E-21
11	61557803	rs102275	*FEN1*	non_coding_transcript_exon_variant	T	C	454288	0.3660	-0.015	0.003	2.02E-09
11	61569830	rs174546	*FADS1*	3_prime_UTR_variant	C	T	456419	0.3178	-0.017	0.003	1.40E-10
11	61570783	rs174547	*FADS1*	intron_variant	T	C	455140	0.3178	-0.017	0.003	1.77E-10
11	61571478	rs174550	*FADS1*	5_prime_UTR_variant	T	C	455140	0.3178	-0.017	0.003	1.61E-10
11	61597212	rs174570	*FADS2*	intron_variant	C	T	420801	0.1413	-0.020	0.003	3.19E-09
11	61597972	rs1535	*FADS2*	intron_variant	A	G	456419	0.3242	-0.017	0.003	6.37E-11
11	61609750	rs174583	*FADS2*	intron_variant	C	T	448670	0.3423	-0.015	0.003	7.82E-09
11	64990041	rs514076	*SLC22A20*	non_coding_transcript_exon_variant	G	C	446691	0.7412	0.017	0.003	1.61E-10
11	65319751	rs11545200	*LTBP3*	missense_variant	G	A	387566	0.0630	-0.029	0.005	8.80E-09
11	65336819	rs3782089	*SSSCA1-AS1*	non_coding_transcript_exon_variant	C	T	453732	0.0698	-0.023	0.004	1.10E-07
11	65386206	rs1193851	*MAP3K11*	missense_variant	C	G	440464	0.3181	-0.014	0.002	1.07E-08
11	65546857	rs610037	*AP5B1*	synonymous_variant	A	C	446618	0.5096	-0.012	0.002	1.95E-07
11	65715204	rs71455793	*TSGA10IP*	missense_variant	G	A	458927	0.0336	-0.058	0.006	1.75E-22
11	65727301	rs491973	*SART1*	missense_variant	A	G	456554	0.4433	-0.015	0.002	9.05E-12
11	66083591	rs150281243	*CD248*	missense_variant	G	A	458927	0.0076	-0.066	0.012	6.49E-08
11	66191859	rs71457718	*NPAS4*	missense_variant	C	A	453210	0.0070	-0.085	0.013	1.30E-11
11	66272237	rs2305535	*CTD-3074O7.11*	missense_variant	G	A	458927	0.2396	0.016	0.003	6.62E-09
11	66297363	rs3816492	*BBS1*	synonymous_variant	C	T	439830	0.2310	0.018	0.003	4.16E-10
11	66826160	rs7112925	*RHOD*	intron_variant	C	T	457648	0.3614	-0.021	0.002	1.94E-19
11	66832528	rs11227673	*RHOD*	intron_variant	G	A	447020	0.4681	-0.015	0.002	7.28E-11
11	68174189	rs4988321	*LRP5*	missense_variant	G	A	458927	0.0437	-0.035	0.005	1.45E-11
11	68201295	rs3736228	*LRP5*	missense_variant	C	T	436922	0.1313	-0.024	0.003	1.96E-13
11	68855363	rs3829241	*MIR3164*	missense_variant	G	A	458927	0.3499	-0.015	0.002	2.53E-10
11	70007354	rs201870990	*ANO1*	missense_variant	G	A	458356	0.0061	0.070	0.013	1.06E-07
11	75282052	rs634552	*SERPINH1*	intron_variant	T	G	457648	0.8373	-0.047	0.003	7.16E-57
11	85436352	rs641393	*SYTL2*	missense_variant	G	A	458927	0.6184	0.012	0.002	1.22E-07
11	94533444	rs138059525	*AMOTL1*	missense_variant	G	A	449393	0.0081	-0.098	0.012	6.51E-17
11	94731822	rs151327191	*KDM4D*	missense_variant	C	G	415677	0.0081	-0.067	0.012	4.32E-08
11	116973929	rs12269901	*AP000936.4*	intron_variant	G	C	451352	0.3306	-0.014	0.002	1.05E-08
11	118574675	rs494459	-	intergenic_variant	C	T	455011	0.3985	0.019	0.002	2.79E-16
11	128586155	rs654723	*FLI1*	intron_variant	C	A	378302	0.6019	0.018	0.002	7.23E-13
12	371410	rs527118	*RP11-283I3.4*	intron_variant	T	C	436216	0.7967	-0.016	0.003	4.71E-08
12	4374373	rs11063069	*CCND2-AS2*	intron_variant	A	G	455178	0.2043	-0.014	0.003	1.02E-07
12	11855624	rs2187642	*ETV6*	intron_variant	A	C	442868	0.5981	-0.023	0.002	1.27E-22
12	11855773	rs2856321	*ETV6*	intron_variant	G	A	442868	0.6193	-0.025	0.002	8.86E-27
12	14488914	rs6488674	-	intergenic_variant	T	G	408012	0.5267	-0.015	0.002	4.26E-10
12	14587301	rs3213764	*ATF7IP*	missense_variant	A	G	458253	0.4716	0.016	0.002	5.60E-12
12	20857467	rs10770705	*SLCO1C1*	intron_variant	A	C	435827	0.6887	-0.024	0.002	2.50E-24
12	20905250	rs6487138	*SLCO1C1*	missense_variant	C	T	435417	0.5241	0.013	0.002	7.30E-09
12	28412372	rs11049488	*CCDC91*	missense_variant	G	A	447870	0.2685	-0.031	0.003	7.54E-35
12	28534415	rs2638953	*CCDC91*	intron_variant	G	C	337234	0.6944	0.025	0.003	8.74E-20
12	28605426	rs10771427	*CCDC91*	missense_variant	G	A	458927	0.7491	-0.014	0.003	6.48E-08
12	28722756	rs10843206	*CCDC91*	intron_variant	C	T	447870	0.5094	0.017	0.002	5.58E-14
12	50901882	rs10876041	*DIP2B*	intron_variant	T	C	422791	0.6178	-0.014	0.002	3.69E-09
12	56636975	rs59626664	*ANKRD52*	missense_variant	C	G	322309	0.0592	0.036	0.006	7.63E-10
12	56660905	rs60542959	*COQ10A*	start_lost	G	T	391956	0.0580	0.034	0.005	1.18E-10
12	56737973	rs2066808	*STAT2*	intron_variant	A	G	434008	0.0889	0.027	0.004	9.64E-10
12	56740682	rs2066807	*STAT2*	missense_variant	C	G	426750	0.0589	0.035	0.005	4.10E-12
12	57146069	rs2277339	*PRIM1*	missense_variant	T	G	458927	0.1135	-0.029	0.003	6.30E-18
12	58015494	rs923828	*ARHGEF25*	missense_variant	G	A	455935	0.3896	0.013	0.002	1.10E-08
12	58062667	rs10876993	-	intergenic_variant	C	T	447870	0.6189	0.014	0.002	1.54E-09
12	58087737	rs4760168	*OS9*	upstream_gene_variant	T	G	422012	0.6270	0.013	0.002	9.12E-08
12	58138971	rs147996581	*TSPAN31*	missense_variant	G	A	443412	0.0025	-0.114	0.022	1.28E-07
12	58162739	rs703842	*METTL21B*	missense_variant	A	G	376583	0.3390	-0.019	0.003	1.41E-12
12	58222672	rs4760332	*CTDSP2*	intron_variant	C	A	443982	0.3307	-0.018	0.002	4.43E-13
12	66351826	rs1351394	*HMGA2*	3_prime_UTR_variant	T	C	458927	0.5363	-0.050	0.002	1.20E-108
12	66358347	rs1042725	*HMGA2*	3_prime_UTR_variant	C	T	458927	0.5042	-0.049	0.002	1.26E-105
12	66359752	rs8756	*HMGA2*	3_prime_UTR_variant	C	A	458927	0.5407	-0.051	0.002	1.21E-110
12	66364509	rs12424086	*HMGA2*	downstream_gene_variant	T	C	458927	0.2008	-0.047	0.003	7.37E-67
12	66394664	rs4026608	-	intergenic_variant	C	T	458927	0.6139	0.022	0.002	7.54E-24
12	66546100	rs8793	*TMBIM4*	missense_variant	A	G	458927	0.4309	0.014	0.002	8.53E-11
12	69140339	rs61743810	*SLC35E3*	missense_variant	G	C	452800	0.0206	-0.039	0.007	8.58E-08
12	69827658	rs10748128	-	intergenic_variant	G	T	458927	0.3786	0.032	0.002	4.71E-44
12	69828681	rs11177669	-	intergenic_variant	G	A	457648	0.2752	0.029	0.002	2.49E-33
12	90231386	rs17783015	-	intergenic_variant	C	T	455275	0.1415	-0.020	0.003	5.42E-10
12	93976954	rs3825199	*SOCS2*	3_prime_UTR_variant	A	G	446151	0.2183	0.040	0.003	2.67E-52
12	95927762	rs3812813	*USP44*	missense_variant	T	C	458927	0.5655	-0.013	0.002	3.31E-09
12	102108345	rs3205421	*CHPT1*	missense_variant	T	C	437065	0.2830	0.016	0.002	2.92E-10
12	102368065	rs7978999	*DRAM1*	intron_variant	T	C	456730	0.4670	-0.021	0.002	1.14E-21
12	102513531	rs2292303	*PARPBP*	intron_variant	G	C	451352	0.0262	-0.048	0.007	2.06E-12
12	102799598	rs5742692	*IGF1*	intron_variant	A	G	453732	0.0345	-0.037	0.006	5.03E-10
12	103077198	rs7296248	-	intergenic_variant	C	T	421920	0.5088	0.014	0.002	1.38E-10
12	103152029	rs12820008	-	intergenic_variant	C	A	432300	0.3193	-0.013	0.002	1.57E-07
12	104354173	rs11612024	*C12orf73*	intron_variant	C	T	447196	0.3307	0.015	0.002	1.07E-10
12	104408832	rs117801489	*GLT8D2*	missense_variant	T	C	458253	0.0148	0.053	0.009	6.48E-10
12	105606172	rs1196761	*APPL2*	intron_variant	G	A	444823	0.5219	0.011	0.002	1.87E-07
12	107174646	rs10861661	*RIC8B*	intron_variant	A	C	417827	0.2342	-0.018	0.003	7.27E-12
12	117383320	rs4076700	*FBXW8*	missense_variant	G	A	442868	0.8117	0.016	0.003	5.22E-08
12	121756084	rs13141	*ANAPC5*	missense_variant	G	A	437065	0.0080	-0.081	0.012	1.23E-11
12	122494809	rs11835818	*BCL7A*	intron_variant	T	C	445917	0.4820	0.017	0.002	8.22E-14

12	122674780	rs11060094	*LRRC43*	missense_variant	C	A	458253	0.1933	-0.017	0.003	2.23E-09
12	122689181	rs7136356	*DIABLO*	missense_variant	C	G	401657	0.3274	0.018	0.002	1.18E-12
12	122864920	rs34292795	*CLIP1*	missense_variant	G	A	448719	0.0237	0.046	0.007	4.97E-11
12	123102921	rs11837038	*KNTC1*	missense_variant	T	G	457940	0.1002	0.024	0.004	1.85E-10
12	123447928	rs4275659	*ABCB9*	intron_variant	T	C	431811	0.6733	-0.014	0.003	5.88E-08
12	123575742	rs1727307	*PITPNM2*	non_coding_transcript_exon_variant	A	G	458253	0.7008	-0.015	0.002	2.29E-09
12	123757861	rs1109559	*CDK2AP1*	upstream_gene_variant	G	A	441345	0.6542	-0.017	0.003	4.08E-11
12	123806219	rs1060105	*SBNO1*	missense_variant	C	T	458253	0.1940	0.033	0.003	1.19E-31
12	123873242	rs28533432	*SETD8*	non_coding_transcript_exon_variant	C	T	456730	0.6707	-0.018	0.002	1.76E-13
12	123921264	rs28434767	*RILPL2*	5_prime_UTR_variant	G	T	419654	0.2748	0.014	0.003	1.57E-07
12	124801226	rs1809889	*FAM101A*	downstream_gene_variant	T	C	405745	0.6926	-0.025	0.003	2.51E-23
12	124826462	rs2229840	*NCOR2*	missense_variant	C	T	458253	0.1601	0.026	0.003	3.77E-19
13	21189941	rs2442455	*RNU2-7P*	missense_variant	G	A	458253	0.1460	0.019	0.003	1.50E-09
13	21562832	rs2770928	*LATS2*	missense_variant	C	T	458253	0.8652	0.024	0.003	2.41E-14
13	33147548	rs7332115	-	intergenic_variant	T	G	455275	0.3619	0.015	0.002	1.51E-10
13	33693837	rs9315204	*STARD13*	intron_variant	C	T	443986	0.2245	-0.015	0.003	2.17E-08
13	50835715	rs2762051	*DLEU1*	intron_variant	C	T	455275	0.1727	0.030	0.003	6.47E-25
13	50842259	rs2066674	*DLEU1*	intron_variant	G	A	457404	0.0380	0.069	0.006	1.90E-35
13	51105334	rs3118905	*DLEU1*	intron_variant	G	A	444226	0.2527	-0.044	0.003	6.79E-62
13	51106555	rs1239947	*DLEU1*	intron_variant	C	T	453732	0.6583	-0.020	0.002	3.04E-17
13	51111355	rs3116602	*DLEU1*	intron_variant	T	G	444123	0.1911	-0.051	0.003	3.44E-65
13	51116901	rs3118914	*DLEU1*	intron_variant	G	T	457648	0.1923	-0.051	0.003	1.02E-68
13	51221618	rs797486	*AC007304.1*	intron_variant	C	A	456125	0.8696	-0.020	0.003	5.41E-10
13	80717156	rs1359790	-	intergenic_variant	G	A	454406	0.2597	0.016	0.002	2.57E-10
13	92015977	rs8002779	-	intergenic_variant	G	A	433651	0.5769	-0.023	0.002	2.81E-23
13	92024574	rs7319045	-	intergenic_variant	A	G	457648	0.6001	-0.024	0.002	2.20E-27
14	23313633	rs17880989	*MMP14*	missense_variant	G	A	448822	0.0226	0.040	0.007	2.15E-08
14	23761094	rs12050260	*PPP1R3E*	intron_variant	T	C	413020	0.6235	0.016	0.002	5.87E-11
14	24707479	rs34354104	*GMPR2*	missense_variant	G	A	458927	0.0417	0.043	0.005	1.08E-15
14	24771285	rs4280164	*LTB4R2*	missense_variant	G	A	458927	0.1905	0.022	0.003	6.37E-15
14	24830850	rs1950500	*NFATC4*	upstream_gene_variant	T	C	455011	0.7028	-0.027	0.002	1.45E-28
14	50901768	rs17780143	*MAP4K5*	missense_variant	G	A	458927	0.0536	0.025	0.005	1.67E-07
14	55265828	rs8022503	-	intergenic_variant	T	C	457404	0.5498	0.018	0.002	5.31E-16
14	60789176	rs4901977	*CTD-2568P8.1*	upstream_gene_variant	C	T	457404	0.3260	0.021	0.002	1.44E-17
14	60903757	rs1254319	*C14orf39*	missense_variant	G	A	447870	0.3196	0.028	0.002	4.50E-31
14	60932752	rs12586711	*C14orf39*	missense_variant	G	A	447541	0.2017	0.018	0.003	4.22E-10
14	60976537	rs33912345	*C14orf39*	missense_variant	C	A	443542	0.5633	-0.035	0.002	4.08E-47
14	61072875	rs10483727	*RP11-1042B17.2*	upstream_gene_variant	T	C	443542	0.5652	-0.034	0.002	7.06E-47
14	68753593	rs911263	*RAD51B*	intron_variant	C	T	420401	0.6850	0.014	0.003	4.88E-08
14	68785077	rs8017304	*RAD51B*	intron_variant	G	A	457404	0.6079	0.014	0.002	1.94E-09
14	70633411	rs41286548	*SLC8A3*	missense_variant	C	T	449393	0.0182	-0.054	0.008	6.75E-12
14	74990746	rs862034	*LTBP2*	intron_variant	A	G	455685	0.6358	0.027	0.002	3.58E-34
14	75322794	rs8014204	*PROX2*	3_prime_UTR_variant	G	A	437739	0.5683	0.013	0.002	3.61E-08
14	75347585	rs10083386	*DLST*	upstream_gene_variant	C	A	436216	0.4736	0.014	0.002	7.45E-10
14	76156609	rs2303345	*TTLL5*	missense_variant	C	T	326725	0.6382	-0.015	0.003	5.75E-08
14	79945162	rs10146997	*NRXN3*	intron_variant	A	G	457648	0.2149	0.014	0.003	5.28E-08
14	92427222	rs7153027	-	intergenic_variant	A	C	429999	0.4236	-0.029	0.002	2.55E-35
14	92441066	rs1051340	*TRIP11*	missense_variant	C	T	456554	0.3220	-0.023	0.002	3.06E-22
14	92459958	rs8007661	*TRIP11*	intron_variant	C	T	457648	0.4822	-0.026	0.002	1.11E-30
14	92485881	rs7155279	*TRIP11*	intron_variant	G	T	361532	0.3748	-0.028	0.003	2.02E-28
14	92548785	rs1048755	*ATXN3*	missense_variant	C	T	458927	0.2578	-0.026	0.003	6.86E-25
14	94844947	rs28929474	*SERPINA1*	missense_variant	C	T	440722	0.0156	0.122	0.009	3.01E-45
14	101349454	rs41286560	*MIR432*	missense_variant	G	T	455897	0.0213	-0.050	0.007	4.39E-12
14	102792631	rs7158139	*ZNF839*	missense_variant	G	A	453488	0.2200	-0.016	0.003	1.43E-08
15	41476209	rs522063	*EXD1*	missense_variant	T	C	458927	0.7457	0.014	0.003	3.97E-08
15	41689166	rs3204853	*NDUFAF1*	missense_variant	C	A	388029	0.2357	-0.016	0.003	6.29E-08
15	41689232	rs1899	*NDUFAF1*	missense_variant	C	T	445265	0.2448	-0.017	0.003	3.06E-10
15	50932357	rs56170748	*TRPM7*	intron_variant	C	T	457404	0.5035	0.012	0.002	5.31E-08
15	51217361	rs2306331	*AP4E1*	missense_variant	T	C	447020	0.4492	0.016	0.002	1.64E-13
15	51530495	rs16964211	*CYP19A1*	intron_variant	G	A	314486	0.0873	-0.043	0.005	1.24E-19
15	51569410	rs2305707	*CYP19A1*	non_coding_transcript_exon_variant	A	G	437739	0.1788	-0.023	0.003	3.36E-15
15	60781513	rs3743266	*RORA*	3_prime_UTR_variant	T	C	432544	0.3109	-0.014	0.002	1.46E-08
15	62259637	rs3784634	*VPS13C*	missense_variant	C	T	332654	0.6061	0.016	0.003	2.24E-08
15	62332980	rs17271305	*VPS13C*	intron_variant	A	G	449393	0.3713	-0.014	0.002	1.20E-08
15	62380259	rs7178424	*NPM1P47*	upstream_gene_variant	C	T	452807	0.4388	-0.019	0.002	1.56E-15
15	65916527	rs3743171	*SLC24A1*	missense_variant	A	T	431612	0.2002	0.019	0.003	1.57E-11
15	70048157	rs10152591	-	regulatory_region_variant	A	C	403244	0.0930	-0.040	0.004	7.20E-24
15	70364352	rs975210	*TLE3*	intron_variant	G	A	452883	0.1704	0.033	0.003	1.09E-30
15	72161403	rs12902421	*MYO9A*	intron_variant	T	C	396842	0.0165	0.059	0.009	1.11E-11
15	72454690	rs71395065	*GRAMD2*	missense_variant	A	G	445813	0.0056	0.101	0.014	4.86E-13
15	72462255	rs34815962	*GRAMD2*	missense_variant	C	T	433651	0.0174	0.063	0.008	2.07E-14
15	72511415	rs3759901	*PKM*	missense_variant	G	A	340406	0.0162	0.060	0.010	4.25E-10
15	74229065	rs893817	*LOXL1*	intron_variant	G	A	437739	0.6514	-0.020	0.002	1.69E-18
15	74328116	rs743580	*PML*	missense_variant	A	G	458927	0.5087	-0.012	0.002	1.34E-08
15	74328141	rs743581	*PML*	missense_variant	G	T	427725	0.3648	-0.017	0.002	1.53E-12
15	74336633	rs5742915	*PML*	missense_variant	T	C	458927	0.4064	0.029	0.002	5.73E-38
15	74487969	rs971756	*STRA6*	missense_variant	A	T	443266	0.1857	-0.017	0.003	2.23E-09
15	74635368	rs6161	*CYP11A1*	missense_variant	C	T	426102	0.0034	0.097	0.018	6.59E-08
15	75755467	rs4886707	*PTPN9*	downstream_gene_variant	C	T	443986	0.2753	0.018	0.003	3.05E-12
15	77335891	rs11636648	*TSPAN3*	3_prime_UTR_variant	C	T	432974	0.6183	-0.014	0.002	6.28E-09
15	84286492	rs2562784	*SH3GL3*	intron_variant	A	G	455685	0.2469	0.029	0.003	3.56E-30
15	84315884	rs2554380	-	intergenic_variant	C	T	430142	0.8103	0.034	0.003	4.41E-31
15	84327771	rs2730081	*ADAMTSL3*	intron_variant	T	C	434297	0.5915	0.013	0.002	1.81E-08
15	84488636	rs4483821	*ADAMTSL3*	missense_variant	A	G	458023	0.4914	0.029	0.002	2.21E-37
15	84539619	rs4144691	*ADAMTSL3*	missense_variant	C	G	437045	0.7999	0.018	0.003	2.14E-10
15	84568158	rs10906982	*ADAMTSL3*	intron_variant	T	A	276680	0.5173	0.039	0.003	4.75E-36
15	84573041	rs7183263	*ADAMTSL3*	intron_variant	T	G	457648	0.5487	0.047	0.002	5.60E-90
15	84580582	rs11259936	*ADAMTSL3*	intron_variant	A	C	449393	0.5483	0.047	0.002	2.60E-88
15	84582124	rs4842838	*ADAMTSL3*	missense_variant	G	T	456554	0.5487	0.047	0.002	1.83E-89
15	84611367	rs34047645	*ADAMTSL3*	missense_variant	G	C	424263	0.1516	-0.034	0.003	3.50E-25
15	84639350	rs2277849	*ADAMTSL3*	missense_variant	C	T	433651	0.2621	-0.021	0.003	1.37E-16
15	84706461	rs950169	*ADAMTSL3*	missense_variant	C	T	437739	0.2510	0.025	0.003	1.20E-20
15	85149771	rs2271433	*ZSCAN2*	missense_variant	G	T	458927	0.8631	0.018	0.003	6.45E-08
15	85200520	rs1051168	*NMB*	missense_variant	G	T	458927	0.2479	0.015	0.003	3.10E-08
15	85635890	rs8032301	*PDE8A*	intron_variant	T	C	457404	0.4496	0.013	0.002	9.80E-10

15	86123170	rs745191	*AKAP13*	missense_variant	G	T	458927	0.2564	0.016	0.003	1.53E-09
15	86123364	rs7177107	*AKAP13*	missense_variant	G	A	458927	0.1974	-0.018	0.003	4.12E-10
15	86278479	rs16943741	*AKAP13*	intron_variant	A	G	449393	0.5127	-0.014	0.002	1.92E-10
15	89345947	rs8028537	*ACAN*	upstream_gene_variant	A	G	436216	0.5056	0.029	0.002	1.10E-37
15	89359689	rs8041863	*ACAN*	intron_variant	T	A	430838	0.5008	0.029	0.002	2.34E-37
15	89386652	rs34949187	*ACAN*	missense_variant	G	A	426926	0.1602	-0.027	0.003	3.58E-18
15	89388905	rs16942341	*ACAN*	synonymous_variant	C	T	457279	0.0364	-0.100	0.006	5.93E-69
15	89390513	rs117116488	*ACAN*	missense_variant	C	T	458927	0.0104	-0.099	0.010	2.52E-22
15	89392786	rs34616796	*ACAN*	missense_variant	G	A	386292	0.0067	-0.098	0.015	5.41E-11
15	89398553	rs35430524	*ACAN*	missense_variant	C	A	447870	0.0978	0.029	0.004	1.90E-15
15	89398605	rs938608	*ACAN*	missense_variant	G	T	423064	0.6059	-0.021	0.002	1.97E-18
15	89398631	rs938609	*ACAN*	missense_variant	T	A	417688	0.6013	-0.017	0.002	6.41E-12
15	89400339	rs2882676	*ACAN*	missense_variant	A	C	388398	0.5981	-0.019	0.003	4.83E-14
15	89400680	rs28407189	*ACAN*	missense_variant	A	G	458927	0.0388	-0.091	0.006	6.33E-60
15	89401109	rs4932439	*ACAN*	missense_variant	A	G	445349	0.8085	-0.036	0.003	5.28E-35
15	89401362	rs34124958	*ACAN*	missense_variant	G	T	431314	0.0060	-0.099	0.015	3.78E-11
15	89401814	rs34546634	*ACAN*	missense_variant	G	A	436216	0.0066	-0.096	0.014	1.03E-11
15	89401989	rs35061438	*ACAN*	missense_variant	C	T	399758	0.0064	-0.095	0.015	2.09E-10
15	89402051	rs1042630	*ACAN*	missense_variant	A	G	458927	0.7251	-0.014	0.003	2.29E-08
15	89415247	rs3817428	*ACAN*	missense_variant	C	G	452026	0.2424	-0.038	0.003	6.34E-48
15	89424870	rs141308595	*HAPLN3*	missense_variant	G	T	452527	0.0008	-0.250	0.035	1.11E-12
15	89450587	rs1878326	*MFGE8*	missense_variant	G	T	456554	0.6367	-0.018	0.002	1.65E-15
15	89804043	rs17803620	*FANCI*	missense_variant	C	T	437739	0.3629	-0.014	0.002	1.52E-09
15	89902032	rs4932217	*CTD-2335A18.2*	upstream_gene_variant	A	C	435181	0.4451	-0.012	0.002	9.84E-08
15	94570578	rs899609	*LINC01581*	intron_variant	T	C	457404	0.5738	0.013	0.002	5.17E-09
15	99194896	rs2871865	*IGF1R*	intron_variant	C	G	452800	0.1295	-0.053	0.003	4.88E-57
15	99212485	rs1319869	*IGF1R*	intron_variant	G	T	454162	0.8531	0.033	0.003	4.40E-23
15	100514614	rs2573652	*ADAMTS17*	missense_variant	T	C	458253	0.6781	0.028	0.002	3.84E-33
15	100516472	rs11634977	*ADAMTS17*	non_coding_transcript_exon_variant	G	A	395566	0.6458	0.025	0.003	4.58E-22
15	100537494	rs12900132	*ADAMTS17*	intron_variant	C	T	351245	0.5638	0.019	0.003	3.48E-13
15	100687967	rs4246302	*ADAMTS17*	intron_variant	A	G	447196	0.3019	0.020	0.002	1.28E-16
15	100692953	rs72755233	*ADAMTS17*	missense_variant	G	A	454504	0.0949	-0.091	0.004	6.17E-133
15	100786271	rs4533267	*ADAMTS17*	intron_variant	A	G	445067	0.7047	-0.031	0.002	1.26E-37
15	100821576	rs7496668	*ADAMTS17*	missense_variant	G	A	458253	0.3636	-0.019	0.002	1.12E-16
15	100843884	rs8041080	*ADAMTS17*	intron_variant	C	T	391855	0.4694	-0.018	0.002	1.57E-14
15	101717888	rs62621399	*CHSY1*	missense_variant	C	T	458253	0.1306	0.024	0.003	7.90E-14
15	101718239	rs62621400	*CHSY1*	missense_variant	C	G	452126	0.0611	-0.057	0.005	9.11E-37
16	624114	rs2071979	*PIGQ*	missense_variant	A	G	413020	0.4420	0.020	0.002	7.94E-17
16	633125	rs1045277	*PIGQ*	missense_variant	T	C	408580	0.4457	0.020	0.002	1.50E-16
16	675680	rs763014	*RAB40C*	non_coding_transcript_exon_variant	T	C	325002	0.4510	0.022	0.003	7.00E-16
16	701656	rs11642546	*LA16c-349E10.1*	missense_variant	C	T	448925	0.2680	0.023	0.003	9.80E-18
16	705360	rs3803697	*LA16c-349E10.1*	missense_variant	T	C	445643	0.4329	0.017	0.002	1.69E-12
16	708275	rs45613635	*LA16c-349E10.1*	missense_variant	C	A	404345	0.2618	0.024	0.003	2.99E-17
16	709001	rs4984906	*LA16c-349E10.1*	missense_variant	C	A	440929	0.4282	0.017	0.002	2.99E-11
16	711905	rs2301426	*WDR90*	synonymous_variant	A	G	398836	0.4316	0.017	0.003	6.33E-11
16	722331	rs3177338	*RHOT2*	missense_variant	C	T	354113	0.4230	0.017	0.003	1.42E-10
16	774692	rs2071950	*CCDC78*	missense_variant	A	G	351544	0.5146	0.021	0.003	2.67E-16
16	2097158	rs2516739	*TSC2*	non_coding_transcript_exon_variant	G	A	398543	0.2294	-0.017	0.003	1.96E-09
16	2140680	rs10960	*PKD1*	missense_variant	T	C	445100	0.1965	-0.023	0.003	3.38E-15
16	2260567	rs26857	*MLST8*	missense_variant	C	T	312750	0.4732	0.016	0.003	6.24E-09
16	4755108	rs78074706	*ANKS3*	missense_variant	G	A	458927	0.0223	0.054	0.007	2.23E-14
16	4812705	rs61733564	*ZNF500*	missense_variant	A	G	431436	0.0349	0.047	0.006	2.42E-15
16	4933939	rs2037912	*UBN1*	missense_variant	G	C	450707	0.5252	-0.014	0.002	3.49E-10
16	4942099	rs1049205	*PPL*	missense_variant	C	T	458927	0.5252	-0.014	0.002	7.39E-10
16	4945687	rs35340520	*PPL*	missense_variant	G	T	458927	0.0686	0.027	0.004	1.08E-10
16	14388305	rs1659127	-	intergenic_variant	G	A	378966	0.3188	0.023	0.003	5.30E-19
16	15129970	rs7200543	*NTAN1*	synonymous_variant	A	G	434692	0.3054	-0.015	0.002	1.86E-09
16	15131962	rs1135999	*NTAN1*	missense_variant	A	G	426008	0.3049	-0.015	0.003	6.35E-09
16	15131974	rs1136001	*NTAN1*	missense_variant	G	T	411789	0.3062	-0.015	0.003	1.48E-09
16	20748331	rs11074471	*THUMPD1*	missense_variant	C	A	437065	0.1378	-0.019	0.003	1.13E-08
16	24804954	rs113388806	*TNRC6A*	missense_variant	A	T	443266	0.0358	0.035	0.006	6.03E-10
16	29998200	rs4077410	*TAOK2*	synonymous_variant	A	G	457648	0.5121	0.013	0.002	2.59E-09
16	30072530	rs9928448	*ALDOA*	intron_variant	T	C	458927	0.4702	0.015	0.002	3.82E-11
16	30958481	rs61738491	*ORAI3*	missense_variant	G	A	452297	0.0079	0.064	0.012	6.55E-08
16	31091390	rs35376811	*RP11-196G11.1*	missense_variant	C	T	448822	0.0068	0.079	0.013	4.86E-10
16	31474091	rs141923065	*ARMC5*	splice_acceptor_variant	A	G	447563	0.0048	0.105	0.015	2.03E-12
16	47684830	rs34667348	*PHKB*	missense_variant	C	A	457668	0.0042	0.118	0.016	5.43E-14
16	67320223	rs3868142	*PLEKHG4*	missense_variant	G	A	436136	0.1092	-0.033	0.004	8.43E-17
16	67325711	rs16957289	*PLEKHG4*	missense_variant	C	T	424117	0.0542	-0.036	0.005	1.57E-12
16	67397580	rs9922085	*LRRC36*	missense_variant	G	C	425348	0.0706	-0.039	0.005	2.03E-15
16	67409180	rs8052655	*LRRC36*	missense_variant	G	A	433763	0.0699	-0.039	0.005	5.17E-16
16	67418957	rs16957415	*LRRC36*	missense_variant	A	G	458927	0.0521	-0.037	0.005	6.28E-14
16	67470505	rs140385822	*ATP6V0D1*	missense_variant	G	A	436090	0.0015	-0.142	0.027	1.24E-07
16	67516945	rs5030980	*AGRP*	missense_variant	C	T	458927	0.0362	-0.052	0.006	1.11E-18
16	67696365	rs35356834	*ACD*	missense_variant	G	A	437150	0.0361	-0.047	0.006	7.52E-15
16	67860637	rs62620177	*CENPT*	missense_variant	C	T	458927	0.0362	-0.046	0.006	2.18E-15
16	67973953	rs5923	*SLC12A4*	missense_variant	G	A	458927	0.0517	-0.031	0.005	4.34E-10
16	67976320	rs4986970	*SLC12A4*	missense_variant	A	T	452026	0.0254	0.041	0.007	1.12E-09
16	69547741	rs4783718	-	regulatory_region_variant	T	C	433843	0.5773	0.023	0.002	1.57E-23
16	69588572	rs1364063	-	TF_binding_site_variant	T	C	458927	0.3971	0.017	0.002	9.84E-14
16	69745145	rs1800566	*NQO1*	missense_variant	G	A	433651	0.2029	-0.015	0.003	2.77E-08
16	69832105	rs4275849	*WWP2*	intron_variant	G	A	447870	0.3949	-0.015	0.002	2.94E-11
16	70548297	rs3931036	*COG4*	missense_variant	G	A	458927	0.9427	-0.027	0.005	5.31E-09
16	71509779	rs10500557	*ZNF19*	missense_variant	C	T	458927	0.0274	-0.035	0.006	4.28E-08
16	71988106	rs9921412	*PKD1L3*	missense_variant	C	T	424497	0.7397	-0.018	0.003	1.05E-10
16	82203758	rs2303262	*MPHOSPH6*	missense_variant	C	T	458927	0.7989	-0.019	0.003	1.95E-12
16	84900645	rs149615348	*CRISPLD2*	missense_variant	G	A	458927	0.0058	-0.087	0.013	9.88E-11
16	84902472	rs148934412	*CRISPLD2*	missense_variant	G	A	452297	0.0007	-0.297	0.039	2.89E-14
16	84987679	rs2326458	-	intergenic_variant	C	A	457648	0.7128	-0.020	0.002	2.11E-16
16	88782205	rs202127176	*CTU2*	missense_variant	G	C	427872	0.0019	-0.154	0.026	1.69E-09
16	88798919	rs201226914	*PIEZO1*	missense_variant	G	T	441336	0.0017	-0.174	0.026	2.00E-11
16	88804734	rs7184427	*RP5-1142A6.7*	missense_variant	A	G	342711	0.8513	0.022	0.004	3.20E-10
16	88808743	rs6500495	*RP5-1142A6.7*	missense_variant	A	G	444396	0.8802	0.022	0.003	7.13E-11
16	89587871	rs4785686	*SPG7*	non_coding_transcript_exon_variant	A	C	404256	0.4492	-0.014	0.002	6.66E-10
16	89704365	rs1126464	*DPEP1*	missense_variant	G	C	417730	0.2348	0.023	0.003	8.01E-17

16	89755903	rs258322	*CDK10*	intron_variant	A	G	430199	0.8779	0.022	0.004	2.16E-09
16	89986144	rs1805008	*TUBB3*	missense_variant	C	T	430276	0.0692	0.029	0.005	1.94E-10
17	1673276	rs1136287	*SERPINF1*	missense_variant	C	T	458253	0.6416	-0.013	0.002	3.35E-08
17	7329134	rs72842820	*C17orf74*	missense_variant	G	A	458927	0.1700	0.022	0.003	4.26E-14
17	7363088	rs9217	*CHRNB1*	3_prime_UTR_variant	T	C	455011	0.3721	0.028	0.002	4.05E-34
17	7366619	rs34914463	*ZBTB4*	missense_variant	T	C	207253	0.0840	0.036	0.006	2.64E-09
17	7417663	rs6761	*POLR2A*	3_prime_UTR_variant	C	T	457648	0.5817	-0.021	0.002	1.89E-20
17	7536527	rs6259	*SHBG*	missense_variant	G	A	458927	0.1025	0.026	0.004	1.79E-12
17	7557419	rs1642763	*ATP1B2*	synonymous_variant	A	G	429362	0.7753	-0.018	0.003	1.18E-10
17	21284223	rs4640244	*KCNJ12*	intron_variant	A	G	456974	0.3724	-0.019	0.002	2.74E-17
17	27889986	rs542939	*TP53I13*	missense_variant	T	C	449290	0.6728	0.025	0.002	1.19E-26
17	27917771	rs3110496	*GIT1*	intron_variant	A	G	431094	0.6696	0.017	0.002	3.56E-13
17	28548810	rs6355	*SLC6A4*	missense_variant	C	G	450149	0.0168	0.046	0.008	2.01E-08
17	29111368	rs11867457	*CRLF3*	missense_variant	A	G	166444	0.1520	-0.039	0.005	6.90E-15
17	29161503	rs11080134	*ATAD5*	missense_variant	A	G	433852	0.3190	0.021	0.002	3.04E-18
17	29247715	rs3760318	*ADAP2*	intron_variant	G	A	455685	0.3752	-0.042	0.002	5.27E-77
17	29629326	rs11080150	*OMG*	intron_variant	A	G	447870	0.3272	0.013	0.002	5.19E-08
17	36922196	rs1043515	*PIP4K2B*	3_prime_UTR_variant	A	G	379356	0.5256	0.024	0.002	9.15E-23
17	38545193	rs13695	*TOP2A*	3_prime_UTR_variant	C	T	444198	0.2284	0.017	0.003	3.89E-10
17	40514201	rs744166	*STAT3*	intron_variant	A	G	454406	0.4374	0.013	0.002	2.27E-08
17	40529835	rs1026916	*STAT3*	intron_variant	A	G	457404	0.6218	-0.014	0.002	1.14E-09
17	40714804	rs615942	*MLX*	missense_variant	C	A	316130	0.5254	0.015	0.003	1.61E-07
17	40725799	rs2292751	*PSMC3IP*	non_coding_transcript_exon_variant	C	T	447870	0.5505	0.013	0.002	2.65E-09
17	42744238	rs9907151	*C17orf104*	missense_variant	A	C	433651	0.1953	0.016	0.003	1.15E-08
17	43208121	rs12946454	*ACBD4*	intron_variant	A	T	451167	0.2521	-0.030	0.003	9.73E-31
17	43212963	rs2291447	*ACBD4*	splice_region_variant	G	T	437739	0.4923	-0.018	0.002	8.05E-16
17	43216281	rs4986172	*ACBD4*	intron_variant	C	T	458927	0.3701	-0.027	0.002	2.66E-30
17	43714850	rs2942168	*AC126544.4*	non_coding_transcript_exon_variant	G	A	393835	0.1795	-0.020	0.004	1.72E-07
17	43923266	rs62054815	*MAPT-AS1*	missense_variant	G	A	424974	0.1821	-0.020	0.004	6.80E-08
17	43923683	rs12185268	*MAPT-AS1*	missense_variant	A	G	417341	0.1794	-0.019	0.004	1.61E-07
17	43924073	rs12373123	*MAPT-AS1*	missense_variant	T	C	429062	0.1819	-0.019	0.004	1.76E-07
17	43924130	rs12373139	*MAPT-AS1*	missense_variant	G	A	447870	0.1806	-0.019	0.004	1.18E-07
17	44061023	rs62063786	*MAPT*	missense_variant	G	A	449393	0.1810	-0.020	0.004	2.05E-08
17	44061036	rs62063787	*MAPT*	missense_variant	T	C	447870	0.1809	-0.020	0.004	2.66E-08
17	44061278	rs17651549	*MAPT*	missense_variant	C	T	458927	0.1807	-0.020	0.004	3.36E-08
17	44067400	rs10445337	*MAPT*	missense_variant	T	C	448920	0.1827	-0.020	0.004	3.96E-08
17	44076665	rs62063857	*MAPT*	missense_variant	A	G	409812	0.1788	-0.020	0.004	4.15E-08
17	44108906	rs34579536	*KANSL1*	missense_variant	A	G	429519	0.1802	-0.020	0.004	9.02E-08
17	44117119	rs34043286	*KANSL1*	missense_variant	A	G	458927	0.1810	-0.019	0.004	4.96E-08
17	45732774	rs11871606	*KPNB1*	intron_variant	C	A	447870	0.5012	0.015	0.002	5.51E-11
17	45768836	rs8070463	*TBKBP1*	upstream_gene_variant	T	C	457648	0.5099	-0.013	0.002	2.02E-08
17	45786621	rs80267077	*TBKBP1*	missense_variant	G	A	373322	0.0983	-0.027	0.004	3.11E-11
17	46022065	rs17679445	*PNPO*	missense_variant	G	A	437739	0.0648	0.024	0.005	8.32E-08
17	46791801	rs4793601	*COX6B1P2*	downstream_gene_variant	A	C	447870	0.4596	0.013	0.002	3.38E-09
17	46939658	rs10278	*CALCOCO2*	missense_variant	C	G	401031	0.2966	0.015	0.003	9.88E-09
17	46988529	rs46521	*UBE2Z*	intron_variant	A	G	457404	0.5070	-0.026	0.002	1.28E-28
17	46988597	rs46522	*UBE2Z*	non_coding_transcript_exon_variant	C	T	457648	0.5069	-0.026	0.002	1.36E-28
17	47005193	rs15563	*UBE2Z*	3_prime_UTR_variant	A	G	455685	0.5068	-0.026	0.002	1.42E-28
17	47039132	rs2291725	*GIP*	missense_variant	T	C	454127	0.5002	-0.025	0.002	1.99E-26
17	47047868	rs3895874	*GIP*	upstream_gene_variant	G	A	343155	0.5377	-0.024	0.003	2.22E-19
17	47390014	rs2072153	*ZNF652*	intron_variant	G	C	443182	0.3127	0.020	0.002	2.00E-16
17	49446154	rs6504712	-	intergenic_variant	A	G	454162	0.2529	0.016	0.003	2.70E-09
17	54773238	rs227731	-	intergenic_variant	T	G	451124	0.4606	0.014	0.002	3.44E-10
17	54778817	rs227724	-	intergenic_variant	A	T	422768	0.3339	0.023	0.002	2.05E-21
17	54850329	rs4794665	-	intergenic_variant	A	G	456554	0.5029	-0.026	0.002	2.31E-33
17	54872439	rs72837329	*C17orf67*	missense_variant	T	C	458927	0.1446	0.018	0.003	2.28E-09
17	59483766	rs8068318	*TBX2*	non_coding_transcript_exon_variant	C	T	455685	0.6752	-0.024	0.002	9.23E-24
17	59497277	rs757608	-	intergenic_variant	A	G	455685	0.6798	-0.042	0.002	4.82E-72
17	59533868	rs3744448	*TBX4*	missense_variant	G	C	441987	0.1559	0.021	0.003	3.74E-12
17	59638769	rs2378871	-	intergenic_variant	A	C	456125	0.5726	-0.023	0.002	1.67E-25
17	61623052	rs35819807	*KCNH6*	missense_variant	C	T	458927	0.2321	0.026	0.003	1.32E-22
17	61666687	rs72845886	*DCAF7*	3_prime_UTR_variant	C	T	458927	0.0535	0.037	0.005	1.11E-14
17	61712964	rs7209435	*MAP3K3*	intron_variant	T	C	395999	0.2847	0.041	0.003	6.19E-53
17	61908556	rs13030	*SMARCD2*	synonymous_variant	C	T	434087	0.3361	-0.036	0.002	1.82E-51
17	61995761	rs151263636	*GH1*	missense_variant	G	A	446371	0.0021	0.139	0.024	6.31E-09
17	62016704	rs2727278	*SCN4A*	3_prime_UTR_variant	A	G	387495	0.0368	0.053	0.009	4.39E-09
17	62020348	rs2058194	*SCN4A*	missense_variant	T	C	456554	0.5351	0.019	0.002	1.57E-17
17	62050528	rs3760238	*CTC-264K15.6*	non_coding_transcript_exon_variant	T	C	457404	0.5020	-0.012	0.002	4.54E-08
17	63554591	rs2240308	*AXIN2*	missense_variant	G	A	435971	0.4976	0.014	0.002	1.06E-09
17	64280153	rs56152251	-	regulatory_region_variant	G	A	436216	0.4312	-0.014	0.002	3.16E-09
17	64318357	rs9912468	*PRKCA*	intron_variant	G	C	429519	0.5823	0.014	0.002	1.30E-09
17	68090207	rs11867479	*AC002539.1*	intron_variant	C	T	436460	0.3352	0.024	0.002	1.01E-24
17	69926109	rs2158917	-	intergenic_variant	C	T	439826	0.2756	0.020	0.002	9.72E-16
17	76700063	rs7220955	*CYTH1*	intron_variant	G	A	446222	0.5546	-0.013	0.002	5.98E-09
17	76799795	rs1057040	*USP36*	missense_variant	G	A	424233	0.5074	-0.016	0.002	8.92E-12
17	76799860	rs3088040	*USP36*	missense_variant	T	C	447870	0.5591	-0.013	0.002	1.22E-08
17	80176641	rs4239020	*RP13-516M14.2*	downstream_gene_variant	C	T	389337	0.7071	-0.016	0.003	1.60E-09
18	12984144	rs6505776	*SEH1L*	missense_variant	C	A	432977	0.6428	-0.014	0.003	6.88E-08
18	13068132	rs578208	*CEP192*	missense_variant	T	C	458253	0.6357	-0.014	0.002	2.07E-08
18	13069782	rs6505780	*CEP192*	missense_variant	C	T	458253	0.6408	-0.014	0.002	1.36E-08
18	13095609	rs474337	*CEP192*	missense_variant	T	C	458253	0.6410	-0.014	0.002	2.31E-08
18	13116432	rs1786263	*CEP192*	missense_variant	G	T	432395	0.6397	-0.014	0.003	8.55E-09
18	20646281	rs10853489	-	intergenic_variant	A	G	456730	0.5609	0.016	0.002	1.01E-12
18	20720973	rs11082304	*CABLES1*	intron_variant	G	T	458253	0.4848	0.034	0.002	8.44E-53
18	20724328	rs4800148	*CABLES1*	intron_variant	G	A	456974	0.7816	0.056	0.003	7.61E-96
18	20727611	rs4800452	*CABLES1*	intron_variant	C	T	458253	0.7810	0.057	0.003	3.37E-99
18	20735408	rs4369779	*CABLES1*	intron_variant	T	C	456974	0.7963	0.061	0.003	1.50E-105
18	21120444	rs1805082	*NPC1*	missense_variant	T	C	458253	0.4773	-0.013	0.002	2.12E-09
18	21140432	rs1805081	*NPC1*	missense_variant	T	C	458253	0.3770	-0.013	0.002	9.30E-09
18	46770186	rs11661691	*DYM*	intron_variant	T	G	381742	0.4651	0.019	0.002	2.74E-15
18	46959500	rs9967417	*DYM*	intron_variant	G	C	428745	0.6097	-0.031	0.002	1.97E-38
18	46976586	rs2156497	*DYM*	intron_variant	A	G	334605	0.3612	-0.030	0.003	3.67E-28
18	46991160	rs8099594	*DYM*	upstream_gene_variant	A	G	457648	0.3643	-0.029	0.002	1.60E-35
18	57751014	rs12957347	-	intergenic_variant	T	C	262451	0.2618	0.023	0.003	2.75E-12
18	57839769	rs571312	-	intergenic_variant	C	A	454406	0.2482	0.027	0.003	3.79E-24

18	57851097	rs17782313	-	intergenic_variant	T	C	457648	0.2440	0.028	0.003	1.87E-26
18	57851763	rs10871777	-	intergenic_variant	A	G	457648	0.2470	0.028	0.003	1.70E-25
18	57882787	rs489693	-	intergenic_variant	C	A	457648	0.3249	0.014	0.002	8.58E-09
18	57884750	rs12970134	-	intergenic_variant	G	A	456554	0.2584	0.018	0.003	3.33E-12
18	74980601	rs77169818	*GALR1*	missense_variant	A	T	452026	0.0452	-0.043	0.005	4.06E-17
19	1124835	rs740495	*SBNO2*	intron_variant	A	G	448735	0.3045	0.013	0.002	7.45E-08
19	2170954	rs12986413	*DOT1L*	intron_variant	A	T	438464	0.4668	0.026	0.002	1.07E-30
19	2177193	rs12982744	*DOT1L*	intron_variant	C	G	440295	0.3526	0.028	0.002	1.32E-31
19	4689635	rs200229921	*DPP9*	missense_variant	C	T	434987	0.0031	0.101	0.019	1.41E-07
19	4910889	rs2261988	*UHRF1*	missense_variant	G	T	386837	0.3344	0.020	0.002	5.97E-16
19	7184762	rs891088	*INSR*	intron_variant	A	G	454839	0.2832	0.025	0.002	6.08E-25
19	7224431	rs7248104	*INSR*	intron_variant	G	A	457648	0.4020	0.015	0.002	2.96E-12
19	8644031	rs4072910	*AC130469.2*	upstream_gene_variant	G	C	452800	0.4960	-0.028	0.002	1.33E-38
19	8669931	rs7255721	*ADAMTS10*	missense_variant	G	C	407195	0.7422	-0.019	0.003	7.27E-13
19	8672000	rs7249094	*ADAMTS10*	intron_variant	G	A	457648	0.4185	-0.020	0.002	1.56E-18
19	10273372	rs2228612	*DNMT1*	missense_variant	T	C	458253	0.0848	0.030	0.004	4.23E-14
19	10742170	rs2288904	*SLC44A2*	missense_variant	A	G	437065	0.7985	-0.021	0.003	2.18E-13
19	10801185	rs8102380	*ILF3*	3_prime_UTR_variant	G	A	456730	0.7065	-0.019	0.002	1.99E-14
19	11275139	rs7188	*KANK2*	3_prime_UTR_variant	A	C	452638	0.3147	-0.017	0.002	3.44E-13
19	12154799	rs67102109	*ZNF878*	missense_variant	G	C	448239	0.0718	0.028	0.004	1.23E-10
19	17283303	rs2279008	*MYO9B*	intron_variant	T	C	438976	0.2480	-0.016	0.003	1.97E-10
19	18557180	rs115932129	*ELL*	missense_variant	C	T	447196	0.0004	-0.270	0.050	7.93E-08
19	19361735	rs1064395	*AC138430.4*	3_prime_UTR_variant	G	A	455880	0.1758	0.018	0.003	6.33E-10
19	19413092	rs17751061	*SUGP1*	missense_variant	C	T	198687	0.1252	0.028	0.005	4.78E-08
19	37441365	rs547483	*ZNF568*	missense_variant	T	C	458927	0.3544	-0.014	0.002	5.17E-08
19	37441980	rs1644634	*ZNF568*	missense_variant	A	G	458927	0.5674	-0.013	0.002	1.27E-07
19	37482151	rs1667354	*ZNF568*	missense_variant	A	G	458927	0.5299	-0.013	0.002	1.75E-07
19	37487632	rs935706	*ZNF568*	missense_variant	G	A	458927	0.5160	-0.013	0.002	1.68E-07
19	37488499	rs1667366	*ZNF568*	stop_lost	T	C	447870	0.5163	-0.013	0.002	1.54E-07
19	41903220	rs10853751	*CTC-435M10.10*	missense_variant	G	A	437739	0.6130	-0.021	0.002	5.24E-19
19	41937095	rs17318596	*B3GNT8*	missense_variant	G	A	356410	0.3608	0.021	0.003	1.51E-15
19	41939297	rs1043413	*ATP5SL*	missense_variant	C	G	181242	0.4145	0.023	0.004	4.14E-10
19	41944237	rs2231940	*ATP5SL*	missense_variant	T	C	437739	0.3873	0.023	0.002	2.71E-21
19	42728836	rs3810151	*ZNF526*	missense_variant	T	C	458927	0.0999	-0.019	0.004	1.78E-07
19	42863035	rs1206038	*MEGF8*	missense_variant	A	G	433651	0.0657	-0.026	0.004	7.94E-09
19	46914547	rs2279517	*CCDC8*	missense_variant	C	G	421304	0.0567	0.029	0.005	1.52E-09
19	46914927	rs75175362	*CCDC8*	missense_variant	C	T	428205	0.0557	0.029	0.005	3.28E-09
19	48198675	rs13346368	*GLTSCR1*	missense_variant	A	G	458927	0.2713	0.014	0.002	2.19E-08
19	55831502	rs61737281	*TMEM150B*	missense_variant	G	A	458927	0.0071	-0.090	0.012	1.99E-13
19	55879672	rs4252548	*IL11*	missense_variant	C	T	458927	0.0249	-0.101	0.007	5.44E-52
19	55993436	rs147110934	*NAT14*	missense_variant	G	T	333240	0.0180	-0.083	0.009	1.10E-19
19	56001665	rs114976626	*SSC5D*	missense_variant	C	T	347386	0.0302	-0.048	0.007	8.72E-12
19	56011573	rs61747393	*SSC5D*	missense_variant	C	T	403522	0.0219	-0.059	0.008	7.55E-15
20	4101800	rs1741344	*SMOX*	non_coding_transcript_exon_variant	C	T	457648	0.6475	-0.023	0.002	1.15E-24
20	6578556	rs6054374	-	intergenic_variant	C	T	347960	0.4090	-0.026	0.003	2.56E-23
20	6620893	rs967417	-	intergenic_variant	G	A	454406	0.4563	-0.038	0.002	6.14E-65
20	6621685	rs2145270	-	intergenic_variant	C	T	458927	0.6285	-0.040	0.002	7.33E-71
20	21142523	rs4815025	*KIZ*	missense_variant	C	G	413535	0.6533	-0.021	0.003	1.05E-16
20	21142813	rs2236178	*KIZ*	missense_variant	T	C	458253	0.6840	-0.020	0.002	2.19E-16
20	21218023	rs6137297	*KIZ*	intron_variant	C	T	444823	0.6638	-0.020	0.002	1.35E-16
20	31950845	rs291671	*CDK5RAP1*	intron_variant	G	A	458927	0.9026	0.028	0.004	2.56E-13
20	32265513	rs2071056	*NECAB3*	intron_variant	A	G	457404	0.3292	-0.028	0.002	1.42E-32
20	32266134	rs35385772	*NECAB3*	missense_variant	C	T	436837	0.0271	-0.057	0.007	7.20E-18
20	32295541	rs910397	*PXMP4*	missense_variant	C	T	445265	0.4918	-0.014	0.002	1.17E-10
20	32333181	rs7274811	*ZNF341*	intron_variant	G	T	424498	0.2370	-0.037	0.003	1.73E-41
20	32955423	rs6087577	*ITCH*	intron_variant	A	G	455040	0.4941	-0.019	0.002	1.43E-16
20	33110846	rs1122174	*DYNLRB1*	intron_variant	T	C	414851	0.8135	0.020	0.003	1.18E-10
20	33411871	rs6088619	*NCOA6*	intron_variant	A	G	452238	0.1132	0.040	0.004	5.03E-30
20	33470694	rs4911163	*ACSS2*	synonymous_variant	C	T	455040	0.6082	0.019	0.002	6.26E-15
20	33488771	rs6120757	*ACSS2*	intron_variant	C	T	453517	0.6187	0.019	0.002	7.37E-15
20	33565755	rs11906160	*MYH7B*	missense_variant	G	A	428934	0.1271	0.024	0.003	4.66E-12
20	33586968	rs41307159	*TRPC4AP*	missense_variant	G	A	455040	0.0159	-0.056	0.008	3.01E-11
20	33734493	rs1415771	*EDEM2*	intron_variant	G	A	451144	0.4665	0.018	0.002	9.22E-15
20	33764554	rs867186	*PROCR*	missense_variant	A	G	441378	0.1066	0.022	0.004	2.59E-09
20	33849179	rs1555322	*MMP24-AS1*	intron_variant	G	A	408576	0.1348	0.024	0.003	4.65E-13
20	33907161	rs6060369	*UQCC1*	intron_variant	T	C	455040	0.4224	0.056	0.002	4.19E-112
20	33909784	rs6088792	*UQCC1*	intron_variant	C	T	427903	0.2889	0.041	0.003	8.49E-56
20	33914208	rs6060373	*UQCC1*	intron_variant	A	G	455040	0.4230	0.056	0.002	5.15E-113
20	33971914	rs4911494	*UQCC1*	missense_variant	C	T	428116	0.5850	-0.056	0.003	1.41E-109
20	33975181	rs6088813	*UQCC1*	intron_variant	C	A	455040	0.5848	-0.056	0.002	2.29E-113
20	34022387	rs224331	*GDF5*	missense_variant	A	C	346829	0.3673	0.055	0.003	1.18E-84
20	34025756	rs143384	*GDF5*	5_prime_UTR_variant	A	G	450519	0.4622	0.071	0.002	3.83E-180
20	34025983	rs78110303	*GDF5*	5_prime_UTR_variant	A	G	439655	0.4184	0.062	0.003	8.19E-128
20	34097353	rs2236164	*CEP250*	intron_variant	T	C	451124	0.2787	0.039	0.003	6.27E-48
20	34116282	rs7261862	*C20orf173*	missense_variant	T	C	455040	0.1727	0.023	0.003	4.75E-14
20	34214173	rs11543239	*CPNE1*	missense_variant	G	A	455040	0.0648	0.030	0.005	3.13E-11
20	34218673	rs12481228	*CPNE1*	missense_variant	G	C	448913	0.1040	0.032	0.004	4.83E-17
20	34219496	rs6579255	*CPNE1*	missense_variant	T	C	455040	0.2099	0.040	0.003	1.00E-42
20	34220755	rs11543244	*CPNE1*	missense_variant	C	T	455040	0.0599	0.031	0.005	6.31E-11
20	34373979	rs6142443	*PHF20*	intron_variant	A	C	187291	0.7074	-0.029	0.004	3.45E-12
20	34432670	rs2425163	*PHF20*	intron_variant	A	G	419833	0.2140	0.041	0.003	1.54E-42
20	34502107	rs17431878	*PHF20*	missense_variant	G	A	455040	0.1024	0.032	0.004	1.02E-17
20	34560609	rs17347958	*CNBD2*	missense_variant	G	A	454063	0.0528	0.032	0.005	6.85E-11
20	34596371	rs6060750	*CNBD2*	missense_variant	C	T	450809	0.2185	0.034	0.003	1.17E-33
20	35590249	rs4812641	-	intergenic_variant	C	A	458927	0.3665	-0.013	0.002	1.41E-08
20	35769592	rs1744769	*MROH8*	synonymous_variant	T	C	458927	0.7992	0.025	0.003	1.44E-18
20	35865054	rs4608	*RPN2*	synonymous_variant	C	T	458927	0.7838	0.023	0.003	5.30E-17
20	47253150	rs2664521	*PREX1*	missense_variant	T	C	385198	0.9692	0.045	0.007	1.60E-11
20	47685320	rs2227946	*CSE1L*	synonymous_variant	G	C	452026	0.2247	0.033	0.003	2.84E-33
20	47841660	rs11553387	*DDX27*	missense_variant	G	T	441885	0.2013	0.037	0.003	4.94E-36
20	47850182	rs238148	*DDX27*	synonymous_variant	C	T	455011	0.7464	0.017	0.003	5.47E-11
20	47865509	rs238209	*DDX27*	missense_variant	G	A	458927	0.7452	0.017	0.003	1.28E-11
20	47865784	rs6512577	*ZNFX1*	missense_variant	C	T	456554	0.2014	0.038	0.003	1.18E-39
20	47903019	rs237743	*ZFAS1*	intron_variant	G	A	454406	0.2089	0.037	0.003	3.97E-39
20	48600631	rs4647958	*SNAI1*	missense_variant	T	C	455685	0.1582	-0.023	0.003	1.66E-13

20	57475191	rs13831	*GNAS*	3_prime_UTR_variant	A	G	451936	0.7234	-0.013	0.002	7.66E-08
20	57758720	rs16982520	-	intergenic_variant	A	G	458927	0.1263	0.025	0.003	1.02E-13
20	57768743	rs56057707	*ZNF831*	missense_variant	C	T	458927	0.1953	0.019	0.003	3.36E-11
20	57769140	rs55786258	*ZNF831*	missense_variant	G	C	441743	0.1935	0.018	0.003	1.74E-10
20	60986019	rs2236200	*CABLES2*	missense_variant	A	C	453156	0.2246	-0.015	0.003	3.52E-08
21	28305212	rs2830585	*ADAMTS5*	missense_variant	C	T	458927	0.1431	-0.018	0.003	4.72E-09
21	35690786	rs2834442	*AP000318.2*	intron_variant	T	A	377878	0.6593	0.021	0.003	8.01E-17
21	39671476	rs2230033	*KCNJ15*	missense_variant	G	A	451454	0.4991	-0.020	0.002	6.32E-20
21	40007704	rs459094	*ERG*	intron_variant	G	T	441011	0.3028	0.014	0.002	1.54E-08
22	17625915	rs35665085	*CECR5*	missense_variant	G	A	458253	0.0514	-0.026	0.005	9.99E-08
22	20789074	rs1005640	*XXbac-B562F10.12*	intron_variant	T	C	455880	0.4319	0.013	0.002	2.30E-09
22	28501414	rs77885044	*TTC28*	missense_variant	C	T	428205	0.0109	-0.066	0.010	1.29E-10
22	35663523	rs2413338	*HMGXB4*	intron_variant	C	T	420831	0.5942	0.014	0.002	1.70E-08
22	38121152	rs9610841	*RP1-37E16.12*	missense_variant	C	A	433651	0.4171	0.013	0.002	9.54E-09
22	38544298	rs2284063	*PLA2G6*	non_coding_transcript_exon_variant	A	G	436460	0.3653	0.015	0.002	1.21E-10
22	38569006	rs738322	*PLA2G6*	intron_variant	A	G	457648	0.4881	0.013	0.002	7.49E-09
22	42095658	rs147348682	*MEI1*	missense_variant	T	G	449763	0.0225	0.039	0.007	4.82E-08
22	45728370	rs6007594	*FAM118A*	missense_variant	G	A	432124	0.3068	0.020	0.003	2.73E-14
22	45749983	rs5764698	*SMC1B*	missense_variant	G	T	416297	0.4776	-0.019	0.002	6.68E-15
22	45813687	rs12172195	*RIBC2*	synonymous_variant	G	A	428473	0.1421	0.021	0.003	1.38E-10
22	45821887	rs1022477	*RIBC2*	synonymous_variant	G	A	437739	0.5185	0.017	0.002	8.08E-13
22	45821935	rs2142662	*RIBC2*	synonymous_variant	G	A	437739	0.1556	0.022	0.003	2.39E-12
22	50278568	rs910799	*ZBED4*	missense_variant	A	G	441750	0.7697	-0.016	0.003	1.73E-08
23	38009121	rs35318931	*SRPX*	missense_variant	G	A	309940	0.0663	-0.027	0.004	1.75E-09
23	55574773	rs3126259	-	intergenic_variant	T	G	306044	0.3594	-0.020	0.003	2.41E-14
23	56889389	rs1930983	-	intergenic_variant	C	T	307809	0.7069	0.022	0.003	1.28E-14
23	57433303	rs717848	*FAAH2*	intron_variant	A	G	308417	0.3095	-0.018	0.003	1.31E-11
23	57622607	rs1997715	*ZXDB*	3_prime_UTR_variant	G	A	305445	0.3176	-0.021	0.003	9.34E-14
23	77025121	rs112792023	*ATRX*	intron_variant	T	G	297979	0.2806	0.015	0.003	1.01E-08
23	77268502	rs2227291	*ATP7A*	missense_variant	G	C	303813	0.2270	0.016	0.003	2.78E-08
23	77913569	rs4077512	*ZCCHC5*	missense_variant	G	A	251879	0.1397	-0.021	0.004	3.02E-09
23	78649193	rs1474563	-	intergenic_variant	C	T	259761	0.5407	0.031	0.002	8.47E-35
23	78944731	rs1353451	-	intergenic_variant	G	T	266870	0.7188	0.024	0.003	5.48E-16
23	99890204	rs1802288	*TSPAN6*	missense_variant	C	T	284664	0.1537	-0.017	0.003	5.92E-08
23	110494841	rs12013711	*CAPN6*	missense_variant	C	G	281372	0.0770	-0.029	0.005	6.20E-08
23	118587003	rs3810755	*SLC25A43*	missense_variant	C	T	286689	0.5802	0.014	0.002	1.05E-08

Supplementary Table 6. ExomeChip variants with Pdiscovery <2e-07 in the European-ancestry meta-analysis (N=381,625). For the functional annotation, we provide the most severe consequence based on the ENSEMBL's Variant Effect Predictor (VEP) tool. The direction of the effect (Beta) and effect allele frequency (EAF) is given for the alternate (Alt) allele.

Chr	Pos (hg19)	rsID	Gene	VEP annotation	Ref	Alt	N	EAF	Beta	SE	P-value
1	2069172	rs425277	*PRKCZ*	intron_variant	C	T	381625	0.2822	0.019	0.003	1.40E-13
1	7913029	rs34305100	*UTS2*	missense_variant	A	G	381625	0.1908	0.021	0.003	1.04E-11
1	7913445	rs13306061	*UTS2*	missense_variant	C	T	381625	0.1906	0.021	0.003	1.41E-11
1	8046672	rs12727642	*PARK7*	upstream_gene_variant	C	A	380346	0.1804	0.018	0.003	3.24E-08
1	9304731	rs2239560	*H6PD*	intron_variant	G	A	375581	0.1551	0.023	0.003	2.67E-12
1	10285709	rs6541085	*MIR1273D*	intron_variant	A	G	372028	0.4773	0.013	0.002	1.10E-07
1	17306675	rs2284746	*MFAP2*	intron_variant	C	G	375498	0.5141	0.041	0.002	1.48E-61
1	17312743	rs3170740	*ATP13A2*	missense_variant	C	T	264850	0.5276	0.043	0.003	1.44E-47
1	17331676	rs3738814	*ATP13A2*	intron_variant	A	G	378383	0.4399	-0.039	0.002	9.44E-57
1	17395480	rs2076599	*PADI2*	3_prime_UTR_variant	G	A	380346	0.6085	0.025	0.002	7.80E-24
1	19765518	rs12045440	*CAPZB*	intron_variant	T	G	381625	0.3404	-0.017	0.002	3.27E-11
1	21031983	rs6702859	*KIF17*	intron_variant	A	G	376860	0.5979	0.014	0.002	1.82E-08
1	21629447	rs213060	*RP5-1071N3.1*	intron_variant	A	C	372028	0.4250	0.013	0.002	1.78E-07
1	22368342	rs2501279	-	regulatory_region_variant	C	T	370395	0.5926	-0.015	0.002	5.61E-10
1	23536891	rs1738475	-	regulatory_region_variant	C	G	374724	0.4063	-0.017	0.003	4.56E-12
1	23537555	rs627304	-	intergenic_variant	T	C	368141	0.4063	-0.017	0.003	2.14E-11
1	26450009	rs17163588	*PDIK1L*	3_prime_UTR_variant	C	T	380346	0.1738	0.028	0.003	1.28E-16
1	26517267	rs41284333	*CNKSR1*	missense_variant	A	G	381625	0.1860	0.022	0.003	1.25E-10
1	26517794	rs11247866	*CNKSR1*	missense_variant	A	G	381625	0.1856	0.022	0.003	1.03E-10
1	26521140	rs11809207	*CNKSR1*	intron_variant	G	A	359133	0.1841	0.023	0.003	2.18E-11
1	26526439	rs17257155	*CATSPER4*	missense_variant	A	G	381625	0.1822	0.023	0.003	2.70E-11
1	26741544	rs7532866	*LIN28A*	intron_variant	A	G	380346	0.3402	-0.023	0.003	1.71E-19
1	26883511	rs2229712	*RPS6KA1*	missense_variant	A	C	283850	0.2206	-0.027	0.003	1.35E-16
1	32092525	rs2271933	*PEF1*	missense_variant	A	G	381625	0.6151	0.014	0.002	3.88E-08
1	32672908	rs3903683	*RP4-622L5.7*	missense_variant	T	G	351178	0.0647	0.032	0.005	3.06E-10
1	32673514	rs150341307	*RP4-622L5.7*	missense_variant	G	C	333756	0.0021	-0.141	0.026	7.92E-08
1	32842319	rs34885668	*BSDC1*	missense_variant	T	C	381625	0.0345	0.035	0.006	1.83E-08
1	38289383	rs12751325	*MTF1*	splice_region_variant	T	C	379252	0.3003	-0.017	0.003	2.46E-11
1	38338795	rs11488569	*INPP5B*	missense_variant	A	G	359266	0.7193	-0.020	0.003	5.76E-13
1	40773149	rs2228564	*COL9A2*	missense_variant	T	C	378144	0.2198	-0.022	0.003	1.58E-14
1	41485902	rs3738368	*SLFNL1*	missense_variant	C	G	180118	0.3155	0.029	0.004	9.57E-15
1	41486245	rs1138293	*SLFNL1*	missense_variant	C	T	381625	0.1966	0.027	0.003	4.06E-19
1	41530871	rs6686842	*SCMH1*	intron_variant	T	C	346608	0.5644	-0.026	0.003	4.01E-25
1	41540902	rs143365597	*SCMH1*	missense_variant	G	A	368141	0.0042	0.188	0.018	1.58E-25
1	41618297	rs114233776	*SCMH1*	missense_variant	G	A	359848	0.0061	-0.119	0.015	1.92E-15
1	41745770	rs2154319	*RP11-399E6.1*	intron_variant	T	C	349913	0.2172	0.039	0.003	2.32E-37
1	51873967	rs41292521	*EPS15*	missense_variant	G	A	377738	0.0196	0.045	0.008	5.07E-08
1	67390468	rs1886686	*MIER1*	missense_variant	C	G	359683	0.7318	0.015	0.003	1.66E-07
1	78623626	rs17391694	-	regulatory_region_variant	C	T	375104	0.1220	0.033	0.004	1.87E-19
1	89123443	rs6699417	*PKN2-AS1*	intron_variant	C	T	381625	0.6036	0.022	0.002	8.91E-19
1	89271574	rs786906	*PKN2*	splice_region_variant	T	C	381625	0.5594	0.021	0.002	8.56E-18
1	89388944	rs7532151	*RP11-82K18.2*	upstream_gene_variant	A	C	327825	0.4928	-0.018	0.003	7.27E-13
1	93009438	rs7515577	*EVI5*	intron_variant	C	A	370749	0.7899	0.018	0.003	2.68E-09
1	93160902	rs2391199	*EVI5*	missense_variant	T	C	381625	0.8956	0.024	0.004	1.78E-09
1	93323971	rs10874746	*FAM69A*	intron_variant	T	C	377738	0.6501	0.020	0.003	7.13E-15
1	93401837	rs12745968	*RP11-386I23.1*	intron_variant	A	G	381625	0.3713	-0.017	0.003	1.32E-11
1	103216881	rs713162	-	intergenic_variant	G	A	380102	0.3795	0.017	0.003	2.96E-12
1	103379918	rs3753841	*COL11A1*	missense_variant	G	A	356606	0.6170	-0.017	0.003	4.06E-11
1	103432657	rs12755987	*COL11A1*	intron_variant	A	G	378383	0.7008	-0.021	0.003	1.85E-14
1	103483514	rs945748	*COL11A1*	intron_variant	C	T	378383	0.7000	-0.020	0.003	7.72E-14
1	113098534	rs6658555	*ST7L*	missense_variant	C	T	381625	0.2539	0.015	0.003	1.71E-08
1	113190807	rs17030613	*CAPZA1*	intron_variant	A	C	381625	0.2171	-0.019	0.003	6.20E-11
1	118868405	rs17038182	-	regulatory_region_variant	G	C	375498	0.2461	-0.044	0.003	4.79E-53
1	118883973	rs12735613	-	intergenic_variant	G	A	381625	0.2358	-0.043	0.003	1.95E-51
1	119234198	rs2764504	-	intergenic_variant	T	C	373933	0.0582	-0.029	0.005	1.19E-08
1	119427467	rs61730011	*TBX15*	missense_variant	A	C	373551	0.0424	-0.059	0.006	1.61E-24
1	119503843	rs984222	*TBX15*	intron_variant	C	G	373405	0.6245	0.016	0.003	1.15E-10
1	146568955	rs11239931	*NBPF13P*	intron_variant	G	A	366845	0.8043	0.018	0.003	1.26E-08
1	149892872	rs11205277	*SF3B4*	upstream_gene_variant	A	G	363055	0.4289	0.043	0.003	5.00E-66
1	149906413	rs11205303	*MTMR11*	missense_variant	T	C	381625	0.3982	0.047	0.002	2.57E-81
1	149998494	rs12027024	-	intergenic_variant	T	C	377876	0.6470	0.015	0.003	2.08E-09
1	150551327	rs11580946	*MCL1*	missense_variant	G	A	359848	0.0137	0.061	0.010	2.16E-09
1	151259543	rs3748545	*PI4KB*	missense_variant	G	A	381625	0.1150	-0.027	0.004	4.20E-13
1	154987704	rs141845046	*ZBTB7B*	missense_variant	C	T	381625	0.0282	0.058	0.007	7.30E-17
1	171753039	rs2232816	*METTL13*	missense_variant	A	G	379252	0.2677	-0.019	0.003	6.32E-12
1	172053287	rs17346452	*DNM3*	intron_variant	T	C	354447	0.2767	0.035	0.003	1.17E-36
1	172189889	rs678962	*DNM3*	intron_variant	T	G	380346	0.2152	0.048	0.003	3.34E-61
1	172410967	rs1063412	*PIGC*	missense_variant	G	A	344488	0.5700	-0.018	0.003	6.70E-12
1	172434812	rs2901656	*C1orf105*	3_prime_UTR_variant	C	T	372028	0.4944	-0.013	0.002	3.71E-08
1	172437592	rs1129942	*C1orf105*	missense_variant	G	A	342493	0.7806	-0.027	0.003	9.35E-19
1	176219438	rs1553770	-	intergenic_variant	C	T	372028	0.5322	-0.015	0.002	1.61E-10
1	176792249	rs1325598	*PAPPA2*	intron_variant	A	G	377104	0.5631	0.029	0.002	5.98E-34
1	176863867	rs2228956	*ASTN1*	missense_variant	T	C	381625	0.8334	0.018	0.003	7.22E-09
1	182973491	rs10752881	-	intergenic_variant	A	G	372028	0.5342	-0.018	0.003	1.19E-12
1	183085755	rs20563	*LAMC1*	missense_variant	A	G	373551	0.5571	-0.019	0.003	1.87E-13
1	183094547	rs20558	*LAMC1*	missense_variant	T	C	381625	0.5569	-0.019	0.003	4.34E-14
1	183106739	rs10797854	*LAMC1*	intron_variant	G	A	348399	0.5564	-0.018	0.003	4.70E-12
1	183495812	rs144712473	*SMG7*	missense_variant	A	G	381625	0.0061	-0.094	0.014	4.97E-11
1	183979248	rs2378792	*COLGALT2*	intron_variant	C	T	368786	0.2351	-0.016	0.003	1.97E-08
1	184020945	rs2274432	*TSEN15*	missense_variant	G	A	367751	0.3504	0.041	0.003	6.55E-57
1	184023529	rs1046934	*TSEN15*	missense_variant	A	C	380687	0.3513	0.040	0.003	8.31E-57
1	218950403	rs2889809	-	intergenic_variant	A	G	372028	0.4410	-0.020	0.002	2.46E-16
1	219009835	rs2647116	-	intergenic_variant	G	A	376860	0.3667	-0.022	0.003	7.41E-18
1	219743719	rs11118346	-	intergenic_variant	C	T	380346	0.4669	-0.016	0.002	1.44E-10
1	223178026	rs144673025	*DISP1*	missense_variant	T	C	381625	0.0079	-0.078	0.013	1.11E-09

1	227935444	rs2236359	*SNAP47*	missense_variant	A	G	375771	0.4102	-0.017	0.002	2.17E-12
2	1756908	rs6726313	-	intergenic_variant	C	T	367832	0.3080	0.015	0.003	7.95E-09
2	9662210	rs10495563	*ADAM17*	3_prime_UTR_variant	G	A	380346	0.6633	0.022	0.003	2.19E-18
2	11323276	rs978906	*PQLC3*	3_prime_UTR_variant	T	C	377973	0.4797	-0.018	0.002	1.43E-12
2	11359120	rs2230774	*ROCK2*	missense_variant	G	T	380346	0.5431	-0.016	0.002	1.13E-10
2	11500314	rs6739310	*AC099344.2*	intron_variant	C	A	372028	0.5514	-0.016	0.002	2.65E-10
2	20205541	rs52826764	*AC079145.4*	missense_variant	C	T	381625	0.0262	-0.071	0.007	2.67E-23
2	20396122	rs6749689	*SDC1*	downstream_gene_variant	T	C	377729	0.5727	0.016	0.002	4.00E-11
2	23898317	rs4665630	*KLHL29*	intron_variant	C	T	357786	0.8926	0.022	0.004	1.76E-08
2	24244603	rs115334231	*MFSD2B*	missense_variant	G	A	381625	0.0599	-0.031	0.005	1.01E-09
2	24247514	rs7561273	*MFSD2B*	intron_variant	A	G	380346	0.5374	0.026	0.002	1.16E-26
2	24692639	rs2119997	-	intergenic_variant	G	A	374251	0.8474	0.020	0.003	9.27E-09
2	24692809	rs2165738	-	intergenic_variant	C	G	365880	0.7341	0.018	0.003	3.75E-10
2	25022598	rs1550116	*CENPO*	missense_variant	A	G	351774	0.1438	-0.020	0.004	3.34E-08
2	25116977	rs7586879	*ADCY3*	intron_variant	C	T	380102	0.3470	-0.027	0.003	9.49E-25
2	25141538	rs11676272	*ADCY3*	missense_variant	A	G	351760	0.4653	-0.031	0.003	1.56E-32
2	25158008	rs713586	-	intergenic_variant	T	C	355960	0.4713	-0.031	0.003	2.60E-33
2	25187599	rs4665736	*AC013267.1*	intron_variant	C	T	376458	0.5333	0.033	0.003	5.34E-39
2	25276284	rs6733301	*EFR3B*	intron_variant	G	A	381625	0.1187	-0.029	0.004	1.18E-14
2	25328703	rs12233132	*EFR3B*	intron_variant	C	T	378823	0.2744	0.026	0.003	1.05E-21
2	25482883	rs7594432	*DNMT3A*	intron_variant	T	C	372028	0.4338	0.038	0.002	5.79E-55
2	27730940	rs1260326	*GCKR*	missense_variant	T	C	381625	0.6047	0.017	0.003	8.37E-11
2	27741237	rs780094	*GCKR*	intron_variant	T	C	364847	0.6124	0.017	0.003	6.40E-10
2	27742603	rs780093	*GCKR*	intron_variant	T	C	355874	0.6152	0.017	0.003	3.24E-10
2	33361425	rs6714546	*LTBP1*	intron_variant	A	G	372272	0.7194	0.032	0.003	2.50E-32
2	33405151	rs6751657	*LTBP1*	intron_variant	T	C	378823	0.5275	0.026	0.002	2.28E-28
2	33527299	rs41464348	*LTBP1*	intron_variant	G	A	377104	0.5106	-0.015	0.002	1.20E-09
2	36673555	rs7562790	*CRIM1*	intron_variant	T	G	381625	0.4097	-0.014	0.002	1.42E-08
2	36690242	rs848534	*CRIM1*	intron_variant	C	T	376860	0.2665	-0.015	0.003	6.31E-08
2	36771309	rs12712508	*FEZ2*	intron_variant	A	G	369655	0.3575	0.018	0.003	4.84E-12
2	36782886	rs848642	*FEZ2*	missense_variant	G	A	381625	0.3162	-0.020	0.003	1.35E-15
2	36810586	rs14291	*FEZ2*	synonymous_variant	T	C	374518	0.3754	0.016	0.003	9.62E-11
2	37995727	rs12615742	-	regulatory_region_variant	C	T	376353	0.4774	0.026	0.002	7.95E-28
2	43519977	rs35720761	*THADA*	missense_variant	C	T	380102	0.1163	0.020	0.004	1.23E-07
2	43732823	rs7578597	*THADA*	missense_variant	T	C	340409	0.0993	0.028	0.004	8.81E-11
2	43806918	rs10495903	*THADA*	intron_variant	C	T	335515	0.1254	0.023	0.004	4.99E-09
2	44547574	rs698761	*SLC3A1*	missense_variant	G	A	369748	0.6758	-0.016	0.003	4.93E-10
2	44768202	rs2341459	*CAMKMT*	intron_variant	T	C	380346	0.7328	-0.019	0.003	2.39E-12
2	45640374	rs3755073	*SRBD1*	missense_variant	C	A	373551	0.0892	-0.023	0.004	6.66E-08
2	46642249	rs2346177	-	intergenic_variant	G	A	340697	0.5075	0.013	0.003	1.21E-07
2	46921285	rs12474201	*SOCS5*	upstream_gene_variant	G	A	363055	0.3529	0.028	0.003	6.57E-28
2	55771161	rs1045910	*PPP4R3B*	missense_variant	A	G	376215	0.9441	0.031	0.005	3.98E-09
2	56008904	rs7577894	-	regulatory_region_variant	T	C	371178	0.4201	-0.021	0.002	8.83E-17
2	56096892	rs3791679	*EFEMP1*	intron_variant	A	G	377104	0.2400	-0.066	0.003	3.07E-117
2	56111309	rs3791675	*EFEMP1*	intron_variant	C	T	376010	0.2496	-0.061	0.003	3.02E-102
2	56354964	rs1023713	*RP11-481J13.1*	intron_variant	C	T	358325	0.4668	0.013	0.002	1.05E-07
2	71627539	rs3771371	*ZNF638*	intron_variant	C	T	367139	0.5678	-0.027	0.003	1.81E-25
2	71633389	rs6714975	*ZNF638*	synonymous_variant	C	T	381625	0.5694	-0.027	0.002	3.76E-27
2	71654175	rs1804020	*ZNF638*	missense_variant	G	A	367375	0.2429	0.024	0.003	2.79E-16
2	71958480	rs2900976	-	intergenic_variant	C	T	380346	0.3437	0.014	0.002	1.34E-08
2	88874891	rs1805165	*EIF2AK3*	missense_variant	C	A	351511	0.7116	-0.029	0.003	1.28E-23
2	88895123	rs13045	*EIF2AK3*	missense_variant	T	C	374086	0.6567	-0.027	0.003	2.75E-24
2	88895351	rs7571971	*EIF2AK3*	5_prime_UTR_variant	T	C	329212	0.7121	-0.030	0.003	7.78E-24
2	88913273	rs867529	*EIF2AK3*	missense_variant	G	C	365855	0.2863	0.028	0.003	2.35E-23
2	89130009	rs17838437	*AC096579.13*	intron_variant	G	T	376215	0.4207	-0.015	0.002	5.90E-10
2	121612659	rs2166898	*GLI2*	intron_variant	G	A	380346	0.1614	-0.031	0.003	7.26E-22
2	134434824	rs7567288	-	regulatory_region_variant	T	C	358569	0.1971	0.017	0.003	2.24E-08
2	135988127	rs59900519	*ZRANB3*	missense_variant	T	A	351014	0.0907	-0.026	0.005	1.02E-08
2	135988416	rs935615	*ZRANB3*	missense_variant	C	T	349067	0.0895	-0.024	0.005	1.01E-07
2	178545566	rs75127279	*PDE11A*	missense_variant	C	T	381625	0.0245	0.041	0.007	4.98E-08
2	178565913	rs17400325	*AC012499.1*	missense_variant	T	C	381625	0.0362	0.035	0.006	1.12E-08
2	178684720	rs7567851	*PDE11A*	intron_variant	G	C	341110	0.0799	0.039	0.005	1.06E-16
2	179474668	rs16866412	*TTN-AS1*	missense_variant	G	A	381625	0.0134	-0.053	0.010	1.35E-07
2	183703336	rs288326	*FRZB*	missense_variant	G	A	377738	0.1167	0.024	0.004	1.50E-10
2	200142847	rs1813849	*SATB2*	intron_variant	T	C	374251	0.8911	0.025	0.004	2.34E-10
2	217878209	rs6435957	-	intergenic_variant	T	C	380346	0.3141	0.018	0.003	8.26E-12
2	217905832	rs13387042	-	intergenic_variant	A	G	375364	0.4845	0.015	0.002	1.08E-10
2	218271898	rs1351164	*DIRC3*	intron_variant	T	C	381625	0.2000	-0.026	0.003	3.23E-18
2	218283303	rs13395110	*DIRC3*	intron_variant	T	G	380102	0.3264	-0.021	0.003	3.51E-16
2	219195799	rs10932775	*CATIP-AS2*	intron_variant	G	A	380102	0.5029	0.017	0.002	3.05E-13
2	219508372	rs3770213	*ZNF142*	missense_variant	A	T	375498	0.3853	-0.018	0.003	9.70E-12
2	219508988	rs3770214	*ZNF142*	missense_variant	T	C	381625	0.6141	0.018	0.003	3.37E-12
2	219509618	rs2230115	*ZNF142*	missense_variant	C	A	381625	0.5762	0.021	0.003	2.28E-16
2	219555262	rs1344642	*STK36*	missense_variant	G	A	381625	0.4401	-0.022	0.003	7.67E-18
2	219562675	rs1863704	*STK36*	missense_variant	G	A	379977	0.3852	-0.017	0.003	4.91E-11
2	219895548	rs56411706	*CCDC108*	missense_variant	C	A	312571	0.0992	-0.032	0.005	1.73E-11
2	219900068	rs17852959	*CCDC108*	missense_variant	C	T	381625	0.0959	-0.035	0.004	1.52E-15
2	219908369	rs12470505	*CCDC108*	upstream_gene_variant	T	G	381625	0.0954	-0.040	0.004	3.93E-20
2	219924961	rs142036701	*IHH*	missense_variant	G	T	373989	0.0008	-0.320	0.040	1.09E-15
2	219934348	rs1052483	*RP11-33O4.1*	non_coding_transcript_exon_variant	G	T	331731	0.0938	-0.041	0.005	7.46E-19
2	219943846	rs6724465	*NHEJ1*	intron_variant	G	A	381625	0.0944	-0.041	0.004	1.39E-20
2	219949184	rs16859517	*NHEJ1*	intron_variant	C	T	381625	0.0356	0.059	0.006	5.96E-21
2	220046840	rs3210652	*FAM134A*	missense_variant	G	A	381625	0.1418	-0.022	0.004	2.74E-09
2	220078652	rs147445258	*ABCB6*	missense_variant	C	T	373551	0.0095	-0.086	0.012	3.43E-13
2	225047744	rs2629046	-	regulatory_region_variant	T	C	380346	0.4513	-0.021	0.002	1.08E-18
2	232263127	rs2290130	*AC017104.6*	missense_variant	G	A	374981	0.2524	-0.016	0.003	2.28E-09
2	232349636	rs4973417	*NCL*	upstream_gene_variant	G	T	350251	0.5556	-0.020	0.002	3.90E-16
2	232796610	rs749052	-	intergenic_variant	T	C	363269	0.0598	-0.058	0.005	2.97E-29
2	232797966	rs2580816	-	intergenic_variant	C	T	380346	0.1933	-0.036	0.003	1.49E-32

2	232944860	rs3100583	*DIS3L2*	intron_variant	G	A	333941	0.6323	0.021	0.003	1.92E-15
2	232982257	rs11677466	*DIS3L2*	intron_variant	A	T	367424	0.0881	0.051	0.004	1.87E-32
2	233077064	rs7571816	*DIS3L2*	intron_variant	A	G	379016	0.0252	-0.060	0.007	2.35E-16
2	233155110	rs6717918	*DIS3L2*	intron_variant	T	C	375774	0.2437	-0.030	0.003	1.32E-25
2	233633460	rs1801251	*KCNJ13*	missense_variant	G	A	381625	0.3354	-0.018	0.003	4.94E-13
2	233699415	rs10211596	*GIGYF2*	intron_variant	G	A	377729	0.5621	0.014	0.002	2.69E-08
2	238336802	rs6719451	*AC112721.2*	upstream_gene_variant	T	C	371878	0.1089	-0.021	0.004	3.68E-08
2	242163359	rs7590653	*ANO7*	missense_variant	G	A	370395	0.2181	-0.016	0.003	5.28E-08
2	242192848	rs7578199	*HDLBP*	missense_variant	T	C	371918	0.2414	-0.017	0.003	3.35E-09
2	242262986	rs12694997	*42615*	intron_variant	G	A	369545	0.2317	-0.016	0.003	1.79E-07
2	242493511	rs4675801	*BOK-AS1*	intron_variant	C	T	380102	0.4587	-0.019	0.002	4.82E-15
3	11641535	rs6772112	*VGLL4*	intron_variant	C	T	332053	0.9437	0.033	0.006	2.91E-09
3	11643465	rs2276749	*VGLL4*	missense_variant	T	C	381625	0.9498	0.032	0.005	4.08E-09
3	14214524	rs2229089	*XPC*	missense_variant	G	A	380721	0.0308	-0.038	0.007	1.22E-08
3	38047954	rs9816693	*PLCD1*	missense_variant	G	C	375498	0.1723	0.022	0.003	6.08E-12
3	41123735	rs10490823	-	intergenic_variant	C	T	378383	0.5473	0.016	0.002	2.38E-10
3	41137672	rs87938	-	intergenic_variant	A	G	381625	0.5550	0.014	0.002	1.60E-08
3	43097765	rs3732858	*FAM198A*	missense_variant	G	A	380893	0.1753	-0.020	0.003	2.24E-10
3	46939587	rs121434601	*PTH1R*	missense_variant	C	T	373551	0.0025	0.154	0.023	1.30E-11
3	47036565	rs17079425	*NBEAL2*	missense_variant	G	A	316189	0.0195	0.049	0.009	9.31E-08
3	47162886	rs76208147	*SETD2*	missense_variant	C	T	375129	0.0190	0.048	0.009	2.24E-08
3	48623124	rs35761247	*COL7A1*	missense_variant	G	A	360383	0.0538	0.043	0.006	4.51E-15
3	49137043	rs144092780	*QARS*	missense_variant	C	T	362624	0.0024	0.123	0.024	1.91E-07
3	49162284	rs34759087	*LAMB2*	missense_variant	C	T	377738	0.1259	0.028	0.004	5.48E-14
3	49162583	rs35713889	*LAMB2*	missense_variant	C	T	355961	0.0394	0.043	0.006	3.28E-12
3	50597092	rs1034405	*C3orf18*	missense_variant	G	A	381625	0.8684	-0.028	0.004	1.06E-14
3	51071713	rs13088462	*DOCK3*	intron_variant	T	C	338671	0.0538	0.057	0.006	4.52E-24
3	52551010	rs79979130	*STAB1*	synonymous_variant	C	T	366295	0.0859	0.026	0.004	7.69E-09
3	52719398	rs1866268	*GNL3*	intron_variant	C	A	380102	0.4273	-0.015	0.003	2.46E-08
3	52727257	rs2289247	*GNL3*	missense_variant	G	A	381625	0.4273	-0.016	0.003	1.53E-08
3	52740182	rs6617	*SPCS1*	missense_variant	C	G	375498	0.4276	-0.016	0.003	1.70E-08
3	52833219	rs2535629	*ITIH3*	intron_variant	G	A	378383	0.3508	-0.021	0.003	1.48E-13
3	52852538	rs4687657	*ITIH4*	missense_variant	G	T	328036	0.2663	-0.019	0.003	2.72E-09
3	52874288	rs6445538	*TMEM110*	3_prime_UTR_variant	T	C	381625	0.2453	-0.019	0.003	1.04E-10
3	53118739	rs2336725	*RP11-894J14.5*	intron_variant	C	T	381625	0.5646	-0.031	0.002	1.04E-36
3	55474073	rs1392224	-	intergenic_variant	A	G	380102	0.4888	0.014	0.002	6.64E-09
3	56530709	rs2054989	-	intergenic_variant	A	G	239445	0.7603	0.020	0.004	4.51E-08
3	56533016	rs978979	-	intergenic_variant	A	G	376860	0.6684	0.017	0.003	8.00E-11
3	56628031	rs7637449	*CCDC66*	missense_variant	G	A	381625	0.5382	0.025	0.003	1.06E-22
3	56650054	rs111934125	*CCDC66*	missense_variant	T	C	381625	0.1124	-0.025	0.004	8.00E-11
3	56658871	rs2291498	*CCDC66*	missense_variant	T	C	371178	0.0984	-0.028	0.004	1.49E-11
3	56667682	rs9835332	*FAM208A*	missense_variant	G	C	375498	0.4608	-0.023	0.003	1.94E-20
3	57528503	rs9311651	*DNAH12*	missense_variant	A	G	378383	0.1591	0.018	0.003	1.04E-07
3	67416322	rs17806888	*SUCLG2*	intron_variant	T	C	381625	0.1140	-0.028	0.004	3.71E-13
3	67426281	rs35494829	*SUCLG2*	missense_variant	T	C	369748	0.1081	-0.029	0.004	6.54E-13
3	72437413	rs9863706	*RYBP*	intron_variant	C	T	381625	0.2157	-0.035	0.003	7.54E-34
3	98512540	rs28489284	*ST3GAL6*	missense_variant	G	A	381625	0.0471	0.028	0.005	1.56E-07
3	98600385	rs9838238	*DCBLD2*	missense_variant	T	C	381625	0.0470	0.029	0.005	1.23E-07
3	114511356	rs12490319	*ZBTB20*	intron_variant	T	C	374251	0.8395	-0.025	0.003	6.47E-15
3	129050756	rs6439167	*RP13-685P2.8*	upstream_gene_variant	T	C	381625	0.7866	0.037	0.003	6.73E-38
3	129284818	rs2625973	*PLXND1*	missense_variant	A	C	381625	0.2713	0.017	0.003	2.88E-09
3	129293256	rs2255703	*PLXND1*	missense_variant	T	C	371247	0.3773	0.016	0.003	8.31E-10
3	134233092	rs10935120	*CEP63*	intron_variant	A	G	380346	0.6794	0.023	0.003	5.53E-20
3	135720540	rs9814557	*PPP2R3A*	missense_variant	A	G	381625	0.3201	-0.020	0.003	8.38E-14
3	135720851	rs6779903	*PPP2R3A*	missense_variant	G	T	381625	0.2720	0.016	0.003	5.41E-09
3	135722264	rs17197552	*PPP2R3A*	missense_variant	A	G	381625	0.3217	-0.020	0.003	4.61E-14
3	135974216	rs9844666	*PCCB*	5_prime_UTR_variant	G	A	381625	0.2418	-0.032	0.003	3.91E-29
3	136574501	rs1052618	*SLC35G2*	missense_variant	A	G	381625	0.6912	-0.021	0.003	1.47E-16
3	141105570	rs724016	*ZBTB38*	5_prime_UTR_variant	A	G	371887	0.4409	0.075	0.002	4.99E-208
3	141134818	rs16851397	*ZBTB38*	intron_variant	A	G	370749	0.0460	0.056	0.006	1.47E-22
3	141137035	rs9825379	*ZBTB38*	intron_variant	G	A	368874	0.0573	0.054	0.005	1.17E-24
3	141143430	rs10513137	*ZBTB38*	intron_variant	G	A	378383	0.0846	0.039	0.004	2.74E-19
3	156862145	rs6809394	*CCNL1*	downstream_gene_variant	C	T	372028	0.3476	-0.016	0.003	2.17E-10
3	157081324	rs11918974	*RP11-550I24.2*	missense_variant	A	G	354284	0.2470	-0.017	0.003	1.17E-09
3	157682536	rs9845687	-	intergenic_variant	T	C	374936	0.7349	-0.017	0.003	1.77E-10
3	157992814	rs7643792	*RSRC1*	intron_variant	A	G	381625	0.4324	0.017	0.002	5.47E-12
3	158104706	rs7648196	*RSRC1*	intron_variant	A	G	192950	0.5093	-0.019	0.003	3.68E-08
3	171780763	rs4894796	*FNDC3B*	intron_variant	A	G	380102	0.5786	0.013	0.002	1.84E-08
3	171969077	rs7652177	*FNDC3B*	missense_variant	C	G	361528	0.5081	0.042	0.002	9.52E-68
3	172165727	rs572169	*GHSR*	synonymous_variant	C	T	378383	0.3131	0.028	0.003	4.90E-27
3	172236440	rs231983	*TNFSF10*	intron_variant	T	G	374487	0.4013	0.020	0.002	1.05E-15
3	183371250	rs11917105	*KLHL24*	intron_variant	T	G	380346	0.2595	-0.014	0.003	1.93E-07
3	183976103	rs11546878	*CAMK2N2*	missense_variant	C	T	352338	0.1778	-0.022	0.003	6.22E-12
3	183995341	rs1001817	*ECE2*	intron_variant	C	T	381625	0.4960	-0.016	0.002	2.50E-11
3	184020542	rs11545169	*PSMD2*	missense_variant	G	T	290994	0.1621	-0.025	0.004	2.01E-11
3	185548683	rs720390	-	intergenic_variant	G	A	381625	0.3814	0.032	0.002	1.20E-37
3	191093175	rs2028574	*CCDC50*	missense_variant	T	A	362281	0.3962	0.014	0.003	1.54E-07
3	191093310	rs4677728	*CCDC50*	missense_variant	A	G	381625	0.3959	0.014	0.003	6.58E-08
3	191114266	rs2293377	*CCDC50*	3_prime_UTR_variant	T	C	381625	0.3709	0.015	0.003	2.34E-09
4	1701317	rs2247341	*SLBP*	synonymous_variant	G	A	366506	0.3460	0.027	0.003	1.58E-25
4	1729556	rs34205238	*TACC3*	missense_variant	G	A	369355	0.1711	-0.021	0.003	3.15E-11
4	1729988	rs1063743	*TACC3*	missense_variant	G	A	322094	0.2552	-0.020	0.003	4.20E-11
4	1732978	rs17680881	*TACC3*	missense_variant	G	A	377429	0.2544	-0.019	0.003	2.11E-11
4	3473139	rs6831256	*DOK7*	intron_variant	A	G	376150	0.4204	-0.013	0.002	1.54E-07
4	5016883	rs11722554	*CYTL1*	missense_variant	G	A	381625	0.0402	-0.049	0.006	2.01E-17
4	5023112	rs10937615	*CYTL1*	upstream_gene_variant	G	A	352474	0.7453	-0.019	0.003	9.69E-12
4	5035587	rs6446315	-	regulatory_region_variant	G	A	378823	0.8288	-0.022	0.003	1.81E-12
4	8503359	rs1949733	*RP11-689P11.2*	intron_variant	A	G	377973	0.6988	0.017	0.003	1.90E-10
4	12963574	rs763318	-	intergenic_variant	G	A	373208	0.4647	-0.026	0.002	2.06E-27

4	17707449	rs61741460	*FAM184B*	missense_variant	C	T	369664	0.0530	-0.034	0.005	3.59E-10
4	17797966	rs7678436	*DCAF16*	downstream_gene_variant	G	A	381625	0.1442	-0.055	0.004	1.44E-51
4	17805379	rs7690457	*DCAF16*	missense_variant	G	A	381625	0.0280	-0.045	0.007	9.28E-11
4	17829990	rs3795243	*NCAPG*	missense_variant	G	C	374724	0.1152	-0.052	0.004	1.87E-39
4	17944840	rs16896068	*LCORL*	intron_variant	G	A	381625	0.1510	-0.065	0.004	3.49E-75
4	17972372	rs2320299	*LCORL*	intron_variant	G	A	381625	0.7303	-0.047	0.003	4.15E-68
4	18017730	rs6830062	*LCORL*	intron_variant	T	C	364582	0.1521	-0.067	0.004	4.18E-75
4	18033488	rs6449353	-	intergenic_variant	T	C	381625	0.1517	-0.067	0.004	5.42E-78
4	25408838	rs34811474	*ANAPC4*	missense_variant	G	A	377876	0.2236	0.021	0.003	1.60E-13
4	39500514	rs1450	*UGDH*	3_prime_UTR_variant	T	C	379252	0.4984	0.013	0.002	5.16E-08
4	40121562	rs794001	*N4BP2*	missense_variant	G	A	344724	0.7676	0.017	0.003	1.15E-08
4	48493237	rs79858408	*ZAR1*	missense_variant	G	A	277710	0.4823	-0.015	0.003	1.35E-07
4	48498290	rs10031777	*FRYL*	downstream_gene_variant	T	C	298554	0.4944	0.018	0.003	1.76E-10
4	48988450	rs3747690	*CWH43*	missense_variant	C	A	356736	0.4824	-0.014	0.002	4.42E-08
4	57797414	rs3796529	*REST*	missense_variant	C	T	126529	0.1845	0.035	0.005	7.85E-11
4	57823476	rs17081935	*RP11-738E22.3*	downstream_gene_variant	C	T	370749	0.1961	0.032	0.003	5.05E-26
4	73178175	rs150270324	*ADAMTS3*	missense_variant	T	C	377738	0.0130	-0.056	0.010	2.38E-08
4	73179445	rs141374503	*ADAMTS3*	missense_variant	C	T	381625	0.0027	-0.119	0.021	1.82E-08
4	73470972	rs1518485	-	intergenic_variant	C	T	372028	0.5439	-0.031	0.003	2.01E-35
4	73472941	rs1589163	-	intergenic_variant	C	T	323434	0.5198	-0.033	0.003	4.44E-36
4	73515313	rs7697556	-	intergenic_variant	T	C	380346	0.5240	-0.033	0.002	1.43E-41
4	81952637	rs74764079	*BMP3*	missense_variant	T	A	359610	0.0246	-0.040	0.008	1.31E-07
4	82149831	rs710841	-	intergenic_variant	C	T	378383	0.2531	0.047	0.003	1.39E-63
4	82318524	rs10028610	-	intergenic_variant	G	A	372028	0.3453	0.027	0.003	5.81E-27
4	87730980	rs61730641	*PTPN13*	missense_variant	C	T	377738	0.0145	-0.086	0.010	1.94E-19
4	103188709	rs13107325	*SLC39A8*	missense_variant	C	T	381625	0.0623	-0.034	0.005	1.96E-12
4	106081636	rs9884482	*TET2*	intron_variant	T	C	358569	0.3878	0.025	0.003	3.44E-23
4	106106353	rs10010325	*TET2*	intron_variant	C	A	349669	0.4880	0.028	0.003	2.22E-28
4	106196951	rs2454206	*TET2*	missense_variant	A	G	379252	0.3686	-0.026	0.003	8.04E-25
4	106317429	rs13787	*PPA2*	missense_variant	C	G	367424	0.4592	-0.015	0.002	2.26E-09
4	109408608	rs1562975	-	intergenic_variant	G	A	377729	0.2979	0.027	0.003	7.40E-26
4	120422407	rs149385790	*PDE5A*	missense_variant	T	G	365908	0.0014	0.257	0.031	7.50E-17
4	120716967	rs7699214	*LINC01365*	downstream_gene_variant	A	G	355718	0.5293	0.014	0.002	3.20E-08
4	122664323	rs28532673	-	intergenic_variant	G	A	369655	0.4126	0.017	0.002	3.12E-12
4	122665514	rs7659604	-	intergenic_variant	C	T	209260	0.4130	0.018	0.003	1.04E-07
4	122748308	rs1507995	*BBS7*	intron_variant	G	A	156040	0.3248	0.022	0.004	2.58E-08
4	123838758	rs12648093	*NUDT6*	missense_variant	A	G	370309	0.7429	-0.017	0.003	4.88E-10
4	135121721	rs116807401	*PABPC4L*	missense_variant	T	C	381625	0.0171	0.065	0.009	1.39E-13
4	144359490	rs28925904	*GAB1*	missense_variant	C	T	381625	0.0186	-0.048	0.008	1.04E-08
4	145485738	rs1980057	-	intergenic_variant	C	T	379016	0.4252	0.014	0.003	1.38E-07
4	145568352	rs7689420	*HHIP-AS1*	non_coding_transcript_exon_variant	T	C	372272	0.8370	0.075	0.003	2.80E-110
4	145574844	rs1812175	*HHIP*	intron_variant	A	G	378383	0.8373	0.075	0.003	4.93E-111
4	145643079	rs6854783	*HHIP*	intron_variant	G	A	380346	0.5902	0.033	0.003	2.75E-37
4	145650021	rs1492820	*HHIP*	intron_variant	G	A	374731	0.5504	0.040	0.003	1.07E-56
4	145658429	rs2639576	*HHIP*	intron_variant	T	C	380102	0.4550	-0.026	0.002	1.32E-25
4	154557616	rs34343821	*KIAA0922*	missense_variant	C	T	361674	0.0113	0.059	0.011	7.75E-08
4	184236868	rs4862155	*WWC2*	missense_variant	G	A	380102	0.0649	-0.038	0.005	2.40E-15
5	31515657	rs55656741	*DROSHA*	missense_variant	G	A	381625	0.4935	0.014	0.002	1.63E-09
5	32784907	rs146301345	*AC026703.1*	missense_variant	G	A	380850	0.0025	0.128	0.022	1.05E-08
5	32830521	rs1173727	-	intergenic_variant	T	C	377104	0.5929	-0.035	0.002	1.65E-46
5	32888818	rs10472828	*CTD-2218G20.1*	upstream_gene_variant	C	T	381625	0.4508	-0.016	0.002	8.82E-11
5	32941161	rs10067052	*CTD-2066L21.3*	intron_variant	G	A	372028	0.4168	-0.015	0.002	1.21E-09
5	33176567	rs11744729	*CTD-2066L21.3*	intron_variant	G	A	357743	0.5504	0.019	0.002	3.07E-14
5	33230034	rs11745439	*CTD-2066L21.3*	intron_variant	A	G	376860	0.7253	0.023	0.003	8.30E-18
5	36954812	rs292182	*NIPBL*	intron_variant	G	A	378823	0.4324	-0.024	0.002	2.62E-22
5	37239240	rs7735138	*C5orf42*	intron_variant	A	C	357778	0.3632	-0.017	0.003	3.03E-11
5	41574561	rs668732	-	intergenic_variant	C	A	372028	0.4790	-0.013	0.002	1.74E-07
5	42473555	rs13188386	*GHR*	intron_variant	G	A	377973	0.2676	-0.019	0.003	7.11E-12
5	42719239	rs6180	*GHR*	missense_variant	A	C	359266	0.4485	-0.021	0.003	1.81E-16
5	42782492	rs2973011	*CCDC152*	intron_variant	T	C	372028	0.4494	-0.021	0.002	8.34E-17
5	54439466	rs1021580	*CDC20B*	missense_variant	G	A	376643	0.8294	-0.019	0.003	5.47E-09
5	54960609	rs4865614	*SLC38A9*	synonymous_variant	A	G	376017	0.6699	-0.028	0.003	1.02E-25
5	54960673	rs4865615	*SLC38A9*	missense_variant	C	G	335008	0.6695	-0.030	0.003	1.58E-26
5	55001899	rs11958779	*SLC38A9*	intron_variant	G	A	380346	0.6934	-0.028	0.003	1.50E-24
5	56031884	rs889312	-	intergenic_variant	C	A	380346	0.7217	0.019	0.003	7.88E-13
5	56155672	rs56069227	*AC008937.2*	missense_variant	A	G	349519	0.0284	-0.039	0.007	7.46E-08
5	56177443	rs702689	*MAP3K1*	missense_variant	G	A	379252	0.7140	0.018	0.003	9.59E-11
5	56177743	rs832582	*MAP3K1*	missense_variant	G	A	379252	0.8190	0.020	0.003	2.29E-10
5	56207123	rs2257505	*SETD9*	missense_variant	T	A	372631	0.7573	0.018	0.003	2.63E-10
5	64766798	rs61736454	*ADAMTS6*	missense_variant	G	A	360412	0.0019	-0.152	0.026	7.82E-09
5	67596088	rs3756668	*PIK3R1*	3_prime_UTR_variant	G	A	376010	0.4408	-0.014	0.002	1.65E-08
5	88354675	rs10037512	*MEF2C-AS1*	intron_variant	T	C	381625	0.4580	-0.029	0.002	3.99E-32
5	88376061	rs1366594	*MEF2C-AS1*	intron_variant	A	C	377104	0.4589	-0.028	0.002	4.30E-30
5	88416354	rs9293511	*MEF2C-AS1*	intron_variant	C	T	379977	0.3685	-0.028	0.003	3.22E-29
5	90151589	rs2247870	*ADGRV1*	missense_variant	G	A	381625	0.5479	0.014	0.002	8.35E-09
5	95539448	rs4869272	*CTD-2337A12.1*	intron_variant	C	T	381625	0.6842	-0.015	0.003	4.97E-09
5	95728898	rs6235	*PCSK1*	missense_variant	C	G	350404	0.2741	0.020	0.003	5.59E-12
5	95728974	rs6234	*PCSK1*	missense_variant	G	C	375498	0.2741	0.019	0.003	1.36E-11
5	108113344	rs13177718	*FER*	intron_variant	C	T	353936	0.0733	-0.032	0.005	2.13E-11
5	122685727	rs1047437	*CEP120*	missense_variant	C	G	375498	0.1652	-0.017	0.003	1.03E-07
5	122718736	rs6595440	*CEP120*	missense_variant	G	C	151761	0.4327	-0.025	0.004	5.02E-11
5	126250812	rs34821177	*MARCH3*	missense_variant	C	T	369748	0.0359	0.034	0.006	4.25E-08
5	127371588	rs10063647	*LINC01184*	intron_variant	A	G	376450	0.4603	0.015	0.002	2.97E-10
5	127668685	rs78727187	*FBN2*	missense_variant	G	T	355312	0.0060	0.183	0.015	2.47E-33
5	127685135	rs154001	*FBN2*	missense_variant	C	T	381625	0.6862	0.020	0.003	4.73E-15
5	127699375	rs374748	*FBN2*	intron_variant	G	A	372272	0.9014	0.023	0.004	1.63E-08
5	131396478	rs40401	*IL3*	missense_variant	C	T	377738	0.2352	-0.017	0.003	4.69E-09
5	131447104	rs247008	-	regulatory_region_variant	A	G	368141	0.6633	0.023	0.003	4.35E-18
5	131607721	rs10479001	*P4HA2*	missense_variant	C	T	351940	0.0430	0.039	0.006	1.23E-10

5	131663062	rs272893	*SLC22A4*	missense_variant	T	C	369664	0.6083	0.031	0.003	4.38E-31
5	131676320	rs1050152	*SLC22A4*	missense_variant	C	T	305232	0.4195	0.021	0.003	1.95E-11
5	131699867	rs274546	*MIR3936*	intron_variant	A	G	374496	0.6076	0.030	0.003	1.86E-30
5	131723288	rs2073643	*SLC22A5*	intron_variant	T	C	377738	0.5344	0.022	0.003	9.50E-18
5	131744574	rs1016988	*C5orf56*	upstream_gene_variant	T	C	377738	0.2047	-0.020	0.003	2.27E-10
5	131770805	rs2188962	*C5orf56*	intron_variant	C	T	365505	0.4081	0.022	0.003	3.34E-16
5	131784393	rs12521868	*C5orf56*	intron_variant	G	T	375727	0.4072	0.023	0.003	2.51E-18
5	131801726	rs2522056	*AC116366.6*	intron_variant	G	A	376459	0.2043	-0.023	0.003	4.40E-13
5	134076812	rs12657663	*CAMLG*	missense_variant	G	A	379977	0.1076	-0.023	0.004	2.41E-09
5	134356705	rs526896	-	intergenic_variant	T	G	380346	0.2737	-0.026	0.003	2.35E-21
5	134364518	rs479632	*C5orf66*	missense_variant	C	G	373646	0.2564	-0.029	0.003	4.49E-25
5	134372685	rs31198	*C5orf66*	intron_variant	T	C	381625	0.2564	-0.030	0.003	6.45E-26
5	135288632	rs62623707	*LECT2*	missense_variant	A	G	381625	0.0435	-0.030	0.006	1.02E-07
5	141573265	rs3910203	-	intergenic_variant	G	A	380102	0.5984	0.013	0.002	7.76E-08
5	168256240	rs4282339	*SLIT3*	intron_variant	G	A	377973	0.2025	-0.031	0.003	4.05E-26
5	170838791	rs11745536	*NPM1*	downstream_gene_variant	G	A	372028	0.5545	-0.022	0.002	1.71E-19
5	171281875	rs4868125	-	intergenic_variant	C	G	371882	0.5905	0.032	0.002	6.65E-39
5	172196752	rs34471628	*DUSP1*	missense_variant	A	G	355545	0.0362	0.048	0.006	4.00E-14
5	172197790	rs34013988	*DUSP1*	missense_variant	C	T	231563	0.0345	0.055	0.008	6.35E-12
5	172755066	rs148833559	*STC2*	missense_variant	C	A	369802	0.0010	0.290	0.037	5.69E-15
5	172984114	rs889014	-	regulatory_region_variant	C	T	380346	0.3543	-0.028	0.002	1.34E-28
5	173003451	rs1077613	*CTB-33O18.3*	upstream_gene_variant	T	C	377729	0.3305	-0.017	0.003	8.41E-12
5	176516631	rs1966265	*FGFR4*	missense_variant	G	A	381625	0.2324	0.048	0.003	2.63E-64
5	176517326	rs422421	*FGFR4*	intron_variant	T	C	376735	0.7880	0.039	0.003	1.14E-38
5	176517797	rs376618	*FGFR4*	missense_variant	C	T	361650	0.7573	0.025	0.003	8.55E-18
5	176554850	rs11954311	-	intergenic_variant	G	A	354618	0.0284	0.059	0.007	1.34E-15
5	176637471	rs28932177	*NSD1*	missense_variant	G	A	350397	0.0281	0.063	0.007	2.38E-17
5	176637576	rs28932178	*NSD1*	missense_variant	T	C	359848	0.1528	0.021	0.003	2.24E-09
5	176722005	rs78247455	*NSD1*	missense_variant	G	A	377738	0.0229	-0.083	0.008	1.86E-26
5	176734179	rs149685981	*RAB24*	missense_variant	C	T	359848	0.0142	0.055	0.010	2.51E-08
5	176830627	rs17876032	*F12*	non_coding_transcript_exon_variant	G	A	364515	0.6519	-0.022	0.003	1.25E-17
5	176842474	rs2731672	*GRK6*	intron_variant	T	C	378383	0.7506	-0.026	0.003	1.02E-19
5	178507069	rs1445846	*RP11-281O15.7*	missense_variant	T	C	381625	0.6704	-0.021	0.003	3.45E-15
5	178507090	rs1445845	*RP11-281O15.7*	missense_variant	G	A	381625	0.6703	-0.021	0.003	1.81E-15
5	178540975	rs1054480	*ADAMTS2*	missense_variant	G	A	343607	0.2932	-0.016	0.003	9.78E-09
5	179731014	rs6879260	*GFPT2*	intron_variant	T	C	381625	0.6123	0.032	0.002	3.96E-39
6	1901495	rs1570534	*GMDS*	intron_variant	C	T	372028	0.6754	0.017	0.003	7.56E-11
6	7211818	rs1334576	*RREB1*	missense_variant	G	A	359848	0.4240	0.014	0.003	1.49E-08
6	7231843	rs9379084	*RREB1*	missense_variant	G	A	294781	0.1136	-0.053	0.004	2.23E-36
6	7247344	rs35742417	*RREB1*	missense_variant	C	A	381625	0.1847	0.032	0.003	5.10E-24
6	7310259	rs10004	*SSR1*	missense_variant	A	G	381625	0.2716	0.021	0.003	1.70E-14
6	7720059	rs12198986	-	intergenic_variant	G	A	381625	0.4662	0.038	0.002	5.07E-56
6	7725760	rs3812163	*BMP6*	upstream_gene_variant	A	T	362089	0.4561	0.039	0.003	6.43E-54
6	17665479	rs6906499	*NUP153*	missense_variant	G	C	374724	0.3085	0.014	0.003	9.19E-08
6	17675246	rs2228375	*NUP153*	missense_variant	T	C	381625	0.3128	0.015	0.003	6.37E-09
6	17699322	rs12199222	*NUP153*	intron_variant	G	T	380346	0.3070	0.014	0.003	1.26E-07
6	19841493	rs1047014	*ID4*	upstream_gene_variant	T	C	377104	0.2480	0.029	0.003	1.03E-25
6	25776949	rs11754288	*SLC17A4*	missense_variant	G	A	377738	0.4319	0.023	0.003	1.68E-17
6	25813150	rs1165196	*SLC17A1*	missense_variant	G	A	377738	0.5521	-0.022	0.003	9.86E-17
6	25823444	rs1183201	*SLC17A1*	intron_variant	A	T	308256	0.5364	-0.022	0.003	8.74E-15
6	25842951	rs1408272	*SLC17A3*	intron_variant	T	G	364907	0.0621	0.029	0.005	9.86E-08
6	25870542	rs1165205	*SLC17A3*	intron_variant	T	A	368369	0.5312	-0.023	0.003	4.25E-17
6	26056604	rs2230653	*HIST1H1C*	missense_variant	G	A	360743	0.0291	-0.044	0.007	1.18E-09
6	26107790	rs198845	*HIST1H1T*	missense_variant	G	T	356525	0.3788	0.035	0.003	1.50E-37
6	26108168	rs2051542	*HIST1H1T*	missense_variant	G	A	377738	0.0727	-0.030	0.005	7.13E-11
6	26108282	rs198844	*HIST1H1T*	missense_variant	C	G	357641	0.5427	0.017	0.003	1.75E-10
6	26200677	rs806794	*HIST1H2AD*	3_prime_UTR_variant	A	G	317367	0.3005	-0.051	0.003	5.66E-66
6	26233387	rs10946808	*HIST1H1D*	non_coding_transcript_exon_variant	A	G	375365	0.3016	-0.049	0.003	1.48E-71
6	26500563	rs13194984	*BTN1A1*	upstream_gene_variant	G	T	376459	0.1250	0.027	0.004	2.94E-12
6	26505362	rs3736781	*BTN1A1*	missense_variant	G	A	377738	0.4618	0.014	0.003	4.56E-08
6	27037080	rs13194491	-	intergenic_variant	C	T	374811	0.0710	0.027	0.005	1.61E-07
6	27178028	rs858985	*RP11-209A2.1*	upstream_gene_variant	T	C	303689	0.8958	0.026	0.005	3.29E-08
6	28916252	rs4947339	*LINC01556*	downstream_gene_variant	C	T	365143	0.4079	-0.022	0.003	2.57E-13
6	29045632	rs9393941	*SAR1P1*	upstream_gene_variant	G	A	374496	0.3980	-0.021	0.003	1.03E-12
6	29080344	rs3749977	*OR2J3*	missense_variant	G	A	375365	0.2409	-0.017	0.003	1.47E-07
6	29084232	rs3129109	*OR2J3*	downstream_gene_variant	T	C	374496	0.6021	0.021	0.003	1.18E-12
6	29191411	rs714470	*XXbac-BPG308J9.3*	upstream_gene_variant	C	A	366737	0.5789	0.017	0.003	8.04E-09
6	29274486	rs9257694	*OR14J1*	missense_variant	T	C	377738	0.5243	0.018	0.003	1.23E-09
6	29350854	rs1419640	*OR5V1*	intron_variant	G	T	363055	0.5567	0.016	0.003	1.48E-07
6	29611229	rs29233	-	intergenic_variant	C	G	315621	0.0562	-0.037	0.007	1.04E-07
6	30281234	rs9295843	*HCG18*	intron_variant	T	A	345633	0.2270	-0.021	0.004	1.66E-07
6	30297529	rs2057727	*HCG18*	synonymous_variant	T	C	373217	0.2322	-0.020	0.004	1.62E-07
6	30851933	rs7757648	*DDR1*	intron_variant	G	A	320859	0.0132	-0.075	0.013	1.11E-08
6	30861729	rs3132572	*DDR1*	intron_variant	G	A	374496	0.8953	-0.028	0.005	1.10E-07
6	30882689	rs6926224	*GTF2H4*	missense_variant	C	T	377738	0.0292	-0.041	0.008	1.63E-07
6	30882803	rs6926723	*GTF2H4*	missense_variant	G	A	376215	0.0292	-0.041	0.008	1.79E-07
6	30914751	rs2517451	*DPCR1*	intron_variant	C	T	366422	0.8920	-0.027	0.005	1.33E-07
6	30920086	rs79792575	*DPCR1*	missense_variant	C	T	377738	0.0292	-0.043	0.008	4.88E-08
6	30994470	rs116633440	*MUC22*	missense_variant	C	G	173447	0.0115	-0.094	0.017	7.83E-08
6	30997824	rs12110785	*MUC22*	missense_variant	T	C	377738	0.1476	-0.024	0.004	1.71E-08
6	31005726	rs2844670	*MUC22*	downstream_gene_variant	G	A	352719	0.8386	-0.023	0.004	1.69E-07
6	31019562	rs2394427	*HCG22*	upstream_gene_variant	G	A	250654	0.1507	-0.028	0.005	2.92E-08
6	31038756	rs2517490	-	regulatory_region_variant	G	T	374496	0.0151	-0.069	0.012	2.35E-09
6	31079994	rs2233976	*PSORS1C1*	missense_variant	C	T	377738	0.0948	-0.035	0.005	2.45E-11
6	31112484	rs130072	*CCHCR1*	missense_variant	C	T	377738	0.0894	-0.042	0.005	1.89E-14
6	31118898	rs11540822	*CCHCR1*	missense_variant	A	T	363537	0.0880	-0.040	0.006	5.82E-13
6	31125257	rs72856718	*CCHCR1*	stop_gained	C	A	305357	0.0912	-0.042	0.006	2.73E-13
6	31129707	rs2073724	*POU5F1*	missense_variant	C	T	369664	0.0893	-0.042	0.005	2.24E-14
6	31132085	rs3130933	*POU5F1*	intron_variant	T	C	353266	0.8683	-0.036	0.005	1.14E-11

6	31158689	rs7759909	*XXbac-BPG299F13.17*	downstream_gene_variant	G	T	292957	0.1133	-0.029	0.005	1.34E-08
6	31159345	rs1265180	*XXbac-BPG299F13.17*	downstream_gene_variant	C	A	339798	0.0176	-0.060	0.011	6.18E-08
6	31162963	rs4713447	*HCG27*	upstream_gene_variant	A	G	377738	0.4298	-0.018	0.003	6.26E-09
6	31165566	rs3094609	*HCG27*	missense_variant	T	C	373217	0.8541	-0.030	0.005	8.12E-10
6	31170713	rs9263873	*HCG27*	3_prime_UTR_variant	T	C	375365	0.4290	-0.018	0.003	1.75E-08
6	31174527	rs2894181	*HCG27*	upstream_gene_variant	A	G	376459	0.4883	-0.018	0.003	3.70E-09
6	31177915	rs3130952	-	regulatory_region_variant	G	A	374496	0.8544	-0.031	0.005	5.38E-10
6	31184196	rs3869109	-	regulatory_region_variant	A	G	363620	0.5825	-0.019	0.003	1.09E-08
6	31190850	rs12662501	*XXbac-BPG299F13.15*	non_coding_transcript_exon_variant	C	T	377738	0.1566	-0.024	0.004	1.23E-08
6	31207920	rs3132499	-	regulatory_region_variant	C	T	373217	0.8545	-0.030	0.005	1.29E-09
6	31232111	rs3130542	*HLA-C*	downstream_gene_variant	A	G	364582	0.7958	-0.021	0.004	1.70E-07
6	31237124	rs1130838	*HLA-C*	missense_variant	T	C	369770	0.6805	-0.024	0.004	5.85E-12
6	31244021	rs2524074	*HLA-C*	non_coding_transcript_exon_variant	G	A	372123	0.6981	-0.026	0.004	1.22E-12
6	31247067	rs7382297	*RPL3P2*	upstream_gene_variant	T	G	314512	0.8542	-0.028	0.005	4.55E-08
6	31252396	rs2524054	*WASF5P*	downstream_gene_variant	A	C	337955	0.7382	-0.031	0.004	1.77E-12
6	31254088	rs2853933	*WASF5P*	downstream_gene_variant	T	C	363628	0.6003	-0.021	0.004	4.28E-09
6	31257625	rs2524040	*XXbac-BPG248L24.13*	upstream_gene_variant	T	C	363628	0.6002	-0.020	0.004	5.37E-09
6	31258837	rs9468925	*XXbac-BPG248L24.13*	upstream_gene_variant	G	A	366870	0.3863	-0.019	0.003	5.74E-09
6	31259579	rs2524163	*XXbac-BPG248L24.13*	upstream_gene_variant	C	T	341826	0.6007	-0.021	0.004	8.10E-09
6	31261276	rs2243868	*XXbac-BPG248L24.13*	upstream_gene_variant	A	G	368149	0.6001	-0.021	0.003	2.57E-09
6	31262169	rs3873379	*XXbac-BPG248L24.13*	intron_variant	T	C	362715	0.3111	-0.018	0.003	4.14E-08
6	31265490	rs2247056	*XXbac-BPG248L24.13*	intron_variant	T	C	356731	0.7395	-0.033	0.004	7.42E-15
6	31265539	rs3905495	*XXbac-BPG248L24.13*	intron_variant	G	A	374496	0.3553	-0.018	0.003	1.38E-08
6	31266190	rs2853922	*XXbac-BPG248L24.13*	intron_variant	A	G	329881	0.6017	-0.022	0.004	6.06E-10
6	31266522	rs2524089	*XXbac-BPG248L24.13*	intron_variant	G	T	364907	0.6009	-0.021	0.003	2.16E-09
6	31272261	rs6457374	*XXbac-BPG248L24.13*	upstream_gene_variant	C	T	165195	0.7497	-0.036	0.006	4.85E-09
6	31273745	rs3873386	*XXbac-BPG248L24.13*	upstream_gene_variant	T	C	373217	0.4032	-0.017	0.003	5.51E-08
6	31321685	rs1058026	*HLA-B*	3_prime_UTR_variant	A	C	361779	0.1721	-0.020	0.004	1.49E-07
6	31328542	rs2523578	*HLA-B*	upstream_gene_variant	G	A	337955	0.7452	-0.032	0.004	5.46E-13
6	31330546	rs2596548	*DHFRP2*	downstream_gene_variant	T	G	376459	0.8313	-0.030	0.004	7.77E-12
6	31331829	rs2523554	*DHFRP2*	downstream_gene_variant	C	T	374496	0.6183	-0.022	0.003	1.33E-11
6	31342484	rs2523644	*FGFR3P1*	upstream_gene_variant	C	T	265963	0.8307	-0.032	0.005	1.83E-09
6	31353593	rs2844529	*ZDHHC20P2*	upstream_gene_variant	G	A	374496	0.3257	-0.018	0.003	8.34E-08
6	31354819	rs4711269	*HLA-S*	upstream_gene_variant	C	T	377738	0.2556	-0.019	0.003	1.15E-07
6	31360341	rs7771971	*XXbac-BPG181B23.7*	downstream_gene_variant	T	C	220329	0.2593	-0.024	0.005	8.39E-08
6	31362930	rs2523467	*XXbac-BPG181B23.7*	non_coding_transcript_exon_variant	C	T	362619	0.3242	-0.018	0.003	1.87E-07
6	31379304	rs2853977	*HCP5*	intron_variant	A	T	342940	0.5403	-0.024	0.003	8.63E-13
6	31380529	rs2256183	*HCP5*	intron_variant	A	G	359104	0.5432	-0.026	0.003	5.74E-16
6	31387373	rs2596530	*HCP5*	intron_variant	G	A	336765	0.5420	-0.025	0.003	3.24E-14
6	31388214	rs2844513	*HCP5*	intron_variant	G	A	342077	0.4260	-0.018	0.003	3.11E-08
6	31488145	rs3130637	*XXbac-BPG16N22.5*	upstream_gene_variant	A	G	361096	0.7586	-0.020	0.004	1.42E-07
6	31491131	rs3093992	*PPIAP9*	upstream_gene_variant	C	A	373217	0.7586	-0.020	0.004	8.35E-08
6	31496915	rs2259435	*AL662801.1*	missense_variant	G	A	357943	0.1713	-0.023	0.004	4.43E-09
6	31496925	rs3093983	*AL662801.1*	missense_variant	G	A	377738	0.8143	-0.024	0.004	7.32E-09
6	31496949	rs78957773	*AL662801.1*	missense_variant	C	T	377738	0.0200	-0.057	0.010	1.23E-08
6	31497835	rs3115537	*AL662801.1*	3_prime_UTR_variant	G	C	362767	0.8140	-0.024	0.004	8.32E-09
6	31498497	rs3093978	*AL662801.1*	non_coding_transcript_exon_variant	C	A	373217	0.8141	-0.024	0.004	9.74E-09
6	31502767	rs3131628	*AL662801.1*	non_coding_transcript_exon_variant	C	T	374496	0.8143	-0.024	0.004	5.11E-09
6	31506801	rs2523512	*DDX39B*	intron_variant	G	A	365299	0.1725	-0.022	0.004	1.36E-08
6	31511857	rs2251824	*DDX39B*	intron_variant	G	A	369820	0.1609	-0.022	0.004	2.57E-08
6	31538244	rs2009658	*LTA*	upstream_gene_variant	C	G	353778	0.1593	-0.023	0.004	5.99E-09
6	31540556	rs2229094	*LTA*	missense_variant	T	C	377738	0.2665	-0.019	0.003	3.66E-09
6	31542308	rs1799964	*LTA*	upstream_gene_variant	T	C	355961	0.2070	-0.020	0.004	2.34E-08
6	31542476	rs1800630	*LTA*	upstream_gene_variant	C	A	367409	0.1576	-0.024	0.004	3.06E-09
6	31564821	rs2844480	*NCR3*	upstream_gene_variant	C	T	373217	0.1957	-0.022	0.004	1.93E-09
6	31572956	rs2844479	-	intergenic_variant	A	C	364899	0.3460	-0.018	0.003	2.92E-08
6	31578772	rs2844477	*AIF1*	upstream_gene_variant	T	C	366422	0.3678	-0.020	0.003	1.57E-09
6	31582025	rs3132451	*AIF1*	upstream_gene_variant	G	C	362767	0.1926	0.026	0.004	4.15E-09
6	31583827	rs2259571	*AIF1*	5_prime_UTR_variant	T	G	377738	0.3671	-0.020	0.003	8.09E-10
6	31585219	rs2857697	*PRRC2A*	upstream_gene_variant	C	T	373521	0.3878	-0.023	0.003	2.61E-12
6	31587561	rs2736176	*AIF1*	upstream_gene_variant	G	C	361134	0.3118	-0.018	0.003	1.19E-07
6	31587870	rs2857694	*AIF1*	upstream_gene_variant	A	T	368339	0.3885	-0.023	0.003	3.75E-12
6	31589676	rs2844472	*AIF1*	intron_variant	A	G	374496	0.3685	-0.021	0.003	3.47E-10
6	31591808	rs3130070	*PRRC2A*	intron_variant	A	G	377738	0.1843	0.026	0.004	3.01E-09
6	31595487	rs2736171	*PRRC2A*	intron_variant	A	G	373521	0.3875	-0.024	0.003	3.73E-13
6	31603591	rs2261033	*BAG6*	non_coding_transcript_exon_variant	A	G	361340	0.4782	-0.025	0.003	2.76E-14
6	31603770	rs11229	*BAG6*	synonymous_variant	A	G	377738	0.1844	0.026	0.004	4.05E-09
6	31610529	rs1077393	*BAG6*	non_coding_transcript_exon_variant	A	G	362619	0.4813	-0.018	0.003	7.30E-08
6	31610686	rs1052486	*BAG6*	missense_variant	A	G	340233	0.4822	-0.018	0.003	3.66E-08
6	31611777	rs760293	*BAG6*	intron_variant	T	C	334398	0.8339	-0.024	0.004	5.11E-08
6	31618761	rs3130050	*BAG6*	intron_variant	G	A	376459	0.8605	-0.026	0.005	1.21E-07
6	31619576	rs3117583	*BAG6*	5_prime_UTR_variant	A	G	374496	0.1844	0.026	0.004	7.12E-09
6	31632134	rs3130618	*XXbac-BPG32J3.22*	missense_variant	C	A	355379	0.1845	0.026	0.004	3.64E-09
6	31812038	rs9267576	*C6orf48*	downstream_gene_variant	T	G	374936	0.8646	-0.029	0.005	6.49E-09
6	31883957	rs644045	*C2*	intron_variant	A	G	363628	0.6574	-0.020	0.004	2.28E-08
6	31888367	rs3130683	*C2*	intron_variant	C	T	368141	0.8627	-0.031	0.005	3.92E-10
6	31912523	rs36221133	*CFB*	missense_variant	T	C	377738	0.0142	-0.079	0.012	1.26E-11
6	31916400	rs537160	*CFB*	intron_variant	A	G	357141	0.6686	-0.025	0.004	1.78E-12
6	31922254	rs630379	*SKIV2L*	intron_variant	A	C	346273	0.7162	-0.022	0.004	2.78E-08
6	31927342	rs440454	*SKIV2L*	non_coding_transcript_exon_variant	A	G	351751	0.7131	-0.023	0.004	2.84E-09
6	31928799	rs419788	*SKIV2L*	intron_variant	T	C	363628	0.7130	-0.023	0.004	2.12E-09
6	31929014	rs437179	*SKIV2L*	missense_variant	A	C	340416	0.7104	-0.022	0.004	2.60E-08
6	31946614	rs6941112	*STK19*	intron_variant	G	A	377738	0.3250	-0.019	0.003	4.52E-09
6	31947460	rs389883	*STK19*	non_coding_transcript_exon_variant	G	T	342481	0.7147	-0.024	0.004	6.20E-10
6	32071893	rs3134954	*TNXB*	intron_variant	C	T	374496	0.8616	-0.029	0.005	2.26E-09
6	32080146	rs3130342	*ATF6B*	intron_variant	A	C	373217	0.8621	-0.027	0.005	1.97E-08
6	32083175	rs8111	*ATF6B*	3_prime_UTR_variant	C	T	374496	0.2940	-0.018	0.003	1.34E-07
6	32088854	rs2228628	*ATF6B*	synonymous_variant	G	C	361993	0.3041	-0.019	0.003	4.58E-08
6	32105001	rs4713505	-	intergenic_variant	G	T	377738	0.3060	-0.018	0.003	7.60E-08

6	32112626	rs3130279	*PRRT1*	downstream_gene_variant	A	G	376459	0.8605	-0.027	0.005	1.73E-08
6	32113980	rs4713506	*PRRT1*	downstream_gene_variant	G	A	377738	0.2922	-0.019	0.003	2.23E-08
6	32119898	rs3131283	*PPT2-EGFL8*	5_prime_UTR_variant	T	C	373217	0.8673	-0.027	0.005	6.54E-08
6	32151222	rs1035798	*PBX2*	splice_region_variant	G	A	364907	0.2593	-0.019	0.003	1.44E-08
6	32151994	rs1800684	*PBX2*	synonymous_variant	A	T	346764	0.8680	-0.029	0.005	1.01E-08
6	32179896	rs2071286	*NOTCH4*	intron_variant	C	T	363628	0.2256	-0.019	0.004	5.94E-08
6	32190028	rs3132946	*NOTCH4*	intron_variant	A	G	376459	0.8661	-0.027	0.005	4.77E-08
6	32411646	rs7192	*HLA-DRA*	missense_variant	T	G	377006	0.5941	-0.019	0.003	3.76E-09
6	32412480	rs7194	*HLA-DRA*	3_prime_UTR_variant	G	A	376459	0.5943	-0.020	0.003	2.54E-09
6	32413459	rs2227139	*HLA-DRA*	downstream_gene_variant	G	A	362619	0.5936	-0.019	0.003	6.27E-09
6	32658310	rs9469220	-	intergenic_variant	G	A	360383	0.4866	-0.022	0.003	4.04E-12
6	32663851	rs6457617	-	intergenic_variant	C	T	374936	0.5043	-0.026	0.003	4.34E-17
6	32663999	rs6457620	-	intergenic_variant	G	C	245314	0.5153	-0.027	0.004	1.34E-12
6	32664458	rs2647012	-	intergenic_variant	T	C	374496	0.6009	-0.026	0.003	1.09E-14
6	32669018	rs1612904	*MTCO3P1*	downstream_gene_variant	C	A	340913	0.6284	-0.026	0.004	1.91E-13
6	32670308	rs2856717	*MTCO3P1*	downstream_gene_variant	A	G	373217	0.6035	-0.025	0.003	5.82E-14
6	32675109	rs9275524	*MTCO3P1*	upstream_gene_variant	T	C	365861	0.5680	-0.021	0.003	3.28E-10
6	32678182	rs6932517	*MTCO3P1*	upstream_gene_variant	C	G	258427	0.5741	-0.021	0.004	6.51E-08
6	32678999	rs9275572	*MTCO3P1*	upstream_gene_variant	A	G	376459	0.5681	-0.022	0.003	5.98E-12
6	32681631	rs9275596	*XXbac-BPG254F23.7*	upstream_gene_variant	C	T	375365	0.6290	-0.026	0.003	8.15E-15
6	33626717	rs2296343	*ITPR3*	intron_variant	T	C	378383	0.2847	0.018	0.003	7.79E-10
6	33665020	rs658087	*UQCC2*	3_prime_UTR_variant	T	A	302464	0.1450	-0.024	0.004	2.25E-08
6	33686103	rs549652	*IP6K3*	downstream_gene_variant	G	A	380102	0.1449	-0.022	0.004	3.89E-09
6	33690796	rs4713668	*IP6K3*	missense_variant	C	T	381625	0.4622	0.020	0.003	3.55E-15
6	33719877	rs943463	-	regulatory_region_variant	T	C	378823	0.8050	0.024	0.003	1.00E-11
6	33723383	rs1536500	-	intergenic_variant	T	C	319051	0.8005	0.022	0.004	1.80E-09
6	33728755	rs2395449	-	intergenic_variant	T	A	353254	0.3770	0.018	0.003	3.23E-11
6	33745071	rs2296748	*LEMD2*	intron_variant	C	T	379252	0.3768	0.019	0.003	2.85E-13
6	33751767	rs2182659	*LEMD2*	intron_variant	A	G	369674	0.8135	0.024	0.004	2.52E-11
6	33755711	rs756138	*LEMD2*	intron_variant	G	C	364357	0.7861	0.019	0.003	7.12E-09
6	33764158	rs751727	*MLN*	intron_variant	A	G	375581	0.8133	0.024	0.004	1.38E-11
6	33775446	rs1547668	*MLN*	upstream_gene_variant	A	G	372028	0.8031	0.021	0.003	1.12E-09
6	34165721	rs7742369	-	regulatory_region_variant	A	G	379252	0.1749	0.053	0.003	1.68E-61
6	34199092	rs2780226	-	regulatory_region_variant	C	T	378383	0.9163	-0.085	0.004	6.12E-83
6	34214322	rs1150781	*HMGA1*	missense_variant	C	G	290508	0.9119	-0.076	0.005	4.48E-49
6	34214524	rs143851251	*HMGA1*	missense_variant	A	G	318109	0.0012	0.223	0.036	4.01E-10
6	34498328	rs41312309	*PACSIN1*	missense_variant	C	T	381625	0.0927	0.032	0.004	1.29E-14
6	34546560	rs2814982	*RP3-391O22.3*	upstream_gene_variant	C	T	381625	0.1143	0.034	0.004	2.67E-18
6	34552797	rs2814944	*C6orf106*	downstream_gene_variant	G	A	380346	0.1599	0.051	0.003	1.07E-50
6	34618893	rs2814993	*C6orf106*	intron_variant	G	A	379977	0.1528	0.056	0.003	2.98E-57
6	34730395	rs34427075	*SNRPC*	synonymous_variant	C	T	381625	0.0143	-0.117	0.010	9.21E-33
6	34826921	rs61732793	*UHRF1BP1*	missense_variant	G	C	374724	0.0476	-0.034	0.006	1.32E-09
6	34827085	rs9469913	*UHRF1BP1*	missense_variant	A	T	158063	0.1663	0.036	0.005	1.50E-12
6	34831856	rs13205210	*UHRF1BP1*	missense_variant	T	C	372036	0.1033	-0.030	0.004	2.24E-13
6	34839644	rs34672415	*UHRF1BP1*	missense_variant	G	A	373551	0.0143	-0.115	0.010	4.23E-31
6	34845449	rs4646949	*TAF11*	intron_variant	T	G	352718	0.2639	-0.020	0.003	5.69E-12
6	34975415	rs2140418	*ANKS1A*	intron_variant	T	C	377104	0.7992	0.017	0.003	1.22E-07
6	35088381	rs2234045	*TCP11*	missense_variant	C	G	375498	0.1386	-0.030	0.004	4.68E-16
6	35108553	rs35693439	*TCP11*	missense_variant	T	G	381625	0.1396	-0.030	0.004	1.86E-16
6	35117399	rs1886243	*TCP11*	upstream_gene_variant	A	C	371878	0.6874	0.019	0.003	8.94E-12
6	35253974	rs2228265	*ZNF76*	missense_variant	C	T	319665	0.0234	0.072	0.008	2.16E-17
6	35285720	rs2395617	*DEF6*	missense_variant	A	C	381625	0.8909	0.025	0.004	1.18E-10
6	35402785	rs4713858	-	intergenic_variant	A	G	380346	0.8538	0.026	0.003	4.78E-14
6	35402805	rs6457821	-	regulatory_region_variant	C	A	358569	0.0157	-0.104	0.010	1.49E-26
6	35411091	rs3800378	*MKRNP2*	intron_variant	G	A	372028	0.6258	0.016	0.003	1.15E-09
6	35423886	rs7761870	*FANCE*	missense_variant	C	T	381625	0.0148	-0.109	0.010	1.23E-29
6	35467891	rs41270076	*TULP1*	synonymous_variant	C	T	381625	0.0255	-0.064	0.007	1.04E-18
6	35765043	rs2766597	*CLPS*	missense_variant	A	G	332584	0.0151	-0.099	0.010	6.35E-22
6	36094188	rs6922865	*MAPK13*	upstream_gene_variant	T	G	371178	0.6388	-0.014	0.003	4.09E-08
6	36198577	rs3748045	*BRPF3*	3_prime_UTR_variant	G	C	285465	0.6286	-0.017	0.003	3.52E-09
6	36339143	rs61730656	*ETV7*	missense_variant	C	T	372028	0.0103	-0.077	0.012	2.91E-11
6	41650736	rs2842643	*TFEB*	downstream_gene_variant	C	T	374731	0.7261	-0.015	0.003	2.24E-08
6	41903798	rs33966734	*CCND3*	stop_gained	C	A	135421	0.0133	-0.140	0.017	5.51E-17
6	44946506	rs9472414	*SUPT3H*	intron_variant	T	A	374724	0.2126	-0.026	0.003	8.81E-19
6	45095163	rs9395066	*SUPT3H*	intron_variant	A	C	369748	0.4082	0.022	0.002	3.66E-19
6	47623292	rs12195173	*ADGRF2*	upstream_gene_variant	G	A	296637	0.6803	0.018	0.003	1.18E-08
6	47646842	rs6907125	*ADGRF2*	missense_variant	A	G	348888	0.6341	0.015	0.003	3.91E-08
6	47649265	rs17541107	*ADGRF2*	missense_variant	T	A	352947	0.3632	-0.015	0.003	4.28E-08
6	47649573	rs10807371	*ADGRF2*	synonymous_variant	C	T	381625	0.6347	0.016	0.003	3.89E-09
6	47649574	rs10807372	*ADGRF2*	missense_variant	A	G	381625	0.6348	0.016	0.003	3.07E-09
6	47649694	rs9381594	*ADGRF2*	missense_variant	A	G	381625	0.6348	0.016	0.003	3.53E-09
6	76173832	rs6903448	*RP11-415D17.1*	intron_variant	C	T	380102	0.1470	-0.032	0.003	1.88E-21
6	76174857	rs2951916	*RP11-415D17.1*	non_coding_transcript_exon_variant	A	G	369664	0.5007	0.025	0.002	3.44E-25
6	76265642	rs9360921	-	regulatory_region_variant	T	G	376597	0.1075	0.048	0.004	5.90E-34
6	76631823	rs76604824	*MYO6*	missense_variant	C	T	380630	0.0118	0.056	0.011	1.41E-07
6	80956208	rs648831	*BCKDHB*	intron_variant	C	T	376860	0.5230	0.034	0.002	7.20E-47
6	81038921	rs1341278	*BCKDHB*	intron_variant	T	G	316942	0.0590	0.044	0.005	6.22E-16
6	81315597	rs9443804	-	regulatory_region_variant	A	G	380102	0.4373	0.020	0.002	1.11E-16
6	81913895	rs2323150	-	intergenic_variant	G	A	345730	0.5163	-0.025	0.003	2.56E-23
6	83838673	rs4706980	*DOPEY1*	missense_variant	G	A	368874	0.1304	0.020	0.004	3.07E-08
6	105378954	rs7759938	-	intergenic_variant	C	T	381625	0.6784	-0.044	0.003	2.78E-59
6	105400837	rs314280	*LIN28B*	upstream_gene_variant	A	G	378383	0.5474	-0.032	0.002	2.12E-39
6	105407662	rs314277	*LIN28B*	intron_variant	A	C	381625	0.8503	-0.038	0.003	9.69E-30
6	105412932	rs314274	*LIN28B*	intron_variant	A	C	380102	0.6648	-0.042	0.003	1.16E-54
6	105417978	rs314268	*LIN28B*	intron_variant	G	A	368786	0.6629	-0.042	0.003	2.78E-53
6	108988184	rs2153960	*FOXO3*	intron_variant	G	A	332784	0.6984	0.019	0.003	8.02E-12
6	108996963	rs3800229	*FOXO3*	intron_variant	G	T	372972	0.7055	0.022	0.003	1.30E-15
6	109013930	rs9486916	-	intergenic_variant	C	T	374251	0.1957	-0.025	0.003	1.47E-15
6	109742015	rs9487094	*PPIL6*	intron_variant	G	A	377973	0.3529	-0.021	0.003	5.13E-15

6	109764535	rs1476387	*PPIL6*	missense_variant	G	T	359848	0.4155	-0.026	0.003	2.07E-22
6	109767931	rs59056467	*SMPD2*	missense_variant	C	T	372028	0.3341	-0.018	0.003	4.07E-11
6	109783941	rs1046943	*ZBTB24*	3_prime_UTR_variant	A	G	378383	0.4196	-0.025	0.003	8.14E-21
6	109827716	rs2277114	*AK9*	missense_variant	C	T	381625	0.3886	-0.021	0.003	7.36E-15
6	109885475	rs10499052	*AK9*	missense_variant	G	A	381625	0.2827	-0.016	0.003	9.13E-09
6	109894773	rs12175588	*AK9*	missense_variant	T	A	363621	0.2323	0.016	0.003	7.43E-08
6	109906342	rs78047280	*AK9*	missense_variant	C	T	257767	0.4033	-0.021	0.003	9.77E-11
6	116387134	rs1999930	-	intergenic_variant	C	T	377104	0.2722	0.018	0.003	3.08E-10
6	116446576	rs1064583	*COL10A1*	missense_variant	A	G	379977	0.3836	0.014	0.003	2.04E-08
6	116783330	rs1057192	*KRT18P22*	missense_variant	G	A	370176	0.2320	-0.017	0.003	2.17E-09
6	117522156	rs961764	-	intergenic_variant	C	G	199891	0.5791	0.026	0.003	6.72E-16
6	126698719	rs9388489	-	intergenic_variant	A	G	377737	0.4600	0.040	0.003	5.40E-55
6	126767600	rs1361108	-	intergenic_variant	C	T	380346	0.4635	0.041	0.003	5.76E-56
6	126835655	rs1490388	-	intergenic_variant	C	T	379016	0.4630	0.042	0.003	4.30E-58
6	126851160	rs1490384	-	intergenic_variant	C	T	377737	0.5062	0.039	0.003	1.77E-52
6	126966308	rs4549631	*PRELID1P1*	downstream_gene_variant	T	C	381625	0.4974	0.037	0.003	6.48E-47
6	127167072	rs13204965	-	intergenic_variant	A	C	319526	0.2388	-0.026	0.003	3.32E-16
6	130322179	rs2876066	-	regulatory_region_variant	C	A	375581	0.0794	-0.034	0.004	2.94E-14
6	130349119	rs6569648	*L3MBTL3*	intron_variant	C	T	369748	0.7691	-0.049	0.003	2.45E-60
6	130354855	rs9388766	*L3MBTL3*	intron_variant	T	C	380102	0.7087	-0.042	0.003	2.07E-53
6	130358428	rs6899976	*L3MBTL3*	intron_variant	G	A	369030	0.7074	-0.042	0.003	5.26E-52
6	130374102	rs9388768	*L3MBTL3*	missense_variant	C	A	378383	0.6746	-0.037	0.003	2.08E-43
6	140273647	rs642858	-	intergenic_variant	G	A	373217	0.2303	-0.016	0.003	5.40E-08
6	141443540	rs2931796	-	intergenic_variant	C	T	372973	0.6328	-0.013	0.002	7.23E-08
6	142548099	rs225717	*VTA1*	downstream_gene_variant	C	T	381625	0.7708	0.024	0.003	9.73E-17
6	142565531	rs1931983	-	intergenic_variant	C	T	358325	0.6906	0.016	0.003	2.44E-09
6	142679572	rs6570507	*ADGRG6*	intron_variant	G	A	375774	0.2873	-0.054	0.003	2.68E-79
6	142691549	rs11155242	*ADGRG6*	missense_variant	A	C	381625	0.1915	-0.039	0.003	1.39E-34
6	142703877	rs4896582	*ADGRG6*	intron_variant	G	A	366421	0.3036	-0.053	0.003	6.23E-77
6	142750516	rs3817928	*ADGRG6*	intron_variant	A	G	345192	0.1933	-0.039	0.003	9.03E-32
6	142767633	rs3748069	*ADGRG6*	downstream_gene_variant	A	G	380346	0.2904	-0.053	0.003	1.05E-78
6	142797289	rs7763064	-	intergenic_variant	G	A	380346	0.2937	-0.052	0.003	7.58E-76
6	152110943	rs543650	*ESR1*	intron_variant	T	G	367628	0.5960	0.025	0.002	6.24E-25
6	155450779	rs148543891	*TIAM2*	missense_variant	A	G	376353	0.0029	-0.124	0.022	1.45E-08
6	158743188	rs1539312	*TULP4*	intron_variant	G	A	380102	0.5098	-0.017	0.002	3.29E-13
6	158910698	rs12206717	*TULP4*	missense_variant	G	A	377738	0.0510	-0.050	0.005	4.78E-20
6	168810725	rs2147457	-	intergenic_variant	A	G	380102	0.4144	-0.022	0.002	1.51E-20
7	1854263	rs6948971	*MAD1L1*	downstream_gene_variant	A	G	375774	0.2065	0.015	0.003	1.99E-07
7	2763102	rs798544	*GNA12*	intron_variant	C	T	378383	0.2963	-0.047	0.003	3.13E-63
7	2789880	rs798502	*GNA12*	intron_variant	A	C	378383	0.2961	-0.049	0.003	1.64E-67
7	2795957	rs798497	*GNA12*	intron_variant	A	G	377104	0.2999	-0.049	0.003	1.49E-68
7	2801803	rs798489	*AMZ1*	splice_donor_variant	C	T	358432	0.2752	-0.048	0.003	3.50E-61
7	2869985	rs1182188	*GNA12*	intron_variant	T	C	377104	0.3033	-0.048	0.003	1.24E-66
7	19616522	rs4470914	*AC007091.1*	intron_variant	C	T	196538	0.1754	0.035	0.004	1.20E-16
7	23502974	rs12534093	*IGF2BP3*	intron_variant	T	A	344325	0.2262	-0.037	0.003	3.61E-34
7	23811800	rs10247878	*STK31*	missense_variant	G	T	369655	0.1601	-0.019	0.003	4.22E-08
7	25871109	rs1055144	-	intergenic_variant	C	T	377104	0.1904	0.024	0.003	2.02E-15
7	25901639	rs12700667	-	regulatory_region_variant	G	A	351092	0.7415	-0.017	0.003	4.85E-09
7	28180556	rs864745	*JAZF1*	intron_variant	T	C	378383	0.4955	-0.031	0.003	4.14E-34
7	28185091	rs849141	*JAZF1*	intron_variant	A	G	381625	0.7111	-0.045	0.003	7.91E-62
7	28189411	rs1635852	*JAZF1*	intron_variant	T	C	377973	0.4953	-0.030	0.003	7.13E-34
7	28189946	rs1708299	*JAZF1*	intron_variant	A	G	376542	0.6981	-0.044	0.003	1.04E-59
7	28196222	rs849134	*JAZF1*	intron_variant	A	G	381625	0.4886	-0.032	0.003	1.18E-36
7	37947103	rs1802074	*SFRP4*	missense_variant	C	T	381625	0.2070	0.018	0.003	1.13E-09
7	38128326	rs6959212	-	intergenic_variant	T	C	285694	0.6705	0.018	0.003	1.19E-09
7	38136277	rs1524058	-	intergenic_variant	T	C	381625	0.5972	0.015	0.002	1.70E-09
7	46201355	rs1007358	-	regulatory_region_variant	A	G	376860	0.2234	0.019	0.003	1.80E-11
7	46437154	rs17172694	-	intergenic_variant	G	T	380102	0.0735	-0.041	0.005	5.10E-19
7	50730452	rs2715094	*GRB10*	intron_variant	G	A	376860	0.7535	-0.016	0.003	3.54E-08
7	50751090	rs10248619	*GRB10*	intron_variant	T	C	377973	0.7777	-0.017	0.003	6.28E-09
7	55855180	rs11982736	*RNU6-1126P*	upstream_gene_variant	G	A	367090	0.1629	-0.018	0.003	5.88E-08
7	92248076	rs42235	*CDK6*	intron_variant	C	T	372272	0.3078	0.057	0.003	2.53E-102
7	92264410	rs2282978	*CDK6*	intron_variant	T	C	380346	0.3390	0.054	0.003	8.40E-99
7	99489571	rs17277546	*TRIM4*	3_prime_UTR_variant	G	A	380113	0.0486	0.034	0.005	3.28E-10
7	100458093	rs7801190	*SLC12A9*	non_coding_transcript_exon_variant	C	G	306850	0.0442	-0.036	0.006	1.92E-08
7	100490077	rs7636	*ACHE*	synonymous_variant	G	A	356606	0.0427	-0.037	0.006	8.59E-10
7	100490797	rs1799805	*ACHE*	missense_variant	G	T	371903	0.0432	-0.036	0.006	1.50E-09
7	129663496	rs11556924	*RP11-306G20.1*	missense_variant	C	T	381625	0.3787	0.014	0.002	7.90E-09
7	132526350	rs4731907	*CHCHD3*	intron_variant	T	C	369655	0.5477	-0.013	0.002	9.36E-08
7	135048804	rs3812265	*CNOT4*	missense_variant	C	T	381625	0.2459	0.018	0.003	1.79E-10
7	135082953	rs77841106	*CNOT4*	missense_variant	G	C	374724	0.1039	0.023	0.004	3.43E-09
7	135123060	rs17480616	*CNOT4*	missense_variant	G	C	366650	0.0281	0.060	0.007	2.31E-17
7	135293128	rs4294134	*NUP205*	intron_variant	A	G	377973	0.8365	-0.021	0.003	2.55E-10
7	137600690	rs273957	*CREB3L2*	missense_variant	C	T	381625	0.6093	0.020	0.002	5.23E-17
7	140244560	rs2293177	*DENND2A*	missense_variant	C	T	379252	0.3241	0.015	0.003	7.97E-09
7	148650634	rs822552	-	intergenic_variant	C	G	374724	0.2678	0.031	0.003	1.49E-31
7	150667210	rs3807375	*KCNH2*	intron_variant	C	T	376010	0.3676	0.017	0.003	7.00E-12
8	13273477	rs7834383	*DLC1*	intron_variant	G	T	378823	0.3400	0.019	0.002	5.49E-15
8	13356802	rs3816747	*DLC1*	missense_variant	G	A	381625	0.9394	0.030	0.005	1.30E-09
8	23148940	rs2272761	*R3HCC1*	missense_variant	G	A	381625	0.5685	0.014	0.002	5.05E-09
8	23150878	rs13530	*R3HCC1*	missense_variant	T	G	381625	0.5700	0.014	0.002	9.46E-09
8	23167353	rs1063582	*LOXL2*	missense_variant	T	G	374783	0.7726	-0.026	0.003	1.55E-19
8	23418444	rs2942202	*SLC25A37*	intron_variant	A	C	338374	0.5003	-0.019	0.003	3.26E-14
8	23423697	rs3736032	*SLC25A37*	missense_variant	G	A	369748	0.0699	0.032	0.005	7.08E-12
8	24116304	rs1013209	-	intergenic_variant	C	T	380346	0.2483	-0.028	0.003	3.02E-25
8	30383013	rs2979531	*RBPMS*	intron_variant	A	G	372028	0.4898	-0.013	0.002	5.24E-08
8	57078933	rs35883156	*PLAG1*	missense_variant	G	T	294899	0.1685	-0.037	0.004	2.98E-23
8	57095808	rs10958476	*PLAG1*	intron_variant	T	C	381625	0.2148	0.045	0.003	4.00E-54
8	57100149	rs7833986	*PLAG1*	intron_variant	G	A	381625	0.1790	-0.036	0.003	2.74E-27

8	57100791	rs13273123	*PLAG1*	intron_variant	A	G	368469	0.1777	-0.036	0.003	3.11E-26
8	57155598	rs9650315	-	intergenic_variant	G	T	357882	0.1314	-0.061	0.004	2.02E-58
8	57179020	rs7815788	-	intergenic_variant	C	T	380346	0.1334	-0.051	0.004	1.38E-44
8	57194163	rs7460090	-	intergenic_variant	T	C	345093	0.1141	-0.064	0.004	1.51E-55
8	57400489	rs2582394	*RP11-17A4.2*	intron_variant	C	T	380102	0.4646	0.014	0.002	1.51E-09
8	77785447	rs16939382	-	intergenic_variant	A	G	380102	0.6372	-0.013	0.002	9.02E-08
8	78093837	rs7821178	-	intergenic_variant	C	A	308014	0.3322	0.030	0.003	5.23E-26
8	78160179	rs7846385	-	intergenic_variant	T	C	380346	0.2829	0.035	0.003	4.99E-38
8	78178485	rs6473015	-	intergenic_variant	A	C	356196	0.2825	0.035	0.003	3.02E-35
8	87568644	rs2304787	*CPNE3*	intron_variant	T	G	377104	0.7379	0.017	0.003	3.88E-10
8	116599199	rs2293889	*TRPS1*	intron_variant	T	G	380346	0.5853	-0.014	0.002	2.26E-09
8	120353267	rs2469997	-	intergenic_variant	G	C	372631	0.8252	0.020	0.003	2.07E-10
8	120744399	rs956749	*TAF2*	missense_variant	C	T	381625	0.0661	0.026	0.005	1.34E-07
8	126490972	rs2954029	*RP11-136O12.2*	intron_variant	A	T	367424	0.4652	0.014	0.002	2.78E-08
8	130760850	rs4144738	*GSDMC*	missense_variant	A	G	381625	0.4522	-0.031	0.002	4.67E-38
8	130762291	rs77681114	*GSDMC*	synonymous_variant	G	A	381625	0.0372	-0.041	0.006	1.28E-11
8	135494742	rs3936152	*ZFAT*	intron_variant	C	T	372028	0.5979	0.015	0.002	2.94E-10
8	135614553	rs112892337	*ZFAT*	missense_variant	G	C	360530	0.0039	0.196	0.019	4.42E-26
8	135622851	rs75596750	*ZFAT*	missense_variant	G	A	377876	0.0009	0.255	0.036	1.54E-12
8	135637337	rs12680655	*ZFAT*	intron_variant	C	G	375498	0.4002	-0.031	0.002	3.76E-35
8	135649848	rs12541381	*ZFAT*	missense_variant	G	A	381625	0.2519	-0.027	0.003	8.80E-24
8	135669810	rs17778003	*ZFAT*	missense_variant	C	T	369655	0.0915	0.023	0.004	2.73E-08
8	144997927	rs7002002	*PLEC*	missense_variant	G	A	371638	0.4108	-0.017	0.003	6.43E-11
8	145001031	rs55895668	*PLEC*	missense_variant	T	C	377429	0.4174	-0.017	0.003	3.83E-11
8	145007187	rs11136336	*PLEC*	missense_variant	G	A	205748	0.4005	-0.019	0.004	1.03E-07
8	145011204	rs6993938	*PLEC*	synonymous_variant	A	G	361786	0.3929	-0.017	0.003	1.96E-10
8	145058986	rs11136343	*PARP10*	missense_variant	A	G	376589	0.3774	-0.017	0.003	2.56E-10
8	145059425	rs11136344	*PARP10*	missense_variant	T	C	381625	0.4215	-0.020	0.003	9.29E-15
9	34660864	rs11575580	*IL11RA*	missense_variant	C	T	381625	0.0163	-0.064	0.009	5.20E-13
9	78542286	rs11144688	*PCSK5*	intron_variant	G	A	376901	0.1265	-0.043	0.004	1.09E-32
9	85126163	rs7866939	*RP11-15B24.5*	intron_variant	T	C	364374	0.3253	0.014	0.003	1.05E-07
9	86617265	rs1982151	*RMI1*	missense_variant	A	G	381625	0.7355	-0.026	0.003	1.19E-21
9	89099362	rs353785	-	intergenic_variant	T	C	375581	0.5151	0.022	0.002	1.84E-19
9	90811182	rs2814828	-	regulatory_region_variant	T	C	381625	0.7622	-0.025	0.003	1.97E-18
9	90835726	rs2778031	-	regulatory_region_variant	T	C	361624	0.7595	-0.025	0.003	1.02E-17
9	90883630	rs10746839	-	intergenic_variant	A	G	378823	0.5773	-0.022	0.002	2.37E-20
9	94486321	rs10761129	*ROR2*	missense_variant	C	T	363055	0.6742	-0.016	0.003	4.39E-10
9	95284982	rs10120210	*ECM2*	missense_variant	T	G	291012	0.5548	-0.016	0.003	1.20E-08
9	95429120	rs9969804	*IPPK*	intron_variant	A	C	381625	0.5601	-0.020	0.002	6.22E-16
9	95555939	rs7868651	-	intergenic_variant	T	G	372028	0.5067	-0.018	0.002	3.42E-13
9	96893945	rs1257763	-	intergenic_variant	A	G	381625	0.9567	-0.047	0.006	2.22E-17
9	97369149	rs1769259	*FBP1*	missense_variant	C	T	381625	0.9400	-0.027	0.005	9.46E-08
9	98209594	rs357564	*PTCH1*	missense_variant	G	A	369802	0.3422	-0.037	0.003	1.05E-47
9	98231008	rs16909898	*PTCH1*	intron_variant	A	G	372272	0.1004	0.039	0.004	1.52E-22
9	98259703	rs10512248	*PTCH1*	intron_variant	T	G	377104	0.3408	0.035	0.003	9.10E-44
9	98319969	rs17370391	-	intergenic_variant	T	C	377876	0.1659	0.024	0.003	1.90E-13
9	98410405	rs10990303	*RP11-180I4.1*	upstream_gene_variant	C	T	380102	0.2247	0.036	0.003	6.78E-36
9	99280421	rs7852498	*CDC14B*	intron_variant	A	G	216353	0.3855	0.026	0.003	8.94E-16
9	99581568	rs34763627	*ZNF782*	missense_variant	T	C	351774	0.1049	0.025	0.004	3.35E-10
9	101748356	rs2075663	*COL15A1*	missense_variant	A	G	381625	0.3857	-0.019	0.002	1.22E-14
9	108925389	rs4452860	-	intergenic_variant	A	G	378823	0.2949	-0.023	0.003	1.97E-17
9	108936674	rs7861820	-	intergenic_variant	T	C	377737	0.4844	-0.016	0.002	6.20E-11
9	108967088	rs2090409	-	intergenic_variant	C	A	374496	0.3266	-0.023	0.003	2.95E-18
9	109132446	rs7048618	*RP11-308N19.1*	intron_variant	G	A	372028	0.6361	0.017	0.003	3.42E-11
9	109599046	rs7027110	-	intergenic_variant	G	A	380346	0.2277	0.029	0.003	1.35E-23
9	109632353	rs4743034	*ZNF462*	intron_variant	G	A	381625	0.2241	0.029	0.003	3.24E-23
9	111660851	rs2230792	*IKBKAP*	missense_variant	C	T	372028	0.1903	0.017	0.003	6.35E-08
9	113807082	rs1468758	-	intergenic_variant	C	T	380346	0.2408	-0.022	0.003	3.63E-15
9	117050998	rs10982134	*COL27A1*	missense_variant	G	A	381625	0.3199	-0.014	0.003	1.24E-07
9	119106881	rs7020782	*PAPPA*	missense_variant	C	A	304764	0.6965	0.019	0.003	3.90E-11
9	119122342	rs751543	*PAPPA*	intron_variant	C	T	351578	0.7075	0.028	0.003	8.03E-25
9	119134796	rs7869550	*PAPPA*	intron_variant	A	G	381625	0.2017	-0.033	0.003	2.88E-29
9	119232655	rs10817896	*ASTN2*	intron_variant	C	T	380102	0.2734	-0.018	0.003	1.73E-11
9	124422403	rs7025486	*DAB2IP*	intron_variant	G	A	380346	0.2632	0.017	0.003	2.57E-10
9	133464084	rs7466269	*FUBP3*	intron_variant	A	G	372272	0.3567	-0.030	0.003	1.46E-32
9	139110654	rs12684650	*QSOX2*	splice_region_variant	C	T	381625	0.3051	-0.030	0.003	8.62E-32
9	139111870	rs7849585	*QSOX2*	intron_variant	G	T	158774	0.3546	0.028	0.004	5.78E-12
9	139121740	rs12338076	*QSOX2*	intron_variant	A	C	356606	0.3325	0.027	0.003	2.68E-25
9	139323311	rs8413	*INPP5E*	3_prime_UTR_variant	T	C	344880	0.4181	0.017	0.003	2.83E-10
9	139368953	rs3812594	*SEC16A*	missense_variant	G	A	370561	0.2718	0.021	0.003	8.92E-14
10	4963327	rs12774134	*AKR1C2*	downstream_gene_variant	C	T	299046	0.1209	-0.036	0.004	6.48E-19
10	12918764	rs7909670	-	intergenic_variant	C	T	292460	0.4539	-0.022	0.003	1.14E-15
10	22839628	rs2230469	*PIP4K2A*	missense_variant	T	C	367429	0.3171	0.014	0.003	5.23E-08
10	25244392	rs274312	*RP11-165A20.3*	upstream_gene_variant	C	T	372028	0.3786	0.014	0.002	4.50E-08
10	63723577	rs10821936	*ARID5B*	intron_variant	C	T	380346	0.6805	-0.014	0.003	7.33E-08
10	69926334	rs10823148	*MYPN*	missense_variant	C	G	373405	0.5214	0.018	0.003	2.30E-12
10	69933921	rs10997975	*MYPN*	missense_variant	G	A	381625	0.4951	0.021	0.003	3.13E-16
10	69933969	rs7916821	*MYPN*	missense_variant	G	A	381625	0.4944	0.021	0.003	3.38E-16
10	69959242	rs7079481	*MYPN*	missense_variant	C	A	285326	0.4928	0.018	0.003	5.29E-10
10	69991853	rs7916697	*RP11-153K11.3*	5_prime_UTR_variant	A	G	377104	0.7440	0.019	0.003	2.12E-10
10	70000881	rs1900004	*RP11-153K11.3*	intron_variant	C	T	377104	0.2489	-0.019	0.003	3.28E-10
10	70011838	rs3858145	-	intergenic_variant	A	G	381625	0.2697	-0.019	0.003	4.39E-11
10	70019371	rs12571093	*KRT19P4*	upstream_gene_variant	G	A	380346	0.1658	-0.020	0.003	1.85E-09
10	70044031	rs4142048	*PBLD*	missense_variant	T	C	338775	0.1982	-0.020	0.003	8.53E-10
10	70332580	rs10823229	*TET1*	missense_variant	A	G	381625	0.3798	0.019	0.003	1.14E-13
10	70332672	rs12773594	*TET1*	missense_variant	T	A	375498	0.1702	-0.021	0.003	1.26E-10
10	70332862	rs12221107	*TET1*	missense_variant	C	T	334827	0.0925	-0.036	0.005	2.60E-15
10	70405539	rs16925541	*TET1*	missense_variant	A	G	380113	0.0881	-0.033	0.004	1.56E-14
10	70405855	rs3998860	*TET1*	missense_variant	A	G	378383	0.8181	0.020	0.003	2.07E-10

10	79580976	rs41274586	*DLG5*	missense_variant	G	A	373551	0.0174	-0.058	0.009	2.72E-11
10	93032943	rs2631681	*PCGF5*	intron_variant	C	T	380102	0.3253	0.025	0.003	8.51E-23
10	97919011	rs41291604	*ZNF518A*	missense_variant	A	G	381625	0.0399	0.031	0.006	9.94E-08
10	99969568	rs11189513	*R3HCC1L*	missense_variant	A	G	343607	0.3170	0.018	0.003	3.08E-11
10	100017453	rs1983864	*RP11-34A14.3*	missense_variant	T	G	381625	0.3419	0.017	0.003	7.11E-12
10	101805442	rs11599750	*CPN1*	intron_variant	C	T	381625	0.3806	-0.017	0.003	5.65E-12
10	101912064	rs2862954	*ERLIN1*	missense_variant	T	C	378383	0.4709	-0.014	0.002	2.16E-08
10	102744331	rs11591349	*MRPL43*	missense_variant	A	T	341990	0.4519	0.018	0.003	4.88E-13
10	104269217	rs2281880	*SUFU*	intron_variant	G	A	380346	0.5375	0.025	0.002	4.02E-25
10	104500659	rs10786706	*SFXN2*	3_prime_UTR_variant	C	T	359277	0.4690	0.020	0.003	4.24E-14
10	104572963	rs284860	*WBP1L*	missense_variant	T	C	379252	0.5905	-0.014	0.003	1.02E-07
10	105659826	rs2487999	*OBFC1*	missense_variant	T	C	381625	0.9028	-0.022	0.004	1.01E-07
10	114169276	rs3736946	*RP11-324O2.3*	missense_variant	A	G	381625	0.1080	-0.020	0.004	8.73E-08
10	121429633	rs2234962	*BAG3*	missense_variant	T	C	381625	0.2167	-0.015	0.003	7.95E-08
10	124165615	rs6585827	*PLEKHA1*	intron_variant	G	A	381625	0.4914	0.016	0.002	3.06E-11
10	124189197	rs1045216	*PLEKHA1*	missense_variant	A	G	293622	0.6168	0.016	0.003	1.08E-08
11	1977552	rs12812	*MRPL23*	missense_variant	G	A	381625	0.1510	0.021	0.003	4.77E-10
11	2169014	rs10770125	*IGF2-AS*	missense_variant	A	G	381625	0.4937	0.022	0.002	3.56E-19
11	2766282	rs2237878	*KCNQ1*	intron_variant	G	A	380346	0.1003	0.035	0.004	5.17E-19
11	2810731	rs2237886	*KCNQ1*	intron_variant	C	T	354682	0.1007	0.050	0.004	2.64E-35
11	8252853	rs110419	*LMO1*	intron_variant	A	G	351774	0.5010	-0.016	0.002	2.25E-11
11	11986061	rs3206824	*DKK3*	missense_variant	T	C	359266	0.7339	0.016	0.003	8.77E-09
11	12698040	rs7926971	*TEAD1*	intron_variant	A	G	381625	0.4531	0.021	0.002	2.41E-19
11	17316029	rs1330	*NUCB2*	intron_variant	C	T	369030	0.3471	0.016	0.003	1.69E-09
11	17351683	rs757081	*NUCB2*	missense_variant	C	G	345647	0.3377	0.019	0.003	7.48E-12
11	18632984	rs10128711	*SPTY2D1*	intron_variant	T	C	327560	0.7252	-0.021	0.003	5.86E-13
11	18645843	rs11024739	*SPTY2D1*	intron_variant	C	A	374251	0.7269	-0.020	0.003	8.53E-14
11	27016360	rs138273386	*FIBIN*	missense_variant	G	A	377738	0.0044	-0.120	0.017	5.79E-12
11	45935689	rs35214605	*PEX16*	missense_variant	C	G	325682	0.0270	-0.041	0.008	1.74E-07
11	46052575	rs16938437	*PHF21A*	intron_variant	C	T	376459	0.0922	-0.033	0.004	5.96E-15
11	47270255	rs2167079	*NR1H3*	missense_variant	C	T	329283	0.3066	0.018	0.003	3.61E-08
11	47286290	rs7120118	*MADD*	intron_variant	T	C	328004	0.3071	0.017	0.003	5.77E-08
11	47290984	rs1449627	*MADD*	5_prime_UTR_variant	T	G	368141	0.3244	0.018	0.003	7.98E-10
11	47298360	rs326214	*MADD*	synonymous_variant	G	A	355379	0.6744	-0.017	0.003	6.37E-09
11	47354787	rs1052373	*MADD*	synonymous_variant	C	T	354682	0.3250	0.018	0.003	1.50E-09
11	47370041	rs3729989	*MYBPC3*	missense_variant	T	C	377738	0.1292	0.020	0.004	8.89E-08
11	47431703	rs61897432	*SLC39A13*	missense_variant	A	G	356525	0.1388	0.020	0.004	1.83E-07
11	47454701	rs10742805	*RAPSN*	downstream_gene_variant	A	G	365768	0.7108	-0.021	0.003	4.84E-12
11	47640429	rs1064608	*Y_RNA*	missense_variant	G	C	297403	0.3497	-0.026	0.003	1.75E-17
11	47650993	rs3817334	*MTCH2*	intron_variant	C	T	346026	0.4087	-0.021	0.003	3.18E-14
11	47663049	rs10838738	*MTCH2*	intron_variant	A	G	376105	0.3516	-0.026	0.003	8.61E-21
11	61557803	rs102275	*FEN1*	non_coding_transcript_exon_variant	T	C	378383	0.3476	-0.016	0.003	3.47E-09
11	61569830	rs174546	*FADS1*	3_prime_UTR_variant	C	T	381625	0.3402	-0.016	0.003	1.80E-08
11	61570783	rs174547	*FADS1*	intron_variant	T	C	380346	0.3403	-0.016	0.003	2.06E-08
11	61571478	rs174550	*FADS1*	5_prime_UTR_variant	T	C	380346	0.3402	-0.016	0.003	1.90E-08
11	61597212	rs174570	*FADS2*	intron_variant	C	T	355541	0.1420	-0.021	0.004	1.07E-08
11	61597972	rs1535	*FADS2*	intron_variant	A	G	381625	0.3418	-0.016	0.003	1.00E-08
11	61609750	rs174583	*FADS2*	intron_variant	C	T	373551	0.3496	-0.015	0.003	2.80E-08
11	64990041	rs514076	*SLC22A20*	non_coding_transcript_exon_variant	G	C	369389	0.7830	0.020	0.003	7.36E-11
11	65319751	rs11545200	*LTBP3*	missense_variant	G	A	339457	0.0670	-0.030	0.005	1.19E-08
11	65336819	rs3782089	*SSSCA1-AS1*	non_coding_transcript_exon_variant	C	T	377104	0.0674	-0.029	0.005	4.94E-09
11	65386206	rs1193851	*MAP3K11*	missense_variant	C	G	364622	0.3354	-0.015	0.003	2.19E-08
11	65546857	rs610037	*AP5B1*	synonymous_variant	A	C	371879	0.5245	-0.013	0.003	8.97E-08
11	65715204	rs71455793	*TSGA10IP*	missense_variant	G	A	381625	0.0393	-0.058	0.006	1.82E-21
11	65727301	rs491973	*SART1*	missense_variant	A	G	379252	0.4484	-0.017	0.002	9.17E-12
11	66083591	rs150281243	*CD248*	missense_variant	G	A	381625	0.0085	-0.067	0.013	1.12E-07
11	66191859	rs71457718	*NPAS4*	missense_variant	C	A	377738	0.0082	-0.085	0.013	1.88E-11
11	66240882	rs2277302	*PELI3*	synonymous_variant	T	C	359848	0.2554	0.017	0.003	1.29E-08
11	66272237	rs2305535	*CTD-3074O7.11*	missense_variant	G	A	381625	0.2514	0.019	0.003	2.37E-10
11	66297363	rs3816492	*BBS1*	synonymous_variant	C	T	365639	0.2517	0.019	0.003	7.66E-10
11	66826160	rs7112925	*RHOD*	intron_variant	C	T	380346	0.3502	-0.025	0.003	9.92E-22
11	66832528	rs11227673	*RHOD*	intron_variant	G	A	371178	0.4374	-0.018	0.003	6.38E-13
11	68174189	rs4988321	*LRP5*	missense_variant	G	A	381625	0.0481	-0.038	0.006	2.84E-12
11	68201295	rs3736228	*LRP5*	missense_variant	C	T	361382	0.1349	-0.028	0.004	4.27E-15
11	68840160	rs3750965	*TPCN2*	missense_variant	A	G	371247	0.3008	0.015	0.003	1.99E-08
11	68855363	rs3829241	*MIR3164*	missense_variant	G	A	381625	0.3918	-0.016	0.002	8.64E-11
11	75282052	rs634552	*SERPINH1*	intron_variant	T	G	380346	0.8607	-0.050	0.003	9.97E-49
11	77909014	rs2510044	*USP35*	missense_variant	G	A	381625	0.1435	0.019	0.004	9.54E-08
11	94533444	rs138059525	*AMOTL1*	missense_variant	G	A	373551	0.0092	-0.096	0.012	9.01E-16
11	94731822	rs151327191	*KDM4D*	missense_variant	C	G	343538	0.0093	-0.068	0.013	5.87E-08
11	116973929	rs12269901	*AP000936.4*	intron_variant	G	C	374724	0.2986	-0.015	0.003	2.93E-08
11	118574675	rs494459	-	intergenic_variant	C	T	378383	0.4137	0.020	0.002	1.98E-16
11	128586155	rs654723	*FLI1*	intron_variant	C	A	328329	0.6239	0.017	0.003	1.76E-10
12	371410	rs527118	*RP11-283I3.4*	intron_variant	T	C	380102	0.8288	-0.017	0.003	4.70E-08
12	4374373	rs11063069	*CCND2-AS2*	intron_variant	A	G	377876	0.2135	-0.015	0.003	1.88E-07
12	7548996	rs4072796	*CD163L1*	missense_variant	C	G	375498	0.0353	0.034	0.006	4.11E-08
12	7549009	rs4072797	*CD163L1*	missense_variant	C	T	378383	0.0355	0.033	0.006	1.44E-07
12	11855624	rs2187642	*ETV6*	intron_variant	A	C	375774	0.6322	-0.024	0.003	5.31E-21
12	11855773	rs2856321	*ETV6*	intron_variant	G	A	375774	0.6474	-0.026	0.003	6.75E-25
12	14488914	rs6488674	-	intergenic_variant	T	G	335539	0.5236	-0.015	0.003	6.34E-09
12	14587301	rs3213764	*ATF7IP*	missense_variant	A	G	381625	0.4874	0.015	0.002	4.32E-10
12	20857467	rs10770705	*SLCO1C1*	intron_variant	A	C	359199	0.6783	-0.025	0.003	1.70E-22
12	20905250	rs6487138	*SLCO1C1*	missense_variant	C	T	379977	0.5421	0.014	0.002	2.29E-09
12	28412372	rs11049488	*CCDC91*	missense_variant	G	A	372028	0.2985	-0.033	0.003	1.34E-33
12	28534415	rs2638953	*CCDC91*	intron_variant	G	C	266937	0.6847	0.029	0.003	7.99E-21
12	28722756	rs10843206	*CCDC91*	intron_variant	C	T	372028	0.4970	0.018	0.002	2.01E-13
12	50901882	rs10876041	*DIP2B*	intron_variant	T	C	369899	0.6270	-0.015	0.003	4.28E-09
12	56636975	rs59626664	*ANKRD52*	missense_variant	C	G	269461	0.0667	0.036	0.006	3.63E-09
12	56660905	rs60542959	*COQ10A*	start_lost	G	T	324756	0.0658	0.035	0.005	1.15E-10

12	56737973	rs2066808	*STAT2*	intron_variant	A	G	367700	0.0683	0.035	0.005	9.06E-12
12	56740682	rs2066807	*STAT2*	missense_variant	C	G	352947	0.0666	0.036	0.005	7.63E-12
12	57146069	rs2277339	*PRIM1*	missense_variant	T	G	381625	0.1049	-0.031	0.004	4.22E-16
12	58010163	rs1564374	*ARHGEF25*	missense_variant	A	G	381625	0.5811	-0.014	0.003	1.41E-08
12	58015494	rs923828	*ARHGEF25*	missense_variant	G	A	378633	0.4202	0.015	0.003	1.05E-08
12	58062667	rs10876993	-	intergenic_variant	C	T	372028	0.6570	0.015	0.003	2.96E-08
12	58087737	rs4760168	*OS9*	upstream_gene_variant	T	G	349669	0.6620	0.015	0.003	5.99E-08
12	58138971	rs147996581	*TSPAN31*	missense_variant	G	A	368141	0.0029	-0.116	0.022	8.26E-08
12	58162739	rs703842	*METTL21B*	missense_variant	A	G	313751	0.3449	-0.020	0.003	1.82E-11
12	58222672	rs4760332	*CTDSP2*	intron_variant	C	A	376214	0.3221	-0.019	0.003	6.55E-13
12	66351826	rs1351394	*HMGA2*	3_prime_UTR_variant	T	C	381625	0.5043	-0.052	0.002	1.01E-96
12	66358347	rs1042725	*HMGA2*	3_prime_UTR_variant	C	T	381625	0.4912	-0.051	0.002	5.99E-96
12	66359752	rs8756	*HMGA2*	3_prime_UTR_variant	C	A	381625	0.5100	-0.052	0.002	2.50E-98
12	66364509	rs12424086	*HMGA2*	downstream_gene_variant	T	C	381625	0.2074	-0.048	0.003	1.31E-59
12	66394664	rs4026608	-	intergenic_variant	C	T	381625	0.6274	0.025	0.002	2.73E-24
12	66546100	rs8793	*TMBIM4*	missense_variant	A	G	381625	0.4291	0.015	0.002	6.34E-11
12	69140339	rs61743810	*SLC35E3*	missense_variant	G	C	375498	0.0224	-0.047	0.008	1.13E-09
12	69827658	rs10748128	-	intergenic_variant	G	T	381625	0.3492	0.036	0.003	2.46E-46
12	69828681	rs11177669	-	intergenic_variant	G	A	380346	0.2675	0.031	0.003	2.05E-29
12	90231386	rs17783015	-	intergenic_variant	C	T	377973	0.1578	-0.019	0.003	5.18E-09
12	93976954	rs3825199	*SOCS2*	3_prime_UTR_variant	A	G	370309	0.2210	0.047	0.003	1.75E-58
12	95927762	rs3812813	*USP44*	missense_variant	T	C	381625	0.5338	-0.014	0.002	6.78E-09
12	102108345	rs3205421	*CHPT1*	missense_variant	T	C	381625	0.2969	0.016	0.003	2.19E-09
12	102368065	rs7978999	*DRAM1*	intron_variant	T	C	380102	0.4634	-0.024	0.002	1.05E-23
12	102513531	rs2292303	*PARPBP*	intron_variant	G	C	374724	0.0182	-0.052	0.009	2.25E-09
12	102799598	rs5742692	*IGF1*	intron_variant	A	G	377104	0.0196	-0.051	0.008	1.12E-09
12	103077198	rs7296248	-	intergenic_variant	C	T	350251	0.5072	0.016	0.002	1.36E-10
12	103152029	rs12820008	-	intergenic_variant	C	A	376860	0.2805	-0.014	0.003	8.95E-08
12	104354173	rs11612024	*C12orf73*	intron_variant	C	T	372028	0.3071	0.018	0.003	2.98E-11
12	104408832	rs117801489	*GLT8D2*	missense_variant	T	C	381625	0.0173	0.053	0.009	8.72E-10
12	105606172	rs1196761	*APPL2*	intron_variant	G	A	369655	0.5217	0.013	0.002	4.32E-08
12	107174646	rs10861661	*RIC8B*	intron_variant	A	C	346158	0.2304	-0.020	0.003	2.58E-11
12	117383320	rs4076700	*FBXW8*	missense_variant	G	A	375774	0.8461	0.018	0.003	6.41E-08
12	121756084	rs13141	*ANAPC5*	missense_variant	G	A	381625	0.0089	-0.082	0.012	1.09E-11
12	122494809	rs11835818	*BCL7A*	intron_variant	T	C	370749	0.4740	0.018	0.002	6.71E-13
12	122674780	rs11060094	*LRRC43*	missense_variant	C	A	381625	0.2058	-0.017	0.003	9.27E-09
12	122689181	rs7136356	*DIABLO*	missense_variant	C	G	331750	0.2982	0.018	0.003	4.14E-11
12	122864920	rs34292795	*CLIP1*	missense_variant	G	A	373551	0.0276	0.048	0.007	1.25E-11
12	123030788	rs7968222	*KNTC1*	missense_variant	G	T	381625	0.1095	0.025	0.004	1.50E-10
12	123102921	rs11837038	*KNTC1*	missense_variant	T	G	381312	0.1070	0.025	0.004	2.05E-10
12	123447928	rs4275659	*ABCB9*	intron_variant	T	C	366177	0.7128	-0.017	0.003	1.66E-09
12	123575742	rs1727307	*PITPNM2*	non_coding_transcript_exon_variant	A	G	381625	0.7125	-0.019	0.003	1.71E-11
12	123757861	rs1109559	*CDK2AP1*	upstream_gene_variant	G	A	374251	0.6894	-0.020	0.003	9.59E-13
12	123806219	rs1060105	*SBNO1*	missense_variant	C	T	381625	0.2046	0.036	0.003	7.73E-32
12	123873242	rs28533432	*SETD8*	non_coding_transcript_exon_variant	C	T	380102	0.6965	-0.021	0.003	1.18E-14
12	123921264	rs28434767	*RILPL2*	5_prime_UTR_variant	G	T	365999	0.2843	0.016	0.003	5.67E-09
12	124337772	rs33935373	*DNAH10*	missense_variant	C	T	381625	0.0409	0.031	0.006	6.77E-08
12	124801226	rs1809889	*FAM101A*	downstream_gene_variant	T	C	353804	0.7207	-0.027	0.003	4.90E-22
12	124826462	rs2229840	*NCOR2*	missense_variant	C	T	381625	0.1615	0.029	0.003	7.32E-19
13	21189941	rs2442455	*RNU2-7P*	missense_variant	G	A	381625	0.1477	0.020	0.003	2.88E-09
13	21562832	rs2770928	*LATS2*	missense_variant	C	T	381625	0.8752	0.025	0.004	3.42E-12
13	33045639	rs798274	*N4BP2L2*	intron_variant	G	A	368225	0.6132	0.014	0.003	2.57E-08
13	33147548	rs7332115	-	intergenic_variant	T	G	377973	0.3788	0.016	0.002	3.96E-11
13	33693837	rs9315204	*STARD13*	intron_variant	C	T	368469	0.2269	-0.018	0.003	2.19E-09
13	33704065	rs3742321	*STARD13*	missense_variant	T	C	360412	0.2262	-0.016	0.003	4.50E-08
13	50835715	rs2762051	*DLEU1*	intron_variant	C	T	377973	0.1879	0.033	0.003	1.30E-26
13	50842259	rs2066674	*DLEU1*	intron_variant	G	A	380102	0.0436	0.073	0.006	2.33E-37
13	51105334	rs3118905	*DLEU1*	intron_variant	G	A	376458	0.2783	-0.047	0.003	1.38E-64
13	51106555	rs1239947	*DLEU1*	intron_variant	C	T	377104	0.6633	-0.023	0.003	1.42E-19
13	51111355	rs3116602	*DLEU1*	intron_variant	T	G	366821	0.2172	-0.051	0.003	5.15E-62
13	51116901	rs3118914	*DLEU1*	intron_variant	G	T	380346	0.2178	-0.051	0.003	1.09E-64
13	51221618	rs797486	*AC007304.1*	intron_variant	C	A	378823	0.8749	-0.022	0.004	6.42E-10
13	51287814	rs2812234	*DLEU7*	intron_variant	G	A	342163	0.3907	-0.014	0.003	1.62E-07
13	80717156	rs1359790	-	intergenic_variant	G	A	377104	0.2764	0.017	0.003	4.38E-10
13	92015977	rs8002779	-	intergenic_variant	G	A	359848	0.5832	-0.022	0.003	1.99E-18
13	92024574	rs7319045	-	intergenic_variant	A	G	380346	0.6095	-0.024	0.002	2.39E-22
14	23313633	rs17880989	*MMP14*	missense_variant	G	A	373551	0.0266	0.041	0.007	1.72E-08
14	23761094	rs12050260	*PPP1R3E*	intron_variant	T	C	360151	0.6489	0.016	0.003	1.78E-10
14	24707479	rs34354104	*GMPR2*	missense_variant	G	A	381625	0.0480	0.045	0.005	3.67E-16
14	24771285	rs4280164	*LTB4R2*	missense_variant	G	A	381625	0.2005	0.027	0.003	3.79E-19
14	24830850	rs1950500	*NFATC4*	upstream_gene_variant	T	C	378383	0.7115	-0.030	0.003	6.25E-30
14	55265828	rs8022503	-	intergenic_variant	T	C	380102	0.5498	0.018	0.002	4.96E-14
14	55448409	rs61741224	*WDHD1*	missense_variant	G	C	375498	0.1067	-0.021	0.004	1.41E-07
14	60789176	rs4901977	*CTD-2568P8.1*	upstream_gene_variant	C	T	380102	0.3029	0.025	0.003	1.24E-20
14	60903757	rs1254319	*C14orf39*	missense_variant	G	A	372028	0.2868	0.032	0.003	1.25E-31
14	60932752	rs12586711	*C14orf39*	missense_variant	G	A	371699	0.2062	0.022	0.003	7.59E-13
14	60976537	rs33912345	*C14orf39*	missense_variant	C	A	375774	0.6089	-0.036	0.003	2.62E-43
14	61072875	rs10483727	*RP11-1042B17.2*	upstream_gene_variant	T	C	375774	0.6097	-0.036	0.003	2.39E-43
14	65475540	rs4466998	*FNTB*	intron_variant	C	A	381625	0.5096	-0.013	0.002	1.77E-07
14	70633411	rs41286548	*SLC8A3*	missense_variant	C	T	373551	0.0205	-0.054	0.008	2.49E-11
14	74990746	rs862034	*LTBP2*	intron_variant	A	G	378383	0.6328	0.026	0.002	1.05E-26
14	75322794	rs8014204	*PROX2*	3_prime_UTR_variant	G	A	381625	0.5432	0.013	0.002	7.75E-08
14	75347585	rs10083386	*DLST*	upstream_gene_variant	C	A	380102	0.4644	0.015	0.002	7.34E-10
14	76156609	rs2303345	*TTLL5*	missense_variant	C	T	292029	0.6698	-0.017	0.003	1.60E-08
14	79945162	rs10146997	*NRXN3*	intron_variant	A	G	380346	0.2158	0.016	0.003	4.07E-08
14	92427222	rs7153027	-	intergenic_variant	A	C	356196	0.4241	-0.031	0.003	1.49E-32
14	92441066	rs1051340	*TRIP11*	missense_variant	C	T	379252	0.3299	-0.024	0.003	6.85E-20
14	92459958	rs8007661	*TRIP11*	intron_variant	C	T	380346	0.4689	-0.027	0.002	2.84E-28
14	92485881	rs7155279	*TRIP11*	intron_variant	G	T	289623	0.3585	-0.030	0.003	1.32E-24

14	92548785	rs1048755	*ATXN3*	missense_variant	C	T	381625	0.2424	-0.027	0.003	4.06E-21
14	94844947	rs28929474	*SERPINA1*	missense_variant	C	T	365451	0.0184	0.124	0.009	1.39E-45
14	101349454	rs41286560	*MIR432*	missense_variant	G	T	381625	0.0242	-0.050	0.007	1.17E-11
14	102792386	rs7158731	*ZNF839*	missense_variant	T	C	310708	0.1763	-0.020	0.004	4.13E-08
14	102792631	rs7158139	*ZNF839*	missense_variant	G	A	376860	0.1762	-0.020	0.003	2.90E-10
15	41476209	rs522063	*EXD1*	missense_variant	T	C	381625	0.7345	0.016	0.003	1.55E-08
15	41689166	rs3204853	*NDUFAF1*	missense_variant	C	A	317471	0.2612	-0.018	0.003	5.23E-09
15	41689232	rs1899	*NDUFAF1*	missense_variant	C	T	369748	0.2611	-0.018	0.003	3.07E-10
15	50932357	rs56170748	*TRPM7*	intron_variant	C	T	380102	0.5106	0.013	0.002	6.55E-08
15	51217361	rs2306331	*AP4E1*	missense_variant	T	C	371178	0.4566	0.018	0.002	1.31E-13
15	51530495	rs16964211	*CYP19A1*	intron_variant	G	A	260475	0.0536	-0.052	0.006	1.58E-16
15	51569410	rs2305707	*CYP19A1*	non_coding_transcript_exon_variant	A	G	381625	0.1502	-0.021	0.003	1.59E-10
15	60781513	rs3743266	*RORA*	3_prime_UTR_variant	T	C	377104	0.3171	-0.015	0.003	5.76E-09
15	62259637	rs3784634	*VPS13C*	missense_variant	C	T	263337	0.5627	0.017	0.003	2.20E-08
15	62332980	rs17271305	*VPS13C*	intron_variant	A	G	373551	0.4029	-0.015	0.003	5.17E-09
15	62380259	rs7178424	*NPM1P47*	upstream_gene_variant	C	T	375505	0.4561	-0.020	0.003	1.52E-14
15	65916527	rs3743171	*SLC24A1*	missense_variant	A	T	375498	0.1881	0.020	0.003	4.95E-11
15	67528374	rs7173826	*AAGAB*	missense_variant	T	G	381625	0.3318	-0.013	0.003	1.36E-07
15	70048157	rs10152591	-	regulatory_region_variant	A	C	347130	0.0924	-0.047	0.004	2.25E-27
15	70364352	rs975210	*TLE3*	intron_variant	G	A	375581	0.1736	0.037	0.003	1.63E-31
15	72161403	rs12902421	*MYO9A*	intron_variant	T	C	324499	0.0177	0.072	0.009	1.80E-14
15	72454690	rs71395065	*GRAMD2*	missense_variant	A	G	381625	0.0063	0.104	0.014	1.92E-13
15	72462255	rs34815962	*GRAMD2*	missense_variant	C	T	359848	0.0185	0.073	0.009	8.72E-17
15	72511415	rs3759901	*PKM*	missense_variant	G	A	276900	0.0170	0.077	0.010	2.40E-13
15	74229065	rs893817	*LOXL1*	intron_variant	G	A	381625	0.6515	-0.023	0.002	1.29E-19
15	74328116	rs743580	*PML*	missense_variant	A	G	381625	0.5030	-0.016	0.002	1.79E-11
15	74328141	rs743581	*PML*	missense_variant	G	T	371611	0.3683	-0.020	0.003	6.04E-15
15	74336633	rs5742915	*PML*	missense_variant	T	C	381625	0.4506	0.031	0.002	7.35E-38
15	74487969	rs971756	*STRA6*	missense_variant	A	T	367424	0.2152	-0.017	0.003	1.05E-08
15	75755467	rs4886707	*PTPN9*	downstream_gene_variant	C	T	368469	0.2486	0.017	0.003	2.07E-09
15	77335891	rs11636648	*TSPAN3*	3_prime_UTR_variant	C	T	376860	0.6643	-0.017	0.003	2.27E-10
15	77335902	rs11636613	*TSPAN3*	3_prime_UTR_variant	A	G	370559	0.6823	-0.016	0.003	2.86E-09
15	84286492	rs2562784	*SH3GL3*	intron_variant	A	G	378383	0.2291	0.033	0.003	8.31E-30
15	84315884	rs2554380	-	intergenic_variant	C	T	356339	0.7860	0.036	0.003	2.28E-31
15	84327771	rs2730081	*ADAMTSL3*	intron_variant	T	C	358889	0.5928	0.013	0.003	1.76E-07
15	84488636	rs4483821	*ADAMTSL3*	missense_variant	A	G	380721	0.4507	0.031	0.002	1.41E-36
15	84568158	rs10906982	*ADAMTSL3*	intron_variant	T	A	212840	0.5283	0.041	0.004	6.46E-31
15	84573041	rs7183263	*ADAMTSL3*	intron_variant	T	G	380346	0.5181	0.049	0.003	3.78E-80
15	84580582	rs11259936	*ADAMTSL3*	intron_variant	A	C	373551	0.5178	0.049	0.003	2.12E-78
15	84582124	rs4842838	*ADAMTSL3*	missense_variant	G	T	379252	0.5183	0.049	0.003	1.78E-79
15	84611367	rs34047645	*ADAMTSL3*	missense_variant	G	C	348421	0.1761	-0.035	0.003	2.29E-25
15	84611805	rs61752778	*ADAMTSL3*	missense_variant	C	T	376215	0.0211	-0.044	0.008	4.18E-08
15	84639350	rs2277849	*ADAMTSL3*	missense_variant	C	T	359848	0.2690	-0.025	0.003	1.01E-18
15	84706461	rs950169	*ADAMTSL3*	missense_variant	C	T	381625	0.2735	0.027	0.003	2.14E-21
15	85200520	rs1051168	*NMB*	missense_variant	G	T	381625	0.2708	0.016	0.003	3.13E-08
15	85635890	rs8032301	*PDE8A*	intron_variant	T	C	380102	0.4377	0.014	0.002	2.55E-09
15	86123170	rs745191	*AKAP13*	missense_variant	G	T	381625	0.2825	0.017	0.003	7.47E-10
15	86123364	rs7177107	*AKAP13*	missense_variant	G	A	381625	0.2219	-0.019	0.003	3.40E-10
15	86278479	rs16943741	*AKAP13*	intron_variant	A	G	373551	0.5129	-0.016	0.002	1.65E-10
15	89345947	rs8028537	*ACAN*	upstream_gene_variant	A	G	380102	0.4876	0.030	0.002	1.92E-34
15	89359689	rs8041863	*ACAN*	intron_variant	T	A	374724	0.4820	0.030	0.002	9.02E-35
15	89386652	rs34949187	*ACAN*	missense_variant	G	A	372272	0.1743	-0.029	0.003	1.67E-19
15	89388905	rs16942341	*ACAN*	synonymous_variant	C	T	379977	0.0263	-0.129	0.007	4.30E-72
15	89390513	rs117116488	*ACAN*	missense_variant	C	T	381625	0.0092	-0.114	0.012	1.09E-21
15	89398553	rs35430524	*ACAN*	missense_variant	C	A	372028	0.1009	0.030	0.004	3.89E-14
15	89398605	rs938608	*ACAN*	missense_variant	G	T	348325	0.6380	-0.026	0.003	6.57E-21
15	89398631	rs938609	*ACAN*	missense_variant	T	A	363034	0.6379	-0.024	0.003	1.46E-19
15	89400339	rs2882676	*ACAN*	missense_variant	A	C	315396	0.6391	-0.025	0.003	8.96E-19
15	89400680	rs28407189	*ACAN*	missense_variant	A	G	381625	0.0267	-0.127	0.007	1.77E-71
15	89401109	rs4932439	*ACAN*	missense_variant	A	G	379016	0.8133	-0.038	0.003	3.07E-33
15	89402051	rs1042630	*ACAN*	missense_variant	A	G	381625	0.7424	-0.015	0.003	8.90E-08
15	89415247	rs3817428	*ACAN*	missense_variant	C	G	374724	0.2740	-0.039	0.003	4.05E-47
15	89424870	rs141308595	*HAPLN3*	missense_variant	G	T	377055	0.0009	-0.267	0.037	2.84E-13
15	89450587	rs1878326	*MFGE8*	missense_variant	G	T	379252	0.6301	-0.019	0.003	1.22E-13
15	89804043	rs17803620	*FANCI*	missense_variant	C	T	381625	0.3851	-0.015	0.002	1.62E-09
15	90903311	rs2589957	*ZNF774*	missense_variant	A	G	381625	0.4681	0.013	0.002	7.33E-08
15	94570578	rs899609	*LINC01581*	intron_variant	T	C	380102	0.5886	0.015	0.002	3.16E-10
15	99194896	rs2871865	*IGF1R*	intron_variant	C	G	375498	0.1052	-0.057	0.004	1.27E-47
15	99212485	rs1319869	*IGF1R*	intron_variant	G	T	376860	0.8937	0.040	0.004	1.35E-24
15	100514614	rs2573652	*ADAMTS17*	missense_variant	T	C	381625	0.6736	0.027	0.003	5.47E-26
15	100516472	rs11634977	*ADAMTS17*	non_coding_transcript_exon_variant	G	A	327132	0.6755	0.027	0.003	1.68E-20
15	100537494	rs12900132	*ADAMTS17*	intron_variant	C	T	286529	0.6308	0.019	0.003	1.99E-11
15	100687967	rs4246302	*ADAMTS17*	intron_variant	A	G	372028	0.3171	0.021	0.003	3.16E-16
15	100692953	rs72755233	*ADAMTS17*	missense_variant	G	A	377876	0.1098	-0.092	0.004	7.09E-130
15	100786271	rs4533267	*ADAMTS17*	intron_variant	A	G	369899	0.7188	-0.032	0.003	3.00E-32
15	100821576	rs7496668	*ADAMTS17*	missense_variant	G	A	381625	0.3359	-0.018	0.003	4.67E-13
15	100843884	rs8041080	*ADAMTS17*	intron_variant	C	T	339914	0.4583	-0.019	0.003	2.31E-13
15	101717888	rs62621399	*CHSY1*	missense_variant	C	T	381625	0.1474	0.025	0.003	9.94E-14
15	101718239	rs62621400	*CHSY1*	missense_variant	C	G	375498	0.0599	-0.062	0.005	2.52E-35
16	624114	rs2071979	*PIGQ*	missense_variant	A	G	360151	0.4308	0.022	0.003	5.17E-17
16	633125	rs1045277	*PIGQ*	missense_variant	T	C	355029	0.4345	0.022	0.003	8.65E-17
16	675680	rs763014	*RAB40C*	non_coding_transcript_exon_variant	T	C	285198	0.4389	0.024	0.003	8.29E-17
16	701656	rs11642546	*LA16c-349E10.1*	missense_variant	C	T	375923	0.2450	0.024	0.003	1.53E-16
16	705360	rs3803697	*LA16c-349E10.1*	missense_variant	T	C	369142	0.3794	0.017	0.003	5.62E-10
16	708275	rs45613635	*LA16c-349E10.1*	missense_variant	C	A	330955	0.2482	0.024	0.003	2.19E-14
16	709001	rs4984906	*LA16c-349E10.1*	missense_variant	C	A	369689	0.3779	0.016	0.003	1.89E-09
16	711905	rs2301426	*WDR90*	synonymous_variant	A	G	327596	0.3765	0.016	0.003	2.07E-08
16	722331	rs3177338	*RHOT2*	missense_variant	C	T	292042	0.3796	0.016	0.003	5.87E-08
16	774692	rs2071950	*CCDC78*	missense_variant	A	G	313052	0.4885	0.022	0.003	3.08E-16

16	2097158	rs2516739	*TSC2*	non_coding_transcript_exon_variant	G	A	347560	0.2173	-0.016	0.003	6.28E-08
16	2140680	rs10960	*PKD1*	missense_variant	T	C	372384	0.1821	-0.024	0.003	1.90E-14
16	2260567	rs26857	*MLST8*	missense_variant	C	T	269592	0.5050	0.017	0.003	4.88E-09
16	4755108	rs78074706	*ANKS3*	missense_variant	G	A	381625	0.0252	0.054	0.007	1.23E-13
16	4812705	rs61733564	*ZNF500*	missense_variant	A	G	357633	0.0319	0.056	0.007	8.61E-17
16	4933939	rs2037912	*UBN1*	missense_variant	G	C	373405	0.5621	-0.016	0.003	2.18E-10
16	4942099	rs1049205	*PPL*	missense_variant	C	T	381625	0.5622	-0.015	0.002	8.39E-10
16	4945687	rs35340520	*PPL*	missense_variant	G	T	381625	0.0742	0.031	0.005	8.68E-12
16	14388305	rs1659127	-	intergenic_variant	G	A	314333	0.3460	0.025	0.003	1.21E-18
16	15129970	rs7200543	*NTAN1*	synonymous_variant	A	G	379252	0.3027	-0.014	0.003	1.08E-07
16	15131974	rs1136001	*NTAN1*	missense_variant	G	T	359848	0.3026	-0.015	0.003	8.23E-08
16	20748331	rs11074471	*THUMPD1*	missense_variant	C	A	381625	0.1391	-0.019	0.004	1.83E-07
16	24804954	rs113388806	*TNRC6A*	missense_variant	A	T	367424	0.0401	0.036	0.006	1.08E-09
16	29998200	rs4077410	*TAOK2*	synonymous_variant	A	G	380346	0.5125	0.015	0.002	2.61E-09
16	30072530	rs9928448	*ALDOA*	intron_variant	T	C	381625	0.4615	0.016	0.002	1.58E-11
16	30958481	rs61738491	*ORAI3*	missense_variant	G	A	381625	0.0092	0.064	0.012	8.17E-08
16	31091390	rs35376811	*RP11-196G11.1*	missense_variant	C	T	373551	0.0080	0.079	0.013	9.44E-10
16	31474091	rs141923065	*ARMC5*	splice_acceptor_variant	A	G	373551	0.0056	0.104	0.015	5.88E-12
16	47684830	rs34667348	*PHKB*	missense_variant	C	A	381625	0.0049	0.121	0.016	3.96E-14
16	67320223	rs3868142	*PLEKHG4*	missense_variant	G	A	368368	0.0809	-0.036	0.005	3.50E-15
16	67325711	rs16957289	*PLEKHG4*	missense_variant	C	T	351774	0.0418	-0.050	0.006	9.93E-16
16	67397580	rs9922085	*LRRC36*	missense_variant	G	C	357580	0.0431	-0.053	0.006	5.67E-18
16	67409180	rs8052655	*LRRC36*	missense_variant	G	A	365995	0.0428	-0.054	0.006	1.08E-18
16	67418957	rs16957415	*LRRC36*	missense_variant	A	G	381625	0.0416	-0.051	0.006	1.38E-17
16	67470505	rs140385822	*ATP6V0D1*	missense_variant	G	A	366511	0.0017	-0.148	0.028	1.27E-07
16	67516945	rs5030980	*AGRP*	missense_variant	C	T	381625	0.0408	-0.053	0.006	2.89E-18
16	67696365	rs35356834	*ACD*	missense_variant	G	A	359848	0.0408	-0.047	0.006	4.26E-14
16	67860637	rs62620177	*CENPT*	missense_variant	C	T	381625	0.0408	-0.047	0.006	5.86E-15
16	67973953	rs5923	*SLC12A4*	missense_variant	G	A	381625	0.0455	-0.043	0.006	1.33E-13
16	67976320	rs4986970	*SLC12A4*	missense_variant	A	T	374724	0.0296	0.041	0.007	1.84E-09
16	69547741	rs4783718	-	regulatory_region_variant	T	C	377729	0.6026	0.027	0.003	3.58E-26
16	69588572	rs1364063	-	TF_binding_site_variant	T	C	381625	0.4228	0.020	0.002	1.59E-16
16	69745145	rs1800566	*NQO1*	missense_variant	G	A	359848	0.1858	-0.020	0.003	7.19E-10
16	69832105	rs4275849	*WWP2*	intron_variant	G	A	372028	0.3678	-0.017	0.003	1.15E-11
16	70548297	rs3931036	*COG4*	missense_variant	G	A	381625	0.9369	-0.029	0.005	4.72E-09
16	71509779	rs10500557	*ZNF19*	missense_variant	C	T	381625	0.0318	-0.036	0.007	2.73E-08
16	71983772	rs1035543	*PKD1L3*	missense_variant	G	C	375498	0.3400	-0.015	0.003	8.16E-08
16	71988106	rs9921412	*PKD1L3*	missense_variant	C	T	351178	0.7378	-0.020	0.003	9.26E-11
16	82203758	rs2303262	*MPHOSPH6*	missense_variant	C	T	381625	0.7846	-0.019	0.003	1.80E-11
16	84900645	rs149615348	*CRISPLD2*	missense_variant	G	A	381625	0.0066	-0.095	0.014	9.13E-12
16	84902472	rs148934412	*CRISPLD2*	missense_variant	G	A	381625	0.0008	-0.297	0.040	7.75E-14
16	84987679	rs2326458	-	intergenic_variant	C	A	380346	0.7363	-0.021	0.003	2.68E-15
16	88782205	rs202127176	*CTU2*	missense_variant	G	C	353201	0.0021	-0.164	0.027	7.42E-10
16	88798919	rs201226914	*PIEZO1*	missense_variant	G	T	369776	0.0019	-0.187	0.027	5.27E-12
16	88804734	rs7184427	*RP5-1142A6.7*	missense_variant	A	G	302165	0.8522	0.024	0.004	1.57E-10
16	88808743	rs6500495	*RP5-1142A6.7*	missense_variant	A	G	369355	0.8764	0.023	0.004	4.80E-10
16	89587871	rs4785686	*SPG7*	non_coding_transcript_exon_variant	A	C	349602	0.4451	-0.013	0.003	1.23E-07
16	89704365	rs1126464	*DPEP1*	missense_variant	G	C	347585	0.2410	0.023	0.003	4.85E-15
16	89755903	rs258322	*CDK10*	intron_variant	A	G	352897	0.8938	0.024	0.004	8.05E-09
16	89986144	rs1805008	*TUBB3*	missense_variant	C	T	356196	0.0819	0.029	0.005	1.50E-10
17	1673276	rs1136287	*SERPINF1*	missense_variant	C	T	381625	0.6417	-0.014	0.003	3.13E-08
17	7329134	rs72842820	*C17orf74*	missense_variant	G	A	381625	0.1787	0.023	0.003	6.08E-13
17	7363088	rs9217	*CHRNB1*	3_prime_UTR_variant	T	C	378383	0.3679	0.030	0.003	7.64E-32
17	7366619	rs34914463	*ZBTB4*	missense_variant	T	C	159643	0.1028	0.034	0.006	2.75E-08
17	7417663	rs6761	*POLR2A*	3_prime_UTR_variant	C	T	380346	0.6010	-0.023	0.003	3.09E-19
17	7536527	rs6259	*SHBG*	missense_variant	G	A	381625	0.1129	0.028	0.004	1.13E-12
17	7557419	rs1642763	*ATP1B2*	synonymous_variant	A	G	376359	0.7704	-0.019	0.003	1.83E-10
17	21284223	rs4640244	*KCNJ12*	intron_variant	A	G	380346	0.3977	-0.020	0.002	8.81E-17
17	27889986	rs542939	*TP53I13*	missense_variant	T	C	372789	0.6569	0.025	0.003	3.72E-23
17	27917771	rs3110496	*GIT1*	intron_variant	A	G	375781	0.6734	0.017	0.003	3.28E-11
17	28548810	rs6355	*SLC6A4*	missense_variant	C	G	373418	0.0190	0.049	0.008	5.94E-09
17	29111368	rs11867457	*CRLF3*	missense_variant	A	G	136791	0.1642	-0.042	0.005	2.25E-15
17	29161503	rs11080134	*ATAD5*	missense_variant	A	G	377738	0.3484	0.021	0.003	1.25E-16
17	29247715	rs3760318	*ADAP2*	intron_variant	G	A	378383	0.3730	-0.045	0.003	2.72E-71
17	29629326	rs11080150	*OMG*	intron_variant	A	G	372028	0.3091	0.016	0.003	1.09E-09
17	36922196	rs1043515	*PIP4K2B*	3_prime_UTR_variant	A	G	326741	0.5566	0.025	0.003	4.06E-22
17	38545193	rs13695	*TOP2A*	3_prime_UTR_variant	C	T	369030	0.2560	0.018	0.003	8.35E-11
17	38640744	rs2290207	*TNS4*	missense_variant	C	T	379252	0.2505	0.015	0.003	1.37E-07
17	40714804	rs615942	*MLX*	missense_variant	C	A	254275	0.5632	0.019	0.003	1.63E-09
17	40725799	rs2292751	*PSMC3IP*	non_coding_transcript_exon_variant	C	T	372028	0.5521	0.017	0.003	1.30E-11
17	42744238	rs9907151	*C17orf104*	missense_variant	A	C	359848	0.1879	0.018	0.003	5.79E-09
17	43208121	rs12946454	*ACBD4*	intron_variant	A	T	373865	0.2634	-0.032	0.003	3.11E-30
17	43212963	rs2291447	*ACBD4*	splice_region_variant	G	T	381625	0.5018	-0.020	0.002	1.02E-16
17	43216281	rs4986172	*ACBD4*	intron_variant	C	T	381625	0.3480	-0.032	0.003	3.90E-35
17	43714850	rs2942168	*AC126544.4*	non_coding_transcript_exon_variant	G	A	328783	0.2019	-0.021	0.004	1.85E-07
17	43923266	rs62054815	*MAPT-AS1*	missense_variant	G	A	351171	0.2056	-0.021	0.004	6.21E-08
17	43923683	rs12185268	*MAPT-AS1*	missense_variant	A	G	343538	0.2028	-0.020	0.004	1.59E-07
17	43924073	rs12373123	*MAPT-AS1*	missense_variant	T	C	351760	0.2065	-0.021	0.004	1.21E-07
17	43924130	rs12373139	*MAPT-AS1*	missense_variant	G	A	372028	0.2034	-0.020	0.004	1.13E-07
17	44061023	rs62063786	*MAPT*	missense_variant	G	A	373551	0.2033	-0.021	0.004	2.28E-08
17	44061036	rs62063787	*MAPT*	missense_variant	T	C	372028	0.2033	-0.021	0.004	3.00E-08
17	44061278	rs17651549	*MAPT*	missense_variant	C	T	381625	0.2035	-0.020	0.004	4.80E-08
17	44067400	rs10445337	*MAPT*	missense_variant	T	C	371618	0.2057	-0.021	0.004	3.78E-08
17	44076665	rs62063857	*MAPT*	missense_variant	A	G	337903	0.2013	-0.021	0.004	3.41E-08
17	44081064	rs8070723	*MAPT*	intron_variant	A	G	381625	0.2044	-0.021	0.004	2.04E-08
17	44108906	rs34579536	*KANSL1*	missense_variant	A	G	355716	0.2029	-0.021	0.004	1.08E-07
17	44117119	rs34043286	*KANSL1*	missense_variant	A	G	381625	0.2035	-0.021	0.004	4.65E-08
17	45732774	rs11871606	*KPNB1*	intron_variant	C	A	372028	0.5100	0.015	0.003	1.44E-09
17	45768836	rs8070463	*TBKBP1*	upstream_gene_variant	T	C	380346	0.5041	-0.013	0.002	6.21E-08

17	45786621	rs80267077	*TBKBP1*	missense_variant	G	A	309280	0.1128	-0.026	0.004	3.78E-10
17	46022065	rs17679445	*PNPO*	missense_variant	G	A	381625	0.0708	0.025	0.005	9.62E-08
17	46939658	rs10278	*CALCOCO2*	missense_variant	C	G	350310	0.2963	0.016	0.003	2.19E-08
17	46988529	rs46521	*UBE2Z*	intron_variant	A	G	380102	0.5329	-0.026	0.003	3.11E-24
17	46988597	rs46522	*UBE2Z*	non_coding_transcript_exon_variant	C	T	380346	0.5328	-0.027	0.003	2.82E-24
17	47005193	rs15563	*UBE2Z*	3_prime_UTR_variant	A	G	378383	0.5328	-0.027	0.003	2.20E-24
17	47039132	rs2291725	*GIP*	missense_variant	T	C	381625	0.5274	-0.026	0.003	8.84E-23
17	47047868	rs3895874	*GIP*	upstream_gene_variant	G	A	280939	0.5607	-0.024	0.003	5.08E-17
17	47390014	rs2072153	*ZNF652*	intron_variant	G	C	364247	0.3059	0.025	0.003	1.49E-21
17	47440466	rs16948048	*ZNF652*	intron_variant	A	G	381625	0.3822	-0.015	0.002	4.81E-10
17	54773238	rs227731	-	intergenic_variant	T	G	374496	0.4502	0.014	0.002	2.57E-09
17	54778817	rs227724	-	intergenic_variant	A	T	366654	0.3448	0.024	0.003	4.39E-21
17	54850329	rs4794665	-	intergenic_variant	A	G	379252	0.5078	-0.026	0.002	9.65E-28
17	54872439	rs72837329	*C17orf67*	missense_variant	T	C	381625	0.1473	0.019	0.003	2.19E-08
17	59483766	rs8068318	*TBX2*	non_coding_transcript_exon_variant	C	T	378383	0.7271	-0.026	0.003	1.70E-22
17	59497277	rs757608	-	intergenic_variant	A	G	378383	0.6753	-0.045	0.003	8.65E-70
17	59533868	rs3744448	*TBX4*	missense_variant	G	C	366145	0.1548	0.024	0.003	1.74E-13
17	59638769	rs2378871	-	intergenic_variant	A	C	378823	0.6151	-0.025	0.002	1.46E-25
17	60440732	rs67568091	-	intergenic_variant	T	C	381625	0.5156	0.013	0.002	1.04E-07
17	61623052	rs35819807	*KCNH6*	missense_variant	C	T	381625	0.2504	0.028	0.003	1.56E-23
17	61666687	rs72845886	*DCAF7*	3_prime_UTR_variant	C	T	381625	0.0622	0.040	0.005	1.08E-15
17	61712964	rs7209435	*MAP3K3*	intron_variant	T	C	334293	0.2787	0.041	0.003	1.20E-46
17	61908556	rs13030	*SMARCD2*	synonymous_variant	C	T	377973	0.3344	-0.034	0.003	1.44E-40
17	62020348	rs2058194	*SCN4A*	missense_variant	T	C	379252	0.5321	0.018	0.002	8.52E-14
17	62050528	rs3760238	*CTC-264K15.6*	non_coding_transcript_exon_variant	T	C	380102	0.4887	-0.013	0.002	1.10E-08
17	63554591	rs2240308	*AXIN2*	missense_variant	G	A	369663	0.5269	0.016	0.002	5.33E-12
17	64280153	rs56152251	-	regulatory_region_variant	G	A	380102	0.4213	-0.013	0.002	7.58E-08
17	64318357	rs9912468	*PRKCA*	intron_variant	G	C	373405	0.5788	0.014	0.002	2.22E-08
17	65870073	rs12602912	*BPTF*	intron_variant	C	T	378823	0.2051	0.016	0.003	9.72E-08
17	68090207	rs11867479	*AC002539.1*	intron_variant	C	T	380346	0.3491	0.025	0.002	2.06E-23
17	69926109	rs2158917	-	intergenic_variant	C	T	364983	0.2667	0.021	0.003	4.78E-14
17	76700063	rs7220955	*CYTH1*	intron_variant	G	A	370380	0.5563	-0.016	0.003	6.11E-10
17	76799795	rs1057040	*USP36*	missense_variant	G	A	350042	0.5367	-0.017	0.003	1.04E-11
17	76799860	rs3088040	*USP36*	missense_variant	T	C	372028	0.5613	-0.016	0.003	5.91E-10
17	80176641	rs4239020	*RP13-516M14.2*	downstream_gene_variant	C	T	314970	0.6788	-0.016	0.003	1.32E-08
18	166819	rs563155	*USP14*	splice_region_variant	T	C	359848	0.2224	0.017	0.003	7.29E-09
18	20646281	rs10853489	-	intergenic_variant	A	G	380102	0.5925	0.017	0.002	2.36E-12
18	20720973	rs11082304	*CABLES1*	intron_variant	G	T	381625	0.5058	0.035	0.002	9.69E-47
18	20724328	rs4800148	*CABLES1*	intron_variant	G	A	380346	0.7885	0.061	0.003	8.03E-91
18	20727611	rs4800452	*CABLES1*	intron_variant	C	T	381625	0.7913	0.062	0.003	1.81E-92
18	20735408	rs4369779	*CABLES1*	intron_variant	T	C	380346	0.7954	0.063	0.003	9.29E-93
18	21120444	rs1805082	*NPC1*	missense_variant	T	C	381625	0.4782	-0.015	0.002	1.67E-09
18	21140432	rs1805081	*NPC1*	missense_variant	T	C	381625	0.4133	-0.014	0.002	4.02E-08
18	44819849	rs10164176	*CTD-2130O13.1*	intron_variant	T	C	380102	0.4564	0.013	0.002	7.43E-08
18	46770186	rs11661691	*DYM*	intron_variant	T	G	329563	0.5061	0.018	0.003	1.45E-12
18	46959500	rs9967417	*DYM*	intron_variant	G	C	372631	0.5795	-0.030	0.002	3.98E-34
18	46976586	rs2156497	*DYM*	intron_variant	A	G	292240	0.3433	-0.032	0.003	4.59E-27
18	46991160	rs8099594	*DYM*	upstream_gene_variant	A	G	380346	0.3442	-0.031	0.003	1.32E-34
18	57751014	rs12957347	-	intergenic_variant	T	C	220129	0.2513	0.026	0.004	1.24E-12
18	57839769	rs571312	-	intergenic_variant	C	A	377104	0.2347	0.031	0.003	2.85E-24
18	57851097	rs17782313	-	intergenic_variant	T	C	380346	0.2346	0.031	0.003	2.13E-24
18	57851763	rs10871777	-	intergenic_variant	A	G	380346	0.2372	0.030	0.003	1.79E-23
18	57882787	rs489693	-	intergenic_variant	C	A	380346	0.3120	0.015	0.003	1.68E-08
18	57884750	rs12970134	-	intergenic_variant	G	A	379252	0.2630	0.018	0.003	2.02E-10
18	74980601	rs77169818	*GALR1*	missense_variant	A	T	374724	0.0470	-0.048	0.006	3.60E-18
19	2170954	rs12986413	*DOT1L*	intron_variant	A	T	363621	0.4709	0.028	0.002	2.15E-28
19	2177193	rs12982744	*DOT1L*	intron_variant	C	G	365127	0.3882	0.029	0.003	1.23E-29
19	4910889	rs2261988	*UHRF1*	missense_variant	G	T	341234	0.3297	0.020	0.003	2.82E-14
19	7184762	rs891088	*INSR*	intron_variant	A	G	377973	0.2630	0.029	0.003	6.31E-26
19	7196565	rs2115386	*INSR*	intron_variant	C	T	351440	0.4948	-0.014	0.002	1.04E-08
19	7224431	rs7248104	*INSR*	intron_variant	G	A	380346	0.4106	0.018	0.002	2.54E-14
19	8644031	rs4072910	*AC130469.2*	upstream_gene_variant	G	C	375498	0.4708	-0.031	0.002	2.77E-39
19	8669931	rs7255721	*ADAMTS10*	missense_variant	G	C	333237	0.7029	-0.019	0.003	6.22E-12
19	8672000	rs7249094	*ADAMTS10*	intron_variant	G	A	380346	0.3865	-0.022	0.002	4.24E-19
19	10273372	rs2228612	*DNMT1*	missense_variant	T	C	381625	0.0637	0.037	0.005	5.98E-14
19	10742170	rs2288904	*SLC44A2*	missense_variant	A	G	381625	0.7906	-0.021	0.003	3.93E-12
19	10801185	rs8102380	*ILF3*	3_prime_UTR_variant	G	A	380102	0.6866	-0.020	0.003	3.47E-14
19	11275139	rs7188	*KANK2*	3_prime_UTR_variant	A	C	376010	0.3258	-0.018	0.003	9.28E-13
19	12128726	rs77897724	*ZNF433*	missense_variant	T	C	354673	0.0014	-0.172	0.033	1.22E-07
19	12154799	rs67102109	*ZNF878*	missense_variant	G	C	371611	0.0717	0.036	0.005	7.20E-14
19	12774208	rs1054486	*WDR83*	missense_variant	G	C	371749	0.2943	-0.014	0.003	1.89E-07
19	17283303	rs2279008	*MYO9B*	intron_variant	T	C	364133	0.2578	-0.016	0.003	1.47E-08
19	19361735	rs1064395	*AC138430.4*	3_prime_UTR_variant	G	A	379252	0.1568	0.026	0.003	4.49E-15
19	19413092	rs17751061	*SUGP1*	missense_variant	C	T	152097	0.1444	0.029	0.005	8.61E-08
19	19790159	rs4808209	*ZNF101*	start_lost	A	C	360412	0.0474	-0.031	0.006	2.74E-08
19	41903220	rs10853751	*CTC-435M10.10*	missense_variant	G	A	381625	0.6029	-0.023	0.003	4.04E-19
19	41937095	rs17318596	*B3GNT8*	missense_variant	G	A	305993	0.3676	0.023	0.003	2.00E-15
19	41939297	rs1043413	*ATP5SL*	missense_variant	C	G	151761	0.3920	0.023	0.004	4.36E-09
19	41944237	rs2231940	*ATP5SL*	missense_variant	T	C	381625	0.3956	0.024	0.003	2.76E-21
19	42728836	rs3810151	*ZNF526*	missense_variant	T	C	381625	0.0992	-0.022	0.004	2.32E-08
19	42863035	rs1206038	*MEGF8*	missense_variant	A	G	359848	0.0513	-0.035	0.006	1.39E-10
19	45296806	rs3208856	*CBLC*	missense_variant	C	T	330127	0.0345	0.036	0.007	1.48E-07
19	46914547	rs2279517	*CCDC8*	missense_variant	C	G	366650	0.0540	0.032	0.005	1.12E-09
19	46914927	rs75175362	*CCDC8*	missense_variant	C	T	373551	0.0537	0.032	0.005	8.77E-10
19	48198675	rs13346368	*GLTSCR1*	missense_variant	A	G	381625	0.2632	0.015	0.003	9.97E-08
19	49116359	rs447802	*RPL18*	missense_variant	T	C	377104	0.2698	0.015	0.003	2.27E-08
19	55831502	rs61737281	*TMEM150B*	missense_variant	G	A	381625	0.0080	-0.095	0.013	7.14E-14
19	55879672	rs4252548	*IL11*	missense_variant	C	T	381625	0.0261	-0.114	0.007	1.02E-57
19	55993436	rs147110934	*NAT14*	missense_variant	G	T	266399	0.0206	-0.084	0.010	2.28E-18

19	56001665	rs114976626	*SSC5D*	missense_variant	C	T	304943	0.0236	-0.066	0.008	4.02E-15
19	56011573	rs61747393	*SSC5D*	missense_variant	C	T	331504	0.0233	-0.062	0.008	1.54E-14
19	56056257	rs56258384	*SBK3*	missense_variant	G	C	320631	0.0234	-0.048	0.008	4.15E-09
20	4101800	rs1741344	*SMOX*	non_coding_transcript_exon_variant	C	T	380346	0.6387	-0.024	0.002	5.10E-22
20	6578556	rs6054374	-	intergenic_variant	C	T	283025	0.4354	-0.030	0.003	9.77E-26
20	6620893	rs967417	-	intergenic_variant	G	A	377104	0.4716	-0.041	0.002	4.57E-64
20	6621685	rs2145270	-	intergenic_variant	C	T	381625	0.6350	-0.044	0.002	2.09E-68
20	21142523	rs4815025	*KIZ*	missense_variant	C	G	359880	0.6775	-0.021	0.003	4.95E-14
20	21142813	rs2236178	*KIZ*	missense_variant	T	C	381625	0.6820	-0.020	0.003	7.51E-14
20	21218023	rs6137297	*KIZ*	intron_variant	C	T	369655	0.6769	-0.020	0.003	2.67E-13
20	31950845	rs291671	*CDK5RAP1*	intron_variant	G	A	381625	0.9055	0.030	0.004	1.91E-12
20	32265513	rs2071056	*NECAB3*	intron_variant	A	G	380102	0.3039	-0.034	0.003	1.51E-36
20	32266134	rs35385772	*NECAB3*	missense_variant	C	T	359535	0.0316	-0.055	0.007	2.37E-16
20	32295541	rs910397	*PXMP4*	missense_variant	C	T	369748	0.4681	-0.016	0.002	6.87E-11
20	32333181	rs7274811	*ZNF341*	intron_variant	G	T	368384	0.2392	-0.039	0.003	2.77E-40
20	32955423	rs6087577	*ITCH*	intron_variant	A	G	377738	0.4900	-0.021	0.003	6.14E-17
20	33110846	rs1122174	*DYNLRB1*	intron_variant	T	C	343507	0.8198	0.022	0.003	2.03E-10
20	33411871	rs6088619	*NCOA6*	intron_variant	A	G	374936	0.1306	0.041	0.004	1.36E-29
20	33470694	rs4911163	*ACSS2*	synonymous_variant	C	T	377738	0.6181	0.023	0.003	1.30E-17
20	33488771	rs6120757	*ACSS2*	intron_variant	C	T	376215	0.6191	0.022	0.003	2.47E-17
20	33565755	rs11906160	*MYH7B*	missense_variant	G	A	351632	0.1144	0.026	0.004	7.90E-11
20	33586968	rs41307159	*TRPC4AP*	missense_variant	G	A	377738	0.0186	-0.056	0.009	5.56E-11
20	33730387	rs6120849	*EDEM2*	intron_variant	C	T	377738	0.2271	0.017	0.003	1.80E-08
20	33734493	rs1415771	*EDEM2*	intron_variant	G	A	373842	0.4625	0.023	0.003	9.13E-20
20	33764554	rs867186	*PROCR*	missense_variant	A	G	365861	0.1035	0.024	0.004	1.16E-08
20	33849179	rs1555322	*MMP24-AS1*	intron_variant	G	A	355961	0.1337	0.026	0.004	7.37E-13
20	33907161	rs6060369	*UQCC1*	intron_variant	T	C	377738	0.3943	0.061	0.003	2.59E-106
20	33909784	rs6088792	*UQCC1*	intron_variant	C	T	354100	0.3051	0.048	0.003	3.34E-62
20	33914208	rs6060373	*UQCC1*	intron_variant	A	G	377738	0.3947	0.061	0.003	1.37E-106
20	33971914	rs4911494	*UQCC1*	missense_variant	C	T	354313	0.6086	-0.062	0.003	2.86E-105
20	33975181	rs6088813	*UQCC1*	intron_variant	C	A	377738	0.6089	-0.062	0.003	2.46E-110
20	34022387	rs224331	*GDF5*	missense_variant	A	C	300279	0.3620	0.061	0.003	2.80E-87
20	34025756	rs143384	*GDF5*	5_prime_UTR_variant	A	G	373217	0.4255	0.074	0.003	5.90E-167
20	34025983	rs78110303	*GDF5*	5_prime_UTR_variant	A	G	371887	0.3824	0.064	0.003	2.41E-117
20	34097353	rs2236164	*CEP250*	intron_variant	T	C	374496	0.2409	0.043	0.003	9.72E-45
20	34116282	rs7261862	*C20orf173*	missense_variant	T	C	377738	0.1550	0.028	0.003	3.50E-15
20	34214173	rs11543239	*CPNE1*	missense_variant	G	A	377738	0.0531	0.041	0.005	3.42E-14
20	34218673	rs12481228	*CPNE1*	missense_variant	G	C	371611	0.1013	0.035	0.004	1.17E-15
20	34219496	rs6579255	*CPNE1*	missense_variant	T	C	377738	0.1853	0.045	0.003	2.35E-41
20	34220755	rs11543244	*CPNE1*	missense_variant	C	T	377738	0.0511	0.040	0.006	8.81E-13
20	34373979	rs6142443	*PHF20*	intron_variant	A	C	146208	0.7481	-0.030	0.005	2.70E-10
20	34432670	rs2425163	*PHF20*	intron_variant	A	G	343991	0.1832	0.046	0.004	7.88E-39
20	34502107	rs17431878	*PHF20*	missense_variant	G	A	377738	0.0995	0.038	0.004	1.52E-18
20	34560609	rs17347958	*CNBD2*	missense_variant	G	A	377738	0.0492	0.036	0.006	1.35E-10
20	34596371	rs6060750	*CNBD2*	missense_variant	C	T	377006	0.1937	0.041	0.003	3.99E-37
20	34635441	rs7265718	*LINC00657*	non_coding_transcript_exon_variant	T	G	87348	0.1206	0.044	0.008	8.17E-08
20	35769592	rs1744769	*MROH8*	synonymous_variant	T	C	381625	0.8000	0.021	0.003	4.39E-12
20	35865054	rs4608	*RPN2*	synonymous_variant	C	T	381625	0.7956	0.022	0.003	3.78E-13
20	47253150	rs2664521	*PREX1*	missense_variant	T	C	325105	0.9643	0.045	0.007	2.59E-11
20	47685320	rs2227946	*CSE1L*	synonymous_variant	G	C	374724	0.2420	0.036	0.003	5.48E-35
20	47841660	rs11553387	*DDX27*	missense_variant	G	T	364583	0.2165	0.039	0.003	6.53E-36
20	47850182	rs238148	*DDX27*	synonymous_variant	C	T	378383	0.7775	0.021	0.003	3.70E-12
20	47865509	rs238209	*DDX27*	missense_variant	G	A	381625	0.7773	0.021	0.003	1.81E-12
20	47865784	rs6512577	*ZNFX1*	missense_variant	C	T	379252	0.2173	0.040	0.003	1.58E-39
20	47903019	rs237743	*ZFAS1*	intron_variant	G	A	377104	0.2176	0.040	0.003	4.76E-39
20	48600631	rs4647958	*SNAI1*	missense_variant	T	C	378383	0.1218	-0.025	0.004	1.39E-11
20	57475191	rs13831	*GNAS*	3_prime_UTR_variant	A	G	374634	0.7047	-0.016	0.003	1.47E-09
20	57758720	rs16982520	-	intergenic_variant	A	G	381625	0.1320	0.028	0.004	1.11E-14
20	57768743	rs56057707	*ZNF831*	missense_variant	C	T	381625	0.2028	0.019	0.003	3.07E-10
20	57769140	rs55786258	*ZNF831*	missense_variant	G	C	365901	0.2028	0.019	0.003	7.45E-10
20	60986019	rs2236200	*CABLES2*	missense_variant	A	C	376655	0.2422	-0.017	0.003	2.91E-09
21	35690786	rs2834442	*AP000318.2*	intron_variant	T	A	314611	0.6605	0.022	0.003	8.78E-16
21	38491095	rs1003719	*TTC3*	intron_variant	A	G	381625	0.5541	-0.013	0.002	1.18E-07
21	39671476	rs2230033	*KCNJ15*	missense_variant	G	A	377651	0.5423	-0.022	0.002	4.73E-20
22	17625915	rs35665085	*CECR5*	missense_variant	G	A	381625	0.0578	-0.028	0.005	2.68E-08
22	20789074	rs1005640	*XXbac-B562F10.12*	intron_variant	T	C	379252	0.4326	0.015	0.002	8.00E-10
22	28501414	rs77885044	*TTC28*	missense_variant	C	T	373551	0.0121	-0.067	0.010	9.47E-11
22	35663523	rs2413338	*HMGXB4*	intron_variant	C	T	374251	0.6250	0.014	0.003	5.85E-08
22	38121152	rs9610841	*RP1-37E16.12*	missense_variant	C	A	359848	0.4363	0.014	0.003	3.72E-08
22	38544298	rs2284063	*PLA2G6*	non_coding_transcript_exon_variant	A	G	380346	0.3544	0.016	0.003	1.94E-10
22	38569006	rs738322	*PLA2G6*	intron_variant	A	G	380346	0.4694	0.013	0.002	3.55E-08
22	42095658	rs147348682	*MEI1*	missense_variant	T	G	377832	0.0252	0.041	0.007	2.25E-08
22	45728370	rs6007594	*FAM118A*	missense_variant	G	A	376010	0.2643	0.020	0.003	2.19E-12
22	45749983	rs5764698	*SMC1B*	missense_variant	G	T	360183	0.5174	-0.019	0.003	1.33E-13
22	45813687	rs12172195	*RIBC2*	synonymous_variant	G	A	351171	0.1446	0.025	0.004	1.29E-11
22	45821887	rs1022477	*RIBC2*	synonymous_variant	G	A	381625	0.4816	0.017	0.003	5.98E-12
22	45821935	rs2142662	*RIBC2*	synonymous_variant	G	A	381625	0.1589	0.024	0.003	1.42E-12
23	38009121	rs35318931	*SRPX*	missense_variant	G	A	262032	0.0757	-0.029	0.005	3.97E-10
23	55574773	rs3126259	-	intergenic_variant	T	G	258136	0.2944	-0.021	0.003	4.41E-13
23	56889389	rs1930983	-	intergenic_variant	C	T	260509	0.7775	0.023	0.003	4.66E-13
23	57433303	rs717848	*FAAH2*	intron_variant	A	G	260509	0.2723	-0.020	0.003	1.01E-11
23	57622607	rs1997715	*ZXDB*	3_prime_UTR_variant	G	A	258145	0.2498	-0.022	0.003	1.24E-12
23	77025121	rs112792023	*ATRX*	intron_variant	T	G	251531	0.2705	0.017	0.003	3.60E-08
23	77268502	rs2227291	*ATP7A*	missense_variant	G	C	255905	0.2135	0.018	0.003	1.43E-08
23	77913569	rs4077512	*ZCCHC5*	missense_variant	G	A	210715	0.1444	-0.023	0.004	2.76E-09
23	78649193	rs1474563	-	intergenic_variant	C	T	217091	0.5850	0.031	0.003	5.74E-31
23	78944731	rs1353451	-	intergenic_variant	G	T	222316	0.7902	0.026	0.003	2.93E-15
23	99890204	rs1802288	*TSPAN6*	missense_variant	C	T	240255	0.1755	-0.018	0.003	3.99E-08

Supplementary Table 7. ExomeChip variants with Pdiscovery<2e-07 in the African- (N=27,494) and South Asian-ancestry (N=29,591) meta-analyses. No variants met array-wide significance in Hispanics or East Asian samples. For the functional annotation, we provide the most severe consequence based on the ENSEMBL's Variant Effect Predictor (VEP) tool. The direction of the effect (Beta) and effect allele frequency (EAF) is given for the

Ancestry	Chr	Pos (hg19)	rsID	Gene	VEP annotation	Ref	Alt	N	EAF	Beta	SE	P-value
African	2	56096892	rs3791679	*EFEMP1*	intron_variant	A	G	27494	0.0684	-0.104	0.017	1.86E-09
African	2	56111309	rs3791675	*EFEMP1*	intron_variant	C	T	27494	0.0712	-0.105	0.017	7.86E-10
African	2	72361960	rs2241057	*CYP26B1*	missense_variant	A	G	27494	0.2906	0.050	0.009	1.13E-07
African	5	33951116	rs35397	*SLC45A2*	intron_variant	G	T	23089	0.2084	0.065	0.012	1.55E-07
African	6	34199092	rs2780226	-	regulatory_region_variant	C	T	27494	0.5803	-0.050	0.009	1.33E-08
African	6	35289024	rs9296146	*DEF6*	missense_variant	G	A	23995	0.0973	-0.099	0.016	3.82E-10
African	12	56704347	rs144428833	*CNPY2*	missense_variant	C	T	27494	0.0036	-0.370	0.071	1.87E-07
African	14	74990746	rs862034	*LTBP2*	intron_variant	A	G	27494	0.6719	0.050	0.009	5.02E-08
African	15	84573041	rs7183263	*ADAMTSL3*	intron_variant	T	G	27494	0.7849	0.058	0.011	6.94E-08
African	15	84582124	rs4842838	*ADAMTSL3*	missense_variant	G	T	27494	0.7847	0.057	0.011	9.04E-08
African	15	89392786	rs34616796	*ACAN*	missense_variant	G	A	23796	0.0957	-0.097	0.016	1.41E-09
African	15	89401362	rs34124958	*ACAN*	missense_variant	G	T	23995	0.0951	-0.098	0.016	9.03E-10
African	15	89401814	rs34546634	*ACAN*	missense_variant	G	A	27494	0.0942	-0.094	0.015	3.38E-10
African	15	89401989	rs35061438	*ACAN*	missense_variant	C	T	23796	0.0952	-0.097	0.016	1.84E-09
African	15	99194896	rs2871865	*IGF1R*	intron_variant	C	G	27494	0.4326	-0.055	0.009	2.67E-10
African	17	61712964	rs7209435	*MAP3K3*	intron_variant	T	C	17226	0.7091	0.074	0.012	1.67E-09
African	17	61908556	rs13030	*SMARCD2*	synonymous_variant	C	T	27494	0.2075	-0.063	0.011	3.51E-09
African	17	62016704	rs2727278	*SCN4A*	3_prime_UTR_variant	A	G	23288	0.5728	0.055	0.010	1.78E-08
African	17	62020348	rs2058194	*SCN4A*	missense_variant	T	C	27494	0.7300	0.056	0.010	7.86E-09
South Asian	8	57078933	rs35883156	*PLAG1*	missense_variant	G	T	29591	0.1478	-0.067	0.012	7.84E-09
South Asian	8	57100149	rs7833986	*PLAG1*	intron_variant	G	A	29591	0.1485	-0.065	0.012	2.40E-08
South Asian	8	57100791	rs13273123	*PLAG1*	intron_variant	A	G	29591	0.1481	-0.067	0.012	1.07E-08
South Asian	8	57155598	rs9650315	-	intergenic_variant	G	T	29591	0.1459	-0.064	0.012	4.23E-08
South Asian	14	21969161	rs145593657	*TOX4*	missense_variant	A	G	29591	0.0096	0.251	0.043	3.44E-09

Supplementary Table 8. Inflation factors (λ_{GC}) for height single-variant analyses based on the different categories of variants present on the ExomeChip. GWAS sentinel SNPs include markers reported in the NHGRI GWAS catalog (for all phenotypes). Ancestry informative markers show strong differentiation between African- and European-ancestry samples. Grid SNPs were selected to provide a scaffold across the genome for identity-by-descent analyses.

	Europe-ancestry		African-ancestry		All	
	Number of variants	**λ_{GC}**	**Number of variants**	**λ_{GC}**	**Number of variants**	**λ_{GC}**
All variants	241419	1.225	208257	1.052	246328	1.235
Minor allele frequency ≥5%	27519	2.746	32073	1.254	28241	2.598
Minor allele frequency <5%	213900	1.125	176184	1.018	218087	1.141
GWAS sentinel SNPs	4827	3.436	4814	1.446	4832	3.366
Ancestry informative markers	3936	1.862	3923	1.542	3937	1.94
Grid SNPs	4890	2.205	4871	1.337	4893	2.347
Synonymous SNPs	4061	1.196	3635	1.136	4137	1.208

Supplementary Table 9. Discovery, validation, and combined results for the height ExomeChip analysis of variants with 2e-7<Pdiscovery≤2e-6. Some of these variants were prioritized because their Pdiscovery <2e-6 in the All-ancestries meta-analysis. The validation studies include 59,804 European-ancestry individuals genotyped on the ExomeChip, 72,613 individuals from deCODE, and 120,084 participants from the UK Biobank. For the functional annotation, we provide the most severe consequence based on the ENSEMBL's Variant Effect Predictor (VEP) tool. The direction of the effect (Beta) and effect allele frequency (EAF) is given for the alternate (Alt) allele.

							GIANT European-ancestry discovery (N=381,625)					Validation studies (N=252,491)					Combined discovery+validation (N=634,116)					
Chr	Pos	rsID	Gene	VEP annotation	Ref	Alt	N	MAF	EAF	Beta	SE	P-value	N	MAF	EAF	Beta	SE	P-value	Het12	N	MAF	EAF	Beta	SE	P-value	Het12
1	6614535	rs4908923	*TAS1R1*	missense_variant	G	A	358569	0.1265	0.8735	0.0188	0.0037	4.99E-07	233787	0.1258	0.8742	0.0084	0.0046	0.069	0	592356	0.1262	0.8738	0.0146	0.0029	4.50E-07	38.7
1	6649228	rs2229330	*KLHL21*	missense_variant	T	G	359848	0.0673	0.0673	-0.0234	0.0049	1.60E-06	233520	0.0689	0.0689	-0.0137	0.0060	0.023	0	593368	0.068	0.068	-0.0195	0.0038	2.45E-07	0
1	25044111	rs4601530	-	intergenic_variant	C	T	380346	0.2598	0.2598	-0.0138	0.0027	3.68E-07	233727	0.2478	0.2478	-0.0105	0.0035	0.003	75.6	614073	0.2552	0.2552	-0.0125	0.0021	4.56E-09	65.8
1	25674785	rs3091242	*TMEM50A*	intron_variant	C	T	353706	0.4563	0.5437	0.0130	0.0026	5.65E-07	199447	0.4604	0.5396	0.0137	0.0034	4.83E-05	0	553153	0.4578	0.5422	0.0132	0.0021	1.17E-10	0
1	46493460	rs1707336	*MAST2*	missense_variant	T	G	381625	0.4369	0.4369	-0.0121	0.0025	2.01E-06	233564	0.4451	0.4451	-0.0136	0.0031	1.13E-05	0	615189	0.4402	0.4402	-0.0127	0.0020	1.06E-10	0
1	47952663	rs517384	*RP4-666022.3*	upstream_gene_variant	T	G	375581	0.1035	0.8965	-0.0179	0.0039	4.84E-06	205168	0.1092	0.8908	-0.0248	0.0051	1.38E-06	65.5	580749	0.1056	0.8944	-0.0205	0.0031	5.28E-11	56.7
1	180886140	rs79485039	*KIAA1614*	missense_variant	C	T	373551	0.0263	0.0263	0.0344	0.0071	1.41E-06	233880	0.0310	0.0310	0.0303	0.0086	4.51E-04	0	607431	0.0282	0.0282	0.0327	0.0055	2.63E-09	0
1	210577884	rs2294851	*HHAT*	missense_variant	G	A	381625	0.1429	0.1429	0.0167	0.0034	1.01E-06	233716	0.1557	0.1557	0.0121	0.0042	0.004	0	615341	0.148	0.148	0.0149	0.0027	1.93E-08	0
1	212237798	rs10863936	*DTL*	intron_variant	G	A	319354	0.4766	0.5234	-0.0118	0.0026	6.89E-06	194327	0.4642	0.5358	-0.0201	0.0033	1.69E-09	0	513681	0.4718	0.5282	-0.0149	0.0021	3.91E-13	40.2
2	224919	rs2290911	*SH3YL1*	splice_region_variant	A	G	381625	0.3505	0.3505	0.0121	0.0026	2.96E-06	233740	0.3531	0.3531	0.0209	0.0032	1.13E-10	0	615365	0.3515	0.3515	0.0156	0.0020	1.60E-14	42.4
2	54120025	rs805408	*PSME4*	missense_variant	A	T	374724	0.3019	0.3019	-0.0139	0.0027	2.01E-07	204071	0.2887	0.2887	-0.0135	0.0036	1.40E-04	0	578795	0.2972	0.2972	-0.0138	0.0021	1.16E-10	0
2	65777628	rs68348245	*AC074391.1*	intron_variant	C	T	372028	0.4707	0.5293	-0.0118	0.0024	9.10E-07	205168	0.4657	0.5343	-0.0164	0.0033	4.65E-07	31.5	577196	0.4689	0.5311	-0.0134	0.0019	3.83E-12	29
2	111949327	rs6738028	*MIR4435-1HG*	upstream_gene_variant	G	C	373405	0.4016	0.5984	0.0094	0.0024	1.30E-04	188882	0.3874	0.6126	0.0076	0.0034	0.029	64.2	562287	0.3969	0.6031	0.0088	0.0020	1.15E-05	48
2	128944424	rs744265	*UGGT1*	intron_variant	T	C	381625	0.3997	0.6003	0.0119	0.0024	8.86E-07	233762	0.4015	0.5985	0.0087	0.0031	0.005	0	615387	0.4003	0.5997	0.0107	0.0019	1.95E-08	0
2	169707428	rs540652	*NOSTRIN*	missense_variant	C	T	160436	0.4658	0.4658	0.0186	0.0036	3.02E-07	211883	0.4559	0.4559	0.0226	0.0032	9.21E-13	0	372319	0.4601	0.4601	0.0209	0.0024	2.11E-18	0
2	171822466	rs4668356	*GORASP2*	synonymous_variant	C	T	377104	0.0687	0.9313	0.0209	0.0048	1.16E-05	230729	0.0751	0.9249	0.0176	0.0065	0.007	0	607833	0.071	0.929	0.0197	0.0038	2.83E-07	0
2	177042633	rs2072590	*HOXD-AS1*	non_coding_transcript_exon_variant	A	C	378383	0.3177	0.6823	-0.0108	0.0026	3.14E-05	233821	0.3250	0.6750	-0.0063	0.0033	0.056	0	612204	0.3205	0.6795	-0.0090	0.0020	8.51E-06	0
2	216577567	rs13022398	*AC012668.2*	intron_variant	C	A	376860	0.3063	0.6937	0.0133	0.0026	2.75E-07	205168	0.3076	0.6924	0.0113	0.0035	0.001	12	582028	0.3067	0.6933	0.0126	0.0021	1.27E-09	0
2	224069989	rs4234047	-	regulatory_region_variant	C	T	380102	0.4320	0.4320	-0.0107	0.0024	8.22E-06	205168	0.4297	0.4297	-0.0078	0.0032	0.015	55.8	585270	0.4312	0.4312	-0.0096	0.0019	5.01E-07	40.6
3	33194990	rs6810039	*SUSD5*	missense_variant	C	A	379977	0.3982	0.3982	-0.0127	0.0025	2.33E-07	233743	0.3988	0.3988	-0.0184	0.0031	2.37E-09	0	613720	0.3984	0.3984	-0.0149	0.0019	8.24E-15	0
3	117574822	rs6438424	*LSAMP*	intron_variant	A	C	381625	0.4876	0.5124	0.0106	0.0024	7.56E-06	203334	0.4927	0.4927	0.0166	0.0032	1.54E-07	0	584959	0.4947	0.5053	0.0128	0.0019	1.71E-11	13.8
3	145790803	rs1449444	*PLOD2*	intron_variant	G	T	346363	0.4558	0.4558	0.0084	0.0025	6.65E-04	205168	0.4505	0.4505	0.0128	0.0033	1.05E-04	12.8	551531	0.4539	0.4539	0.0100	0.0020	4.42E-07	12.4
3	169300219	rs1344555	*MECOM*	intron_variant	C	T	377104	0.1944	0.1944	-0.0143	0.0030	1.98E-06	233035	0.1988	0.1988	-0.0130	0.0038	6.24E-04	0	610139	0.1961	0.1961	-0.0138	0.0024	4.88E-09	0
3	187446211	rs2229362	*BCL6*	missense_variant	C	T	139102	0.1404	0.1404	0.0183	0.0036	4.69E-07	233841	0.1645	0.1645	0.0088	0.0040	0.030	0	572943	0.1512	0.1512	0.0140	0.0027	2.03E-07	20.9
4	140115744	rs11941589	-	intergenic_variant	G	A	380102	0.4382	0.5618	-0.0113	0.0024	2.14E-06	205168	0.4450	0.5550	-0.0164	0.0032	3.71E-07	0	585270	0.4406	0.5594	-0.0131	0.0019	8.19E-12	0
4	152355268	rs2709828	*FAM160A1*	intron_variant	C	T	358569	0.4521	0.5479	-0.0113	0.0025	5.82E-06	233726	0.4384	0.5616	-0.0105	0.0030	5.76E-04	0	592295	0.4466	0.5534	-0.0109	0.0019	1.28E-08	0
5	39397132	rs11959928	*DAB2*	intron_variant	T	A	356735	0.4327	0.4327	0.0125	0.0025	6.64E-07	201559	0.4181	0.4181	0.0103	0.0033	0.002	85.5	558294	0.4273	0.4273	0.0117	0.0020	4.67E-09	78.7
5	57147676	rs1816392	-	intergenic_variant	G	A	375581	0.0503	0.0503	-0.0252	0.0053	2.27E-06	205168	0.0507	0.0507	-0.0113	0.0073	0.120	0	580749	0.0504	0.0504	-0.0204	0.0043	2.24E-06	16.4
5	98228403	rs61759467	*CHD1*	missense_variant	T	A	371611	0.0129	0.0129	-0.0462	0.0102	6.55E-06	204468	0.0147	0.0147	-0.0218	0.0132	0.098	38.4	576079	0.0136	0.0136	-0.0370	0.0081	4.79E-06	44.2
5	102338811	rs35658696	*PAM*	missense_variant	A	G	381625	0.0484	0.0484	-0.0253	0.0055	3.76E-06	233656	0.0530	0.0530	-0.0305	0.0068	8.47E-06	0	615281	0.05	0.05	-0.0273	0.0043	1.63E-10	0
5	140562739	rs61743469	*PCDHB16*	missense_variant	G	A	381625	0.0594	0.0594	0.0250	0.0052	1.58E-06	179812	0.0655	0.0655	0.0247	0.0070	4.33E-04	10.2	561437	0.0615	0.0615	0.0248	0.0042	2.63E-09	0
6	43273604	rs2242416	*CRIP3*	intron_variant	A	G	379977	0.3996	0.6004	0.0127	0.0025	4.34E-07	233722	0.3887	0.6113	0.0160	0.0031	2.22E-07	25.5	613699	0.3953	0.6047	0.0140	0.0019	6.55E-13	11.2
6	56919443	rs61740375	*KIAA1586*	missense_variant	A	G	368149	0.0863	0.0863	0.0217	0.0044	8.52E-07	233756	0.0839	0.0839	0.0129	0.0055	0.020	35.7	601905	0.0853	0.0853	0.0183	0.0034	1.15E-07	35.6
6	134013272	rs9493698	*TARID*	intron_variant	A	G	375774	0.2467	0.2467	0.0135	0.0028	1.02E-06	233676	0.2389	0.2389	0.0036	0.0035	0.308	0	609450	0.2437	0.2437	0.0097	0.0022	7.77E-06	52
6	136227558	rs7752169	*PDE7B*	intron_variant	T	C	380102	0.4598	0.5402	0.0120	0.0024	4.31E-07	205168	0.4699	0.5301	0.0114	0.0032	3.71E-04	0	585270	0.4634	0.5366	0.0118	0.0019	6.40E-10	0
6	146125793	rs3811102	*RP11-545I5.3*	missense_variant	A	T	375498	0.4218	0.4218	-0.0128	0.0025	3.71E-07	232672	0.4204	0.4204	-0.0137	0.0031	1.28E-05	0	608170	0.4212	0.4212	-0.0132	0.0020	2.15E-11	0
7	41470093	rs1079866	-	intergenic_variant	C	G	366654	0.1407	0.1407	0.0164	0.0035	2.29E-06	233700	0.1358	0.1358	0.0112	0.0044	0.011	41.8	600354	0.1388	0.1388	0.0144	0.0027	1.24E-07	30.4
7	44578500	rs35803101	*NPC1L1*	missense_variant	G	A	351760	0.0037	0.0037	0.0857	0.0196	1.21E-05	228105	0.0041	0.0041	0.0230	0.0254	0.365	42.4	579865	0.0038	0.0038	0.0623	0.0155	5.91E-05	58.9
7	72904810	rs17145713	*BAZ1B*	intron_variant	C	T	381625	0.1859	0.1859	0.0166	0.0033	3.68E-07	233772	0.1944	0.1944	0.0155	0.0040	9.45E-05	0	615397	0.1893	0.1893	0.0162	0.0025	1.48E-10	0
7	73482987	rs41511151	*ELN*	missense_variant	G	A	343448	0.0042	0.0042	-0.0861	0.0183	2.63E-06	218793	0.0070	0.0070	-0.0606	0.0191	0.002	13.4	562241	0.0055	0.0055	-0.0739	0.0132	2.31E-08	7.2
7	115327840	rs1026713	-	intergenic_variant	T	C	367081	0.1023	0.1023	0.0155	0.0039	8.24E-05	205168	0.0996	0.0996	0.0100	0.0053	0.058	0	572249	0.1013	0.1013	0.0135	0.0032	1.78E-05	0
8	42226805	rs3136797	*POLB*	missense_variant	C	G	332909	0.0178	0.0178	0.0437	0.0092	1.95E-06	233757	0.0210	0.0210	0.0259	0.0104	0.013	0	566666	0.0192	0.0192	0.0359	0.0069	1.88E-07	0
8	76147954	rs16939046	*CASC9*	intron_variant	T	C	325884	0.0916	0.0916	-0.0206	0.0044	3.74E-06	178301	0.0899	0.0899	-0.0078	0.0060	0.190	0	504185	0.091	0.091	-0.0160	0.0036	7.01E-06	11.9
8	124460546	rs13265801	*WDYHV1*	intron_variant	A	G	381625	0.3433	0.3433	-0.0132	0.0027	1.12E-06	233735	0.3378	0.3378	-0.0052	0.0032	0.102	11.1	615360	0.341	0.341	-0.0098	0.0021	1.86E-06	49.2
8	129192271	rs2019960	-	intergenic_variant	T	C	379252	0.2086	0.2086	-0.0134	0.0029	4.36E-06	233747	0.2208	0.2208	-0.0204	0.0035	8.03E-09	86.7	612999	0.2135	0.2135	-0.0163	0.0023	5.45E-13	82.7
9	74039166	rs1935338	*TRPM3*	intron_variant	T	C	368786	0.2444	0.7556	0.0132	0.0028	2.36E-06	205168	0.2433	0.7567	0.0069	0.0037	0.064	0	573954	0.244	0.756	0.0109	0.0022	1.04E-06	11.1
9	76184436	rs157117	*RP11-128I7.1*	upstream_gene_variant	A	G	371178	0.3424	0.3424	0.0112	0.0025	1.07E-05	233509	0.3416	0.3416	0.0085	0.0031	0.007	0	604687	0.342	0.342	0.0101	0.0020	3.05E-07	0
9	136996067	rs28473627	*WDR5*	upstream_gene_variant	A	G	372028	0.3955	0.6045	-0.0126	0.0025	3.27E-07	205168	0.3744	0.6256	-0.0111	0.0033	9.19E-04	0	577196	0.3881	0.6119	-0.0120	0.0020	1.22E-09	0
10	89336834	rs7914810	-	intergenic_variant	A	G	380102	0.4774	0.5226	-0.0123	0.0024	2.32E-07	205168	0.4631	0.5369	-0.0061	0.0033	0.060	0	585270	0.4724	0.5276	-0.0102	0.0019	1.25E-07	0
11	9537904	rs10743108	*ZNF143*	missense_variant	G	C	241639	0.0375	0.9625	0.0345	0.0088	9.56E-05	201755	0.0259	0.9741	0.0417	0.0103	5.25E-05	48.3	443394	0.0326	0.9674	0.0375	0.0067	2.21E-08	27.7
11	30394734	rs2183848	*RP4-710M3.1*	downstream_gene_variant	G	A	380102	0.2831	0.2831	-0.0130	0.0026	7.47E-07	205168	0.2788	0.2788	-0.0178	0.0036	6.09E-07	47.7	585270	0.2816	0.2816	-0.0147	0.0021	3.84E-12	39.9
11	70007354	rs201870990	*ANO1*	missense_variant	G	A	381625	0.0072	0.0072	0.0691	0.0133	2.16E-07	233872	0.0065	0.0065	0.0483	0.0185	0.009	0	615497	0.007	0.007	0.0620	0.0108	9.94E-09	0
11	85436352	rs641393	*SYTL2*	missense_variant	G	A	381625	0.3581	0.6419	0.0125	0.0026	1.23E-06	233289	0.3625	0.6375	0.0177	0.0032	4.03E-08	2.5	614914	0.3598	0.6402	0.0145	0.0020	5.42E-13	18.3
11	101919831	rs10895241	*C11orf70*	intron_variant	G	A	364256	0.3815	0.3815	-0.0111	0.0025	9.94E-06	205168	0.3923	0.3923	-0.0085	0.0033	0.010	46.1	569424	0.3855	0.3855	-0.0101	0.0020	3.84E-07	27
12	53731891	rs10876432	*SP7*	intron_variant	G	A	381625	0.2881	0.7119	-0.0133	0.0028	1.41E-06	233783	0.3206	0.6794	-0.0030	0.0032	0.354	0	615408	0.302	0.698	-0.0089	0.0021	2.08E-05	58.9
13	41109429	rs2755237	*AL133318.1*	downstream_gene_variant	A	C	369748	0.1497	0.1497	-0.0161	0.0034	2.76E-06	233775	0.1450	0.1450	-0.0180	0.0043	2.73E-05	63.4	603523	0.1479	0.1479	-0.0169	0.0027	3.35E-10	46.3
13	101708310	rs2044137	*NALCN*	intron_variant	G	A	377104	0.2306	0.2306	-0.0142	0.0028	5.06E-07	233743	0.2339	0.2339	-0.0105	0.0037	0.004	0	610847	0.2319	0.2319	-0.0128	0.0022	1.05E-08	0
14	45403699	rs117295933	*KLHL28*	missense_variant	C	A	348676	0.0161	0.0161	-0.0451	0.0094	1.55E-06	233879	0.0246	0.0246	-0.0363	0.0103	4.13E-04	0	582555	0.02	0.02	-0.0411	0.0069	3.05E-09	0
14	50901768	rs17780143	*MAP4K5*	missense_variant	G	A	381625	0.0532	0.0532	0.0267	0.0053	4.44E-07	233816	0.0600	0.0600	0.0076	0.0063	0.224	0	615441	0.056	0.056	0.0187	0.0040	3.43E-06	56.7
14	63855760	rs6573513	*PPP2R5E*	intron_variant	C	T	376860	0.0881	0.0881	-0.0185	0.0042	1.09E-05	205168	0.0850	0.0850	-0.0198	0.0060	9.77E-04	60.1	582028	0.0871	0.0871	-0.0190	0.0034	3.92E-08	40.6
14	68785077	rs8017304	*RADS1B*	intron_variant	G	A	380102	0.3710	0.6290	0.0125	0.0025	7.01E-07	205168	0.3572	0.6428	0.0078	0.0034	0.022	0.3	585270	0.3661	0.6339	0.0108	0.0020	8.89E-08	8.1
15	34520687	rs116858574	*SLC12A6*	missense_variant	T	C	381625	0.0138	0.0138	0.0470	0.0097	1.16E-06	229869	0.0144	0.0144	0.0283	0.0124	0.022	80	611494	0.014	0.014	0.0399	0.0076	1.60E-07	73.8
15	44153571	rs150494621	*Y_RNA*	missense_variant	C	T	381625	0.0075	0.0075	0.0630	0.0131	1.56E-06	227404	0.0143	0.0143	0.0538	0.0150	3.42E-04	5.8	609029	0.0105	0.0105	0.0590	0.0099	2.32E-09	0
16	73793552	rs2063506	-	intergenic_variant	A	G	380893	0.4549	0.5451	-0.0105	0.0024	9.27E-06	232437	0.4765	0.5235	-0.0117	0.0030	8.66E-05	0	613330	0.4633	0.5367	-0.0110	0.0019	3.34E-09	0
16	87350773	rs3748393	*C16orf95*	missense_variant	C	A	381625	0.3476	0.3476	-0.0109	0.0025	1.00E-05	233295	0.3261	0.3261	-0.0067	0.0033	0.041	32.2	614920	0.3398	0.3398	-0.0094	0.0020	1.96E-06	25.2
17	49446154	rs6504712	-	intergenic_variant	A	G	376860	0.2225	0.2225	0.0146	0.0029	4.62E-07	205168	0.2332	0.2332	0.0056	0.0038	0.133	0	582028	0.2265	0.2265	0.0112	0.0023	9.03E-07	40.1
17	67081278	rs77542162	*ABCA6*	missense_variant	A	G	280300	0.0169	0.0169	0.0493	0.0104	2.17E-06	226061	0.0229	0.0229	0.0509	0.0102	5.58E-07	85.7	506361	0.02	0.02	0.0501	0.0073	5.57E-12	78.6
18	13069782	rs6505780	*CEP192*	missense_variant	C	T	381625	0.3861	0.6139	-0.0127	0.0027	1.92E-06	233650	0.3961	0.6039	-0.0151	0.0032	2.58E-06	5.4	615275	0.3901	0.6099	-0.0136	0.0020	2.63E-11	0
19	1124835	rs740495	*SBNO2*	intron_variant	A	G	372908	0.2772	0.2772	0.0133	0.0027	5.63E-07	179697	0.2580	0.2580	0.0038	0.0039	0.325	0	552605	0.2711	0.2711	0.0103	0.0022	2.80E-06	60
19	13001547	rs11085824	*GCDH*	upstream_gene_variant	A	G	373551	0.3635	0.3635	0.011	0.003	1.50E-05	233699	0.3813	0.3813	0.012	0.003	1.32E-04	0	607250	0.3705	0.3705	0.011	0.002	7.96E-09	0
19	18123738	rs7259041	*ARRDC2*	missense_variant	T	C	381625	0.2327	0.2327	-0.013	0.003	1.60E-06	233205	0.2188	0.2188	-0.017	0.004	5.34E-06	15.3	614830	0.2275	0.2275	-0.015	0.002	4.75E-11	0
19	37441365	rs547483	*ZNF568*	missense_variant	T	C	381625	0.3589	0.3589	-0.012	0.003	6.72E-06	233676	0.3752	0.3752	-0.011	0.003	3.90E-04	45.3	615301	0.3658	0.3658	-0.012	0.002	1.03E-08	19.3
20	39832628	rs17265513	*ZHX3*	missense_variant	T	C	369748	0.2048	0.2048	0.014	0.003	1.10E-05	233804	0.2012	0.2012	0.012	0.004	0.003	0	603552	0.2034	0.2034	0.013	0.002	1.10E-07	0
20	54824557	rs61735259	*MC3R*	missense_variant	C	A	369748	0.0013	0.0013	-0.134	0.032	2.95E-05	179794	0.0021	0.0021	-0.092	0.036	0.012	71.1	549542	0.0016	0.0016	-0.115	0.024	1.56E-06	52.6
21	28305212	rs2830585	*ADAMTS5*	missense_variant	C	T	381625	0.1551	0.1551	-0.017	0.003	2.31E-07	233624	0.1503	0.1503	-0.012	0.004	0.002	29.6	615249	0.1532	0.1532	-0.015	0.003	3.27E-09	19.7
22	24255296	rs4822455	-	intergenic_variant	C	T	381625	0.4092	0.5908	0.012	0.002	1.43E-06	233390	0.4247	0.5753	0.011	0.003	2.73E-04	0	615015	0.4151	0.5849	0.012	0.002	1.55E-09	0
22	33048216	rs5754188	*SYN3*	intron_variant	T	G	374251	0.2019	0.2019	-0.012	0.003	9.20E-05	205168	0.2228	0.2228	-0.009	0.004	0.015	48.1	579419	0.2098	0.2098	-0.011	0.002	4.60E-06	26.7
22	50278568	rs910799	*ZBED4*	missense_variant	A	G	373982	0.1929	0.8071	-0.011	0.003	2.48E-04	233810	0.1951	0.8049	-0.011	0.004	0.007	0	607792	0.1938	0.8062	-0.011	0.002	5.13E-06	0
23	73641569	rs6647476	*SLC16A2*	missense_variant	T	C	218919	0.4121	0.4121	0.015	0.003	8.31E-07	203690	0.4100	0.4100	0.010	0.003	0.004	0	422609	0.4112	0.4112	0.012	0.002	2.46E-08	0
23	105152282	rs209373	*NRK*	missense_variant	G	A	259423	0.2184	0.2184	-0.011	0.003	2.79E-04	205718	0.2260	0.2260	-0.020	0.004	2.03E-07	68.4	465141	0.2213	0.2213	-0.014	0.002	1.27E-09	69
23	118587003	rs3810755	*SLC25A43*	missense_variant	C	T	240566	0.4195	0.5805	0.013	0.003	1.01E-06	205692	0.4377	0.5623	0.020	0.003	1.10E-09	8.4	446258	0.4265	0.5735	0.016	0.002	2.52E-14	41.9

Supplementary Table 10. 11 variants are more strongly associated with height under a recessive rather than additive genetic model. We provide results for the discovery sample (GIANT ALL- or European-ancestry Recessive and Additive models), the validation set, and the combined analysis (discovery+validation). For the functional annotation, we provide the most severe consequence based on the ENSEMBL's Variant Effect Predictor (VEP) tool. The direction of the effect (Beta) is given for the Alt-Alt genotype (recessive model) or the Alt allele (additive model). The effect allele frequency (EAF) is given for the alternate (Alt) allele.

							GIANT All- or European-ancestry discovery (Recessive model)						GIANT All- or European-ancestry discovery (Additive model)						Validation studies (N=252,491) (Recessive model)							Combined discovery+validation (Recessive model)						
Meta-analysis	Chr	Pos (hg19)	rsID	Gene	VEP annotation	Ref	Alt	N	MAF	EAF	Beta	SE	P-value	N	MAF	EAF	Beta	SE	P-value	N	MAF	EAF	Beta	SE	P-value	HetI2	N	MAF	EAF	Beta	SE	P-value	HetI2
ALL-ANCESTRY	5	112176756	rs459552	*APC*	missense_variant	T	A	449259	0.2200	0.7800	-0.020	0.003	4.29E-10	449259	0.2200	0.7800	-0.014	0.003	2.34E-07	237460	0.2283	0.7717	-0.013	0.005	0.008	0	686719	0.2225	0.7775	0.018	0.003	2.28E-11	0
ALL-ANCESTRY	5	135288632	rs62623707	*LECT2*	missense_variant	A	G	458253	0.0366	0.0366	-0.227	0.035	1.26E-10	458253	0.0382	0.0382	-0.028	0.005	3.07E-07	252431	0.0505	0.0505	-0.246	0.039	#######	57.1	710684	0.0429	0.0429	-0.236	0.026	1.72E-19	36.2
ALL-ANCESTRY	6	80196848	rs1875845	*LCA5*	missense_variant	C	T	445497	0.3225	0.3225	0.028	0.005	1.35E-08	445497	0.3225	0.3225	0.011	0.002	8.83E-06	223714	0.3148	0.3148	0.025	0.007	#######	0	669211	0.3200	0.3200	-0.027	0.004	2.54E-11	0
ALL-ANCESTRY	10	63723577	rs10821936	*ARID5B*	intron_variant	C	T	457648	0.3291	0.6709	-0.017	0.003	2.65E-08	457648	0.3291	0.6709	-0.012	0.002	1.39E-07	252274	0.3340	0.6660	-0.017	0.005	#######	0	709922	0.3306	0.6694	0.017	0.003	3.31E-11	0
ALL-ANCESTRY	10	79616605	rs1248696	*DLG5*	missense_variant	T	C	457279	0.0881	0.9119	-0.021	0.004	2.59E-07	457279	0.0881	0.9119	-0.018	0.004	1.81E-06	252310	0.1085	0.8915	-0.016	0.006	0.006	0	709589	0.0948	0.9052	-0.020	0.003	6.51E-09	0
ALL-ANCESTRY	11	11986061	rs3206824	*DKK3*	missense_variant	T	C	411207	0.2552	0.7448	0.020	0.003	3.35E-10	411207	0.2552	0.7448	0.016	0.003	1.46E-09	252417	0.2568	0.7432	0.016	0.005	#######	0	663624	0.2557	0.7443	0.019	0.003	5.47E-13	0
ALL-ANCESTRY	16	78343690	rs9927661	*WWOX*	intron_variant	G	A	443983	0.3537	0.3537	-0.023	0.005	3.01E-07	443983	0.3537	0.3537	-0.011	0.002	6.65E-07	217993	0.3423	0.3423	-0.017	0.007	0.013	0	661976	0.3501	0.3501	0.021	0.004	1.37E-08	0
ALL-ANCESTRY	23	66941751	rs137852591	*AR*	missense_variant	C	G	280075	0.0021	0.0021	-0.304	0.061	7.05E-07	280075	0.0022	0.0022	-0.110	0.024	4.13E-06	110065	0.0080	0.0080	-0.333	0.058	#######	41.5	390140	0.0052	0.0052	-0.319	0.042	2.67E-14	0
ALL-ANCESTRY	23	110494841	rs12013711	*CAPN6*	missense_variant	C	G	281372	0.0770	0.0770	-0.061	0.011	1.91E-08	281372	0.0770	0.0770	-0.029	0.005	6.20E-08	104344	0.0243	0.0243	0.001	0.031	0.971	63	385716	0.0713	0.0713	-0.054	0.010	1.31E-07	57.8
EUROPEAN	7	128573967	rs4728142	*IRF5*	upstream_gene_variant	G	A	380346	0.4390	0.4390	-0.022	0.004	2.06E-07	380346	0.4390	0.4390	-0.013	0.002	2.39E-07	252281	0.4556	0.4556	-0.010	0.005	0.039	0	632627	0.4459	0.4459	-0.017	0.003	1.30E-07	32.6
EUROPEAN	17	17409560	rs7946	*PEMT*	missense_variant	C	T	369280	0.2692	0.7308	0.019	0.003	2.77E-08	369280	0.2692	0.7308	0.013	0.003	1.14E-06	221787	0.2491	0.7509	0.012	0.005	0.013	39	591067	0.2627	0.7373	0.017	0.003	1.67E-09	35.3

Supplementary Table 11. 606 ExomeChip variants associated with adult height variation. These variants remained significant after conditional analyses and GCTA "joint" modelling. LocusID match the locus numbers assigned in the Wood et al., Nature Genetics, 2014 article. We report 120 new height loci. We provide the most severe consequence based on the ENSEMBL's Variant Effect Predictor (VEP) tool. The direction of the effect (Beta) and effect allele frequency (EAF) is given for the alternate (Alt) allele. All results are for the additive model.

Chr	Pos (hg19)	rsID	LocusID	Novel	Source	Gene	VEP annotation	Ref	Alt	GIANT Discovery (unconditional results) N	MAF	EAF	Beta	SE	P-value	P-value, after conditioning with RAREMETAL (if applicable, only discovery studies)	P-value (discovery studies - GCTA joint)	Validation studies (unconditional results) N	MAF	EAF	Beta	SE	P-value	Combined (discovery+validation, unconditional results) N	MAF	EAF	Beta	SE	P-value	P-value (Combined Analysis - GCTA joint)
1	2069172	rs425277	1		unconditional	PRKCZ	intron_variant	C	T	381625	0.2820	0.2820	0.019	0.003	1.40E-13	NA	2.02E-13	252376	0.2671	0.2671	0.021	0.003	5.35E-10	634001	0.2755	0.2755	0.020	0.002	8.29E-19	6.01E-24
1	7913029	rs34305100	427	yes	unconditional	UTS2	missense_variant	A	G	381625	0.1910	0.1910	0.021	0.003	1.04E-11	NA	2.66E-12	251150	0.1958	0.1958	0.023	0.004	2.59E-09	632775	0.1928	0.1928	0.022	0.002	4.32E-20	6.38E-29
1	9304731	rs2239560	2		unconditional	H6PD	intron_variant	G	A	375581	0.1550	0.1550	0.023	0.003	2.67E-12	NA	7.57E-12	223714	0.1484	0.1484	0.028	0.005	4.73E-10	599295	0.153	0.1530	0.025	0.003	8.11E-23	3.36E-16
1	10285709	rs6541085	428		unconditional	MIR1273D	intron_variant	A	G	372028	0.4770	0.4770	0.013	0.002	1.10E-07	NA	9.07E-08	223714	0.4796	0.4796	0.023	0.003	1.70E-12	595742	0.4777	0.4777	0.016	0.002	2.15E-20	1.43E-15
1	17306675	rs2284746	4		unconditional	MFAP2	intron_variant	C	G	375498	0.4860	0.5140	0.041	0.002	1.48E-61	NA	5.19E-62	237449	0.4761	0.5239	0.038	0.003	6.89E-33	612947	0.4832	0.5168	0.040	0.002	2.85E-124	5.02E-88
1	19765518	rs12045440	5		unconditional	CAPZB	intron_variant	T	G	381625	0.3400	0.3400	-0.017	0.002	3.27E-11	NA	9.03E-12	252018	0.3510	0.3510	-0.013	0.003	3.56E-05	633643	0.3431	0.3431	-0.016	0.002	5.58E-21	5.54E-16
1	21629447	rs213060	6		unconditional	RP5-1071N3.1	intron_variant	A	C	372028	0.4250	0.4250	0.013	0.002	1.78E-07	NA	2.71E-08	223714	0.4397	0.4397	0.013	0.003	1.10E-04	595742	0.429	0.4290	0.013	0.002	3.93E-14	1.25E-11
1	22368342	rs2501279	6		unconditional	-	regulatory_region_variant	C	T	370395	0.4070	0.5930	-0.015	0.002	5.61E-10	NA	2.55E-09	223714	0.4056	0.5944	-0.019	0.003	5.69E-09	594109	0.4066	0.5934	-0.016	0.002	3.83E-21	1.19E-15
1	23536891	rs1738475	7		unconditional	-	regulatory_region_variant	C	G	374724	0.4060	0.4060	-0.017	0.003	4.56E-12	NA	1.76E-12	252289	0.4068	0.4068	-0.016	0.003	4.04E-07	627013	0.4064	0.4064	-0.016	0.002	3.09E-14	1.69E-15
1	25674785	rs3091242	539		validation	TMEM50A	intron_variant	C	T	353706	0.4563	0.5437	0.0130	0.0026	5.65E-07	NA	NA	199447	0.4604	0.5396	0.0137	0.0034	4.83E-05	553153	0.4578	0.5422	0.0132	0.0021	1.17E-10	2.61E-12
1	26450009	rs17163588	8		1st conditional round	PDIK1L	3_prime_UTR_variant	C	T	380346	0.1740	0.1740	0.028	0.003	1.28E-16	5.10E-11	1.28E-14	252176	0.1700	0.1700	0.026	0.004	4.86E-10	632522	0.1726	0.1726	0.027	0.002	3.71E-29	2.86E-36
1	26741544	rs7532866	8		unconditional	LIN28A	intron_variant	A	G	380346	0.3400	0.3400	-0.023	0.003	1.71E-19	NA	2.97E-15	252319	0.3458	0.3458	-0.022	0.003	7.97E-12	632665	0.3427	0.3427	-0.022	0.002	9.60E-25	1.66E-16
1	27138393	rs12748152	8		2nd conditional rounc	RN7SL165P	upstream_gene_variant	C	T	381625	0.0810	0.0810	0.023	0.005	4.73E-07	1.43E-07	6.80E-09	252365	0.0926	0.0926	0.016	0.005	0.002	633990	0.0864	0.0864	0.020	0.004	4.73E-08	2.49E-07
1	32092525	rs2271933	9		unconditional	PEF1	missense_variant	A	G	381625	0.3850	0.6150	0.014	0.002	3.88E-08	NA	4.11E-09	252332	0.3842	0.6158	0.013	0.003	3.12E-05	633957	0.3848	0.6152	0.014	0.002	3.97E-16	6.35E-12
1	32672908	rs3903683	9		unconditional	RP4-622L5.7	missense_variant	T	G	351178	0.0650	0.0650	0.032	0.005	3.06E-10	NA	4.10E-10	199413	0.0641	0.0641	0.034	0.007	6.04E-07	550591	0.0647	0.0647	0.033	0.004	5.00E-16	4.12E-14
1	32673514	rs150341307	9		1st conditional round	RP4-622L5.7	missense_variant	G	C	333756	0.0020	0.0020	-0.141	0.026	7.92E-08	8.55E-08	1.88E-08	246575	0.0040	0.0040	-0.116	0.025	3.83E-06	580331	0.003	0.0030	-0.128	0.018	1.34E-12	1.18E-12
1	38338795	rs11488569	10		unconditional	INPP5B	missense_variant	A	G	359266	0.2810	0.7190	-0.020	0.003	5.76E-13	NA	1.11E-13	252238	0.2679	0.7321	-0.017	0.003	4.90E-07	611504	0.2753	0.7247	-0.019	0.002	8.16E-17	5.33E-24
1	40773149	rs2228564	11		unconditional	COL9A2	missense_variant	T	C	378144	0.2200	0.2200	-0.022	0.003	1.58E-14	NA	4.69E-13	252061	0.2287	0.2287	-0.019	0.004	1.81E-07	630205	0.2236	0.2236	-0.021	0.002	2.90E-19	2.22E-23
1	41540902	rs143365597	11		1st conditional round	SCMH1	missense_variant	G	A	368141	0.0040	0.0040	0.188	0.018	1.58E-25	2.86E-27	2.67E-27	223714	0.0061	0.0061	0.169	0.024	9.42E-13	591855	0.0047	0.0047	0.181	0.014	1.35E-36	2.03E-39
1	41618297	rs114233776	11		2nd conditional rounc	SCMH1	missense_variant	G	A	359848	0.0060	0.0060	-0.119	0.015	1.92E-15	1.92E-13	1.69E-13	252491	0.0060	0.0060	-0.110	0.019	1.32E-08	612339	0.006	0.0060	-0.116	0.012	1.80E-22	7.88E-20
1	41745770	rs2154319	11		unconditional	RP11-399E6.1	intron_variant	T	C	349913	0.2170	0.2170	0.039	0.003	2.32E-37	NA	5.22E-38	223714	0.2195	0.2195	0.043	0.004	8.60E-28	573627	0.2179	0.2179	0.040	0.002	1.48E-64	1.02E-84
1	46493460	rs1707336	540		validation	MAST2	missense_variant	T	G	381625	0.4369	0.4369	-0.0121	0.0025	2.01E-06	NA	NA	233564	0.4451	0.4451	#####	0.0031	1.13E-05	615189	0.4402	0.4402	-0.013	0.002	1.06E-10	8.52E-12
1	47952663	rs517384	541		validation	RP4-666O22.3	upstream_gene_variant	T	G	375581	0.1035	0.8965	-0.0179	0.0039	4.84E-06	NA	NA	205168	0.1092	0.8908	#####	0.0051	1.38E-06	580749	0.1056	0.8944	-0.021	0.0031	5.28E-11	8.00E-12
1	51873967	rs41292521	14		unconditional	EPS15	missense_variant	G	A	377738	0.0200	0.0200	0.045	0.008	5.07E-08	NA	5.08E-08	252442	0.0228	0.0228	0.065	0.010	7.60E-11	630180	0.0211	0.0211	0.053	0.006	2.56E-17	1.29E-18
1	67390468	rs1886686	16		unconditional	MIER1	missense_variant	C	G	359683	0.2680	0.7320	0.015	0.003	1.66E-07	NA	1.66E-07	229646	0.2676	0.7324	0.014	0.004	8.13E-05	589329	0.2678	0.7322	0.015	0.002	1.97E-10	6.40E-14
1	78623626	rs17391694	17		unconditional	-	regulatory_region_variant	C	T	375104	0.1220	0.1220	0.033	0.004	1.87E-19	NA	1.89E-19	252294	0.1412	0.1412	0.033	0.004	5.25E-14	627398	0.1309	0.1309	0.033	0.003	5.96E-29	3.87E-28
1	89123443	rs6699417	19		unconditional	PKN2-AS1	intron_variant	C	T	381625	0.3960	0.6040	0.022	0.002	8.91E-19	NA	2.05E-18	252313	0.4093	0.5907	0.029	0.003	3.46E-20	633938	0.3999	0.6001	0.024	0.002	5.55E-46	8.18E-34
1	93323971	rs10874746	20		unconditional	FAM69A	intron_variant	T	C	377738	0.3500	0.6500	0.020	0.003	7.13E-15	NA	1.64E-14	252293	0.3434	0.6566	0.019	0.003	8.24E-09	630031	0.347	0.6530	0.019	0.002	1.27E-18	1.60E-21
1	103216881	rs713162	22		1st conditional round	-	intergenic_variant	G	A	380102	0.3790	0.3790	0.017	0.003	2.96E-12	1.03E-07	NA	223714	0.3855	0.3855	0.019	0.003	1.64E-08	603816	0.3819	0.3819	0.018	0.002	1.35E-15	2.02E-10
1	103432657	rs12755987	22		unconditional	COL11A1	intron_variant	A	G	378383	0.2990	0.7010	-0.021	0.003	1.85E-14	NA	1.53E-14	252174	0.3000	0.7000	-0.027	0.003	2.96E-15	630557	0.2995	0.7005	-0.023	0.002	1.07E-25	1.54E-22
1	113190807	rs17030613	23		unconditional	CAPZA1	intron_variant	A	C	381625	0.2170	0.2170	-0.019	0.003	6.20E-11	NA	4.11E-11	252265	0.2020	0.2020	-0.021	0.004	4.53E-08	633890	0.2111	0.2111	-0.020	0.002	6.15E-17	1.14E-22
1	118868405	rs17038182	24		unconditional	-	regulatory_region_variant	G	C	375498	0.2460	0.2460	-0.044	0.003	4.79E-53	NA	6.30E-45	252404	0.2605	0.2605	-0.047	0.004	9.49E-42	627902	0.2522	0.2522	-0.045	0.002	1.58E-88	6.17E-100
1	119427467	rs61730011	24		unconditional	TBX15	missense_variant	A	C	373551	0.0420	0.0420	-0.059	0.006	1.61E-24	NA	3.13E-16	247716	0.0459	0.0459	-0.056	0.007	4.19E-15	621267	0.0436	0.0436	-0.058	0.005	2.79E-36	2.84E-20
1	146568955	rs11239931	25		unconditional	NBPF13P	intron_variant	G	A	366845	0.1960	0.8040	0.018	0.003	1.26E-08	NA	3.96E-08	223714	0.1848	0.8152	0.006	0.004	0.126	590559	0.1921	0.8079	0.014	0.002	8.69E-09	2.46E-11
1	149902342	rs145659444	26		1st conditional round	MTMR11	missense_variant	C	T	350397	0.0070	0.0070	0.067	0.015	4.16E-06	1.00E-08	3.44E-08	252440	0.0064	0.0064	0.083	0.019	7.11E-06	602837	0.0068	0.0068	0.073	0.012	3.03E-10	3.54E-13
1	149906413	rs11205303	26		unconditional	MTMR11	missense_variant	T	C	381625	0.3980	0.3980	0.047	0.002	2.57E-81	NA	9.08E-80	252022	0.4090	0.4090	0.051	0.003	1.34E-60	633647	0.4012	0.4012	0.048	0.002	1.53E-180	3.86E-124
1	150551327	rs11580946	26		unconditional	MCL1	missense_variant	G	A	359848	0.0140	0.0140	0.061	0.010	2.16E-09	NA	NA	252268	0.0152	0.0152	0.085	0.012	7.86E-12	612116	0.0145	0.0145	0.070	0.008	1.55E-19	3.14E-12
1	150658971	rs11204697	26		1st conditional round	GOLPH3L	intron_variant	C	T	380346	0.4020	0.4020	0.007	0.003	0.00587	8.55E-08	NA	252339	0.4030	0.4030	0.010	0.003	0.002	632685	0.4025	0.4025	0.008	0.002	1.38E-04	4.27E-09
1	151259543	rs3748545	27		unconditional	PI4KB	missense_variant	G	A	381625	0.1150	0.1150	-0.027	0.004	4.20E-13	NA	5.65E-10	252418	0.1072	0.1072	-0.018	0.005	7.34E-04	634043	0.1121	0.1121	-0.024	0.003	1.24E-13	2.35E-11
1	154987704	rs141845046	430	yes	unconditional	ZBTB7B	missense_variant	C	T	381625	0.0280	0.0280	0.058	0.007	7.30E-17	NA	5.08E-17	252394	0.0246	0.0246	0.061	0.010	4.46E-10	634019	0.0268	0.0268	0.059	0.006	3.46E-25	1.92E-22
1	172053287	rs17346452	30		1st conditional round	DNM3	intron_variant	T	C	354447	0.2770	0.2770	0.035	0.003	1.17E-36	3.82E-18	5.57E-15	244685	0.2799	0.2799	0.032	0.003	9.43E-21	599132	0.2783	0.2783	0.034	0.002	2.06E-50	3.80E-35
1	172189889	rs678962	30		unconditional	DNM3	intron_variant	T	G	380346	0.2150	0.2150	0.048	0.003	3.34E-61	NA	4.10E-42	251880	0.2162	0.2162	0.048	0.004	5.79E-39	632226	0.2155	0.2155	0.048	0.002	9.45E-95	7.09E-96
1	172206026	rs4916245	30		3rd conditional round	DNM3	intron_variant	G	A	365616	0.4780	0.4780	-0.009	0.002	0.000305	7.49E-08	NA	223714	0.4924	0.4924	-0.013	0.003	9.03E-05	589330	0.4819	0.4819	-0.010	0.002	4.03E-09	6.17E-09
1	172437592	rs1129942	30		2nd conditional rounc	C1orf105	missense_variant	G	A	342493	0.2190	0.7810	-0.027	0.003	9.35E-19	2.13E-17	4.58E-17	252196	0.2328	0.7672	-0.028	0.004	6.31E-15	594689	0.2247	0.7753	-0.027	0.002	1.10E-32	6.42E-33
1	176219438	rs1553770	31		unconditional	-	intergenic_variant	C	T	372028	0.4680	0.5320	-0.015	0.002	1.61E-10	NA	2.53E-12	223714	0.4830	0.5170	-0.013	0.003	2.60E-05	595742	0.4723	0.5277	-0.015	0.002	8.99E-18	2.04E-14
1	176521349	rs11583447	31		1st conditional round	PAPPA2	intron_variant	T	G	315802	0.4300	0.4300	0.013	0.003	8.36E-07	7.55E-12	NA	223714	0.4142	0.4142	0.012	0.003	2.43E-04	539516	0.423	0.4230	0.013	0.002	1.38E-08	3.92E-19
1	176792249	rs1325598	31		unconditional	PAPPA2	intron_variant	A	G	377104	0.4370	0.5630	0.029	0.002	5.98E-34	NA	1.67E-35	251835	0.4451	0.5549	0.028	0.003	8.77E-21	628939	0.4395	0.5605	0.029	0.002	1.07E-66	3.35E-57
1	180886140	rs79485039	537	yes	validation	KIAA1614	missense_variant	C	T	373551	0.0263	0.0263	0.0344	0.0071	1.41E-06	NA	NA	233880	0.0310	0.0310	0.0303	0.0086	4.51E-04	607431	0.0282	0.0282	0.0327	0.0055	2.63E-09	1.65E-08
1	183094547	rs20558	32		unconditional	LAMC1	missense_variant	T	C	381625	0.4430	0.5570	-0.019	0.003	4.34E-14	NA	1.83E-16	252333	0.4405	0.5595	-0.014	0.003	6.92E-06	633958	0.4418	0.5582	-0.017	0.002	1.58E-14	1.19E-19
1	183495812	rs144712473	32		1st conditional round	SMG7	missense_variant	A	G	381625	0.0060	0.0060	-0.094	0.014	4.97E-11	6.04E-12	2.76E-12	248709	0.0078	0.0078	-0.067	0.017	8.94E-05	630334	0.0067	0.0067	-0.083	0.011	1.61E-14	1.59E-17
1	184020945	rs2274432	32		unconditional	TSEN15	missense_variant	G	A	367751	0.3500	0.3500	0.041	0.003	6.55E-57	NA	3.43E-58	244000	0.3529	0.3529	0.047	0.003	2.12E-47	611751	0.3513	0.3513	0.044	0.002	1.11E-87	4.00E-108
1	210577884	rs2294851	538	yes	validation	HHAT	missense_variant	G	A	381625	0.1429	0.1429	0.0167	0.0034	1.01E-06	NA	NA	233716	0.1557	0.1557	0.0121	0.0042	0.004	615341	0.148	0.1480	0.0149	0.0027	1.93E-08	1.24E-07
1	219009835	rs2647116	36		unconditional	-	intergenic_variant	G	A	376860	0.3670	0.3670	-0.022	0.003	7.41E-18	NA	6.09E-16	223714	0.3622	0.3622	-0.019	0.003	2.27E-08	600574	0.3649	0.3649	-0.021	0.002	3.83E-20	3.23E-22
1	219743719	rs11118346	36		unconditional	-	intergenic_variant	C	T	380346	0.4670	0.4670	-0.016	0.002	1.44E-10	NA	2.17E-09	252295	0.4464	0.4464	-0.017	0.003	5.33E-08	632641	0.4608	0.4608	-0.016	0.002	3.92E-22	5.04E-13
1	223178026	rs144673025	432	yes	unconditional	DISP1	missense_variant	T	C	381625	0.0080	0.0080	-0.078	0.013	1.11E-09	NA	6.29E-10	252399	0.0072	0.0072	-0.086	0.018	1.22E-06	634024	0.0077	0.0077	-0.081	0.011	1.27E-14	5.16E-14
1	227935444	rs2236359	39		unconditional	SNAP47	missense_variant	A	G	375771	0.4100	0.4100	-0.017	0.002	2.17E-12	NA	7.74E-13	252267	0.4208	0.4208	-0.020	0.003	3.80E-11	628038	0.4132	0.4132	-0.018	0.002	7.02E-27	1.43E-19
2	224919	rs2290911	567	yes	validation	SH3YL1	splice_region_variant	A	G	381625	0.3505	0.3505	0.0121	0.0026	2.96E-06	NA	NA	233740	0.3531	0.3531	0.0209	0.0032	1.13E-10	615365	0.3515	0.3515	0.0156	0.002	1.60E-14	7.11E-15
2	1756908	rs6726313	41		unconditional	-	intergenic_variant	C	T	367832	0.3080	0.3080	0.015	0.003	7.95E-09	NA	5.86E-09	223714	0.3054	0.3054	0.012	0.004	8.78E-04	591546	0.3069	0.3069	0.014	0.002	2.50E-09	3.86E-13
2	9662210	rs10495563	433		unconditional	ADAM17	3_prime_UTR_variant	G	A	380346	0.3370	0.6630	0.022	0.003	2.19E-18	NA	3.70E-18	252377	0.3268	0.6732	0.014	0.003	1.06E-05	632723	0.3323	0.6677	0.018	0.002	5.90E-17	4.94E-20
2	11323276	rs978906	434		unconditional	PQLC3	3_prime_UTR_variant	T	C	377973	0.4800	0.4800	-0.018	0.002	1.43E-12	NA	9.30E-13	252230	0.4997	0.5003	-0.015	0.003	1.85E-06	630203	0.4861	0.4861	-0.017	0.002	3.68E-24	2.27E-18
2	20205541	rs52826764	44		unconditional	MATN3	missense_variant	C	T	381625	0.0260	0.0260	-0.071	0.007	2.67E-23	NA	6.41E-20	231140	0.0282	0.0282	-0.084	0.010	6.60E-19	612765	0.0268	0.0268	-0.076	0.006	3.74E-41	1.40E-34
2	24247514	rs7561273	45		unconditional	MFSD2B	intron_variant	A	G	380346	0.4630	0.5370	0.026	0.002	1.16E-26	NA	9.88E-21	252015	0.4619	0.5381	0.025	0.003	1.49E-16	632361	0.4627	0.5373	0.026	0.002	1.65E-53	2.40E-31
2	25187599	rs4665736	45		1st conditional round	AC013267.1	intron_variant	C	T	376458	0.4670	0.5330	0.033	0.003	5.34E-39	1.03E-09	1.11E-11	252013	0.4816	0.5184	0.030	0.003	4.06E-22	628471	0.4741	0.5259	0.032	0.002	1.85E-48	3.76E-14
2	25482883	rs7594432	45		unconditional	DNMT3A	intron_variant	T	C	372028	0.4340	0.4340	0.038	0.002	5.79E-55	NA	6.87E-31	223714	0.4311	0.4311	0.040	0.003	1.99E-34	595742	0.4332	0.4332	0.038	0.002	4.81E-113	1.71E-40
2	27730940	rs1260326	46		unconditional	GCKR	missense_variant	T	C	381625	0.3950	0.6050	0.017	0.003	8.37E-11	NA	3.25E-11	252041	0.3831	0.6169	0.021	0.003	1.02E-10	633666	0.3895	0.6105	0.019	0.002	1.22E-17	8.40E-22
2	33361425	rs6714546	47		unconditional	LTBP1	intron_variant	A	G	372272	0.2810	0.7190	0.032	0.003	2.50E-32	NA	1.29E-30	250490	0.2860	0.7140	0.035	0.003	9.47E-26	622762	0.2832	0.7168	0.033	0.002	1.66E-50	1.06E-60
2	33405151	rs6751657	47		1st conditional round	LTBP1	intron_variant	T	C	378823	0.4720	0.5280	0.026	0.002	2.28E-28	9.67E-27	1.10E-24	223714	0.4744	0.5256	0.022	0.003	4.65E-12	602537	0.4727	0.5273	0.025	0.002	7.45E-49	1.13E-32
2	36782886	rs848642	48		unconditional	FEZ2	missense_variant	G	A	381625	0.3160	0.3160	-0.020	0.003	1.35E-15	NA	2.56E-15	252372	0.3103	0.3103	-0.029	0.003	7.79E-19	633997	0.3134	0.3134	-0.024	0.002	1.05E-27	3.74E-34
2	37995727	rs12615742	48		unconditional	-	regulatory_region_variant	C	T	376353	0.4770	0.4770	0.026	0.002	7.95E-28	NA	2.00E-27	223714	0.4952	0.4952	0.026	0.003	3.41E-15	600067	0.482	0.4820	0.026	0.002	3.60E-52	4.50E-36
2	38298139	rs1800440	48		1st conditional round	RMDN2	missense_variant	T	C	381625	0.1810	0.1810	-0.016	0.003	2.13E-07	1.00E-07	6.14E-08	252300	0.1911	0.1911	-0.014	0.004	3.72E-04	633925	0.1848	0.1848	-0.015	0.002	1.60E-10	7.86E-15
2	43732823	rs7578597	50		unconditional	THADA	missense_variant	T	C	340409	0.0990	0.0990	0.028	0.004	8.81E-11	NA	2.66E-10	252277	0.1049	0.1049	0.011	0.005	0.032	592686	0.1013	0.1013	0.021	0.003	9.40E-12	3.61E-11
2	44768202	rs2341459	51		unconditional	CAMKMT	intron_variant	T	C	380346	0.2670	0.7330	-0.019	0.003	2.39E-12	NA	1.64E-12	252398	0.2612	0.7388	-0.027	0.004	7.40E-15	632744	0.2645	0.7355	-0.022	0.002	4.98E-23	2.72E-28
2	45640374	rs3755073	435		unconditional	SRBD1	missense_variant	C	A	373551	0.0890	0.0890	-0.023	0.004	6.66E-08	NA	NA	252151	0.0790	0.0790	-0.023	0.006	4.35E-05	625702	0.0856	0.0856	-0.023	0.003	1.72E-12	1.48E-13
2	46921285	rs12474201	52		unconditional	SOCS5	upstream_gene_variant	G	A	363055	0.3530	0.3530	0.028	0.003	6.57E-28	NA	1.54E-26	229730	0.3645	0.3645	0.027	0.003	1.15E-16	592785	0.3582	0.3582	0.028	0.002	9.53E-36	1.37E-41
2	56096892	rs3791679	54		unconditional	EFEMP1	intron_variant	A	G	377104	0.2400	0.2400	-0.066	0.003	3.07E-117	NA	5.96E-117	251899	0.2196	0.2196	-0.077	0.004	6.91E-96	629003	0.232	0.2320	-0.070	0.002	5.78E-200	5.02E-264
2	65777628	rs68148245	570	yes	validation	AC074391.1	intron_variant	C	T	372028	0.4707	0.5293	-0.0118	0.0024	9.10E-07	NA	NA	205168	0.4657	0.5343	#####	0.0033	4.65E-07	577196	0.4689	0.5311	-0.013	0.0019	3.83E-12	2.86E-14
2	71633389	rs6714975	56		unconditional	ZNF638	synonymous_variant	C	T	381625	0.4310	0.5690	-0.027	0.002	3.76E-27	NA	2.88E-27	252171	0.4315	0.5685	-0.031	0.003	4.87E-24	633796	0.4312	0.5688	-0.028	0.002	1.57E-63	4.08E-45
2	88895123	rs13045	57		unconditional	EIF2AK3	missense_variant	C	T	374086	0.3430	0.6570	-0.027	0.003	2.75E-24	NA	2.79E-24	252199	0.3345	0.6655	-0.030	0.003	2.89E-20	626285	0.3391	0.6609	-0.029	0.002	6.98E-38	1.26E-47
2	121612659	rs2166898	60		unconditional	GLI2	intron_variant	G	A	380346	0.1610	0.1610	-0.031	0.003	7.26E-22	NA	7.35E-22	252070	0.1695	0.1695	-0.035	0.004	7.77E-18	632416	0.164	0.1640	-0.032	0.002	4.21E-41	5.29E-58
2	128944424	rs744265	565	yes	validation	UGGT1	intron_variant	T	C	381625	0.3997	0.6003	0.0119	0.0024	8.86E-07	NA	NA	233762	0.4015	0.5985	0.0087	0.0031	0.005	615387	0.4003	0.5997	0.0107	0.0019	1.95E-08	1.20E-08
2	134434824	rs7567288	61		unconditional	-	regulatory_region_variant	T	C	358569	0.1970	0.1970	0.017	0.003	2.24E-08	NA	6.46E-08	252282	0.1939	0.1939	0.020	0.004	7.94E-08	610851	0.1958	0.1958	0.018	0.002	7.50E-15	1.10E-18
2	135988127	rs59900519	62		unconditional	ZRANB3	missense_variant	T	A	351014	0.0910	0.0910	-0.026	0.005	1.02E-08	NA	2.93E-08	252398	0.0682	0.0682	-0.032	0.007	9.16E-07	603412	0.0825	0.0825	-0.028	0.004	1.11E-12	7.81E-12
2	178684720	rs7567851	67		unconditional	PDE11A	intron_variant	G	C	341110	0.0800	0.0800	0.039	0.005	1.06E-16	NA	1.48E-17	246470	0.0740	0.0740	0.028	0.006	3.14E-06	587580	0.0775	0.0775	0.034	0.004	3.16E-19	6.75E-18
2	179474668	rs16866412	436		unconditional	TTN	missense_variant	G	A	381625	0.0130	0.0130	-0.053	0.010	1.35E-07	NA	6.98E-09	252397	0.0101	0.0101	-0.019	0.015	0.215	634022	0.0121	0.0121	-0.042	0.008	3.44E-07	5.42E-08
2	183703336	rs288326	68		unconditional	FRZB	missense_variant	G	A	377738	0.1170	0.1170	0.024	0.004	1.50E-10	NA	1.24E-10	252229	0.1134	0.1134	0.025	0.005	1.55E-07	629967	0.1155	0.1155	0.024	0.003	1.61E-15	2.30E-15
2	200142847	rs1813849	437	yes	unconditional	SATB2	intron_variant	T	C	374251	0.1090	0.8910	0.025	0.004	2.34E-10	NA	2.34E-10	223714	0.1079	0.8921	0.014	0.005	0.009	597965	0.1086	0.8914	0.021	0.003	4.84E-11	2.56E-12
2	216577567	rs13022398	566		validation	AC012668.2	intron_variant	C	A	376860	0.3063	0.6937	0.0133	0.0026	2.75E-07	NA	NA	205168	0.3076	0.6924	0.0113	0.0035	0.001	582028	0.3067	0.6933	0.0126	0.0021	1.27E-09	9.69E-10
2	217878209	rs6435957	72		1st conditional round	-	intergenic_variant	T	C	380346	0.3140	0.3140	0.018	0.003	8.26E-12	5.65E-12	NA	252110	0.3272	0.3272	0.019	0.003	3.16E-09	632456	0.3202	0.3202	0.019	0.002	3.52E-17	2.82E-23
2	218271898	rs1351164	72		unconditional	DIRC3	intron_variant	T	C	381625	0.2000	0.2000	-0.026	0.003	3.23E-18	NA	1.52E-17	252300	0.2003	0.2003	-0.023	0.004	1.50E-09	633925	0.2001	0.2001	-0.025	0.002	5.25E-26	1.09E-35
2	219195799	rs10932775	72		unconditional	CATIP-AS2	intron_variant	G	A	380102	0.4970	0.5030	0.017	0.002	3.05E-13	NA	6.69E-10	223714	0.4870	0.4870	0.017	0.003	8.97E-08	603816	0.4986	0.4986	0.017	0.002	1.00E-23	8.23E-12
2	219555262	rs1344642	72		3rd conditional round	STK36	missense_variant	G	A	381625	0.4400	0.4400	-0.022	0.003	7.67E-18	1.53E-10	2.26E-10	252130	0.4447	0.4447	-0.026	0.003	3.22E-16	633755	0.4422	0.4422	-0.024	0.002	7.31E-28	6.68E-16
2	219924961	rs142036701	72		1st conditional round	IHH	missense_variant	T	C	373989	0.0010	0.0010	-0.320	0.040	1.09E-15	1.36E-15	4.19E-16	244985	0.0031	0.0031	-0.263	0.043	1.48E-09	618974	0.002	0.0020	-0.294	0.029	1.85E-23	1.36E-23
2	219943846	rs6724465	72		2nd conditional rounc	NHEJ1	intron_variant	G	A	381625	0.0940	0.0940	-0.041	0.004	1.39E-20	3.61E-15	6.36E-17	252277	0.0962	0.0962	-0.048	0.005	4.71E-19	633902	0.0948	0.0948	-0.043	0.003	8.05E-42	1.25E-37
2	219949184	rs16859517	72		unconditional	NHEJ1	intron_variant	C	T	381625	0.0360	0.0360	0.059	0.006	5.96E-21	NA	7.07E-15	252355	0.0358	0.0358	0.064	0.008	1.12E-15	633980	0.0359	0.0359	0.061	0.005	8.20E-37	1.35E-24
2	220078652	rs147445258	72		3rd conditional round	ABCB6	missense_variant	C	T	373551	0.0095	0.0095	-0.086	0.012	3.43E-13	1.77E-13	3.27E-12	198495	0.0090	0.0090	-0.064	0.018	4.40E-04	572046	0.0097	0.0097	-0.079	0.010	2.47E-15	5.14E-15
2	225047744	rs2629046	74		unconditional	-	regulatory_region_variant	T	C	380346	0.4510	0.4510	-0.021	0.002	1.08E-18	NA	3.14E-19	252278	0.4650	0.4650	-0.024	0.003	2.40E-15	632624	0.4553	0.4553	-0.022	0.002	2.27E-39	7.65E-29
2	232263127	rs2290130	75		unconditional	AC017104.6	missense_variant	G	A	374981	0.2520	0.2520	-0.016	0.003	2.28E-09	NA	NA	252216	0.2333	0.2333	-0.017	0.004	9.54E-07	627197	0.2442	0.2442	-0.017	0.002	4.60E-13	2.95E-15
2	232349636	rs4973417	75		1st conditional round	NCL	upstream_gene_variant	G	T	350251	0.4440	0.5560	-0.020	0.002	3.90E-16	7.36E-12	1.16E-17	223714	0.4612	0.5388	-0.019	0.003	1.86E-09	573965	0.4488	0.5512	-0.020	0.002	1.91E-31	5.72E-25
2	232796610	rs749052	75		2nd conditional rounc	-	intergenic_variant	T	C	363269	0.0600	0.0600	-0.058	0.005	2.97E-29	7.86E-12	4.64E-28	246757	0.0608	0.0608	-0.068	0.006	1.75E-26	610026	0.0603	0.0603	-0.062	0.004	1.58E-55	2.55E-23
2	232797966	rs2580816	75		unconditional	-	intergenic_variant	C	T	380346	0.1930	0.1930	-0.036	0.003	1.49E-32	NA	NA	252302	0.1935	0.1935	-0.041	0.004	2.96E-26	632648	0.1932	0.1932	-0.038	0.002	1.72E-57	3.19E-20
2	232982257	rs11677466	75		1st conditional round	DIS3L2	intron_variant	A	T	367424	0.0880	0.0880	0.051	0.004	1.87E-32	1.10E-22	3.90E-26	248496	0.0927	0.0927	0.047	0.005	2.26E-19	615920	0.0897	0.0897	0.050	0.003	7.84E-55	6.68E-45
2	233077064	rs7571816	75		3rd conditional round	DIS3L2	intron_variant	A	G	379016	0.0250	0.0250	-0.060	0.007	2.35E-16	6.22E-11	6.27E-14	252435	0.0230	0.0230	-0.079	0.010	2.58E-15	631451	0.0243	0.0243	-0.066	0.006	6.46E-31	1.98E-13
2	233633460	rs1801251	75		unconditional	KCNJ13	missense_variant	G	A	381625	0.3350	0.3350	-0.018	0.003	4.94E-13	NA	7.81E-13	252292	0.3642	0.3642	-0.026	0.003	3.84E-16	633917	0.3489	0.3489	-0.022	0.002	2.16E-23	4.93E-25
2	238336802	rs6719451	438	yes	unconditional	AC112721.2	upstream_gene_variant	T	C	371878	0.1090	0.1090	-0.021	0.004	3.68E-08	NA	7.77E-08	223714	0.1057	0.1057	-0.015	0.005	0.004	595592	0.1078	0.1078	-0.019	0.003	3.61E-09	8.68E-11
2	242493511	rs4675801	76		unconditional	BOK-AS1	intron_variant	C	T	380102	0.4590	0.4590	-0.019	0.002	4.82E-15	NA	7.47E-16	223714	0.4667	0.4667	-0.024	0.003	8.54E-14	603816	0.4611	0.4611	-0.020	0.002	3.27E-33	3.18E-23
3	11641535	rs6772112	78		unconditional	VGLL4	intron_variant	C	T	332053	0.0560	0.9440	0.033	0.006	2.91E-09	NA	4.48E-09	217993	0.0578	0.9422	0.026	0.007	1.78E-04	550046	0.0568	0.9432	0.030	0.005	3.75E-11	2.93E-09
3	14214524	rs2229089	78		unconditional	XPC	missense_variant	G	A	380721	0.0310	0.0310	-0.038	0.007	1.22E-08	NA	1.88E-08	252238	0.0345	0.0345	-0.020	0.008	0.017	632959	0.0325	0.0325	-0.030	0.005	1.29E-08	2.93E-09
3	33194990	rs6810039	579	yes	validation	SUSD5	missense_variant	C	A	379977	0.3982	0.3982	-0.0127	0.0025	2.33E-07	NA	NA	233743	0.3988	0.3988	#####	0.0031	2.37E-09	613720	0.3984	0.3984	-0.015	0.0019	8.24E-15	7.48E-15
3	38047954	rs9816693	79		unconditional	PLCD1	intron_variant	G	C	375498	0.1720	0.1720	0.022	0.003	6.08E-12	NA	1.09E-11	251989	0.1762	0.1762	0.026	0.004	1.02E-10	627487	0.1735	0.1735	0.023	0.002	1.88E-22	3.34E-32
3	41123735	rs10490823	80		unconditional	-	intergenic_variant	C	T	378383	0.4530	0.5470	0.016	0.002	2.38E-10	NA	1.73E-10	252258	0.4460	0.5540	0.013	0.003	4.22E-05	630641	0.4509	0.5491	0.015	0.002	3.95E-19	2.81E-16
3	43097765	rs3732858	439	yes	unconditional	FAM198A	missense_variant	G	A	380893	0.1750	0.1750	-0.020	0.003	2.24E-10	NA	4.70E-10	252356	0.1676	0.1676	-0.020	0.004	1.07E-06	633249	0.1724	0.1724	-0.020	0.002	1.45E-16	2.89E-23
3	46939587	rs121434601	440	yes	unconditional	PTH1R	missense_variant	C	T	373551	0.0030	0.0030	0.154	0.023	1.30E-11	NA	2.30E-14	248519	0.0025	0.0025	0.192	0.031	5.48E-10	622070	0.0028	0.0028	0.168	0.019	1.14E-19	1.21E-21
3	47162886	rs76208147	440	yes	1st conditional round	SETD2	missense_variant	C	T	375129	0.0190	0.0190	0.048	0.009	2.24E-08	2.68E-08	2.72E-08	248666	0.0161	0.0161	0.062	0.012	2.22E-07	623795	0.0179	0.0179	0.053	0.007	1.65E-13	2.01E-14
3	49162284	rs34759087	442	yes	unconditional	LAMB2	missense_variant	C	T	377738	0.1260	0.1260	0.028	0.004	5.48E-14	NA	1.71E-15	252326	0.1134	0.1134	0.025	0.005	4.58E-07	630064	0.1209	0.1209	0.027	0.003	7.35E-18	8.91E-25
3	49162583	rs35713889	442		1st conditional round	LAMB2	missense_variant	C	T	355961	0.0390	0.0390	0.043	0.006	3.28E-12	2.55E-13	NA	252327	0.0450	0.0450	0.060	0.007	1.33E-16	608288	0.0414	0.0414	0.050	0.005	3.49E-27	9.38E-12
3	51071713	rs13088462	81		unconditional	DOCK3	intron_variant	T	C	338671	0.0540	0.0540	0.057	0.006	4.52E-24	NA	6.61E-23	223328	0.0505	0.0505	0.056	0.007	2.07E-14	561999	0.0526	0.0526	0.057	0.005	3.34E-34	1.38E-19
3	52551010	rs79979130	82		unconditional	STAB1	synonymous_variant	C	T	366295	0.0860	0.0860	0.026	0.004	7.69E-09	NA	NA	217530	0.0833	0.0833	0.035	0.006	5.40E-09	583825	0.0851	0.0851	0.029	0.003	5.13E-18	2.70E-14
3	53118739	rs2336725	82		unconditional	RP11-894J14.5	intron_variant	C	T	381625	0.4350	0.5650	-0.031	0.002	1.04E-36	NA	1.78E-37	252289	0.4375	0.5625	-0.030	0.003	7.11E-22	633914	0.4358	0.5642	-0.031	0.002	2.78E-74	4.54E-41
3	55474073	rs1392224	83		unconditional	-	intergenic_variant	A	G	380102	0.4890	0.4890	0.014	0.002	6.64E-09	NA	1.21E-09	223714	0.4997	0.4997	0.015	0.003	1.51E-06	603816	0.492	0.4920	0.014	0.002	2.16E-17	4.19E-15
3	56628031	rs7637449	84		unconditional	CCDC66	missense_variant	G	A	381625	0.4620	0.5380	0.025	0.003	1.06E-22	NA	8.65E-24	252277	0.4719	0.5281	0.024	0.003	2.45E-14	633902	0.4668	0.5332	0.024	0.002	1.47E-29	7.76E-32
3	57528503	rs9311651	84		unconditional	DNAH12	missense_variant	A	G	378383	0.1590	0.1590	0.018	0.003	1.04E-07	NA	NA	251732	0.1674	0.1674	0.012	0.004	0.007	630115	0.1618	0.1618	0.016	0.002	1.01E-10	3.10E-17
3	67416322	rs17806888	87		unconditional	SUCLG2	intron_variant	T	C	381625	0.1140	0.1140	-0.028	0.004	3.71E-13	NA	3.34E-13	252269	0.1128	0.1128	-0.025	0.005	1.51E-07	633894	0.1135	0.1135	-0.027	0.003	2.32E-18	4.14E-19
3	72437413	rs9863706	89		unconditional	RYBP	intron_variant	C	T	381625	0.2160	0.2160	-0.035	0.003	7.54E-34	NA	6.99E-34	252383	0.2199	0.2199	-0.034	0.004	1.30E-20	634008	0.2176	0.2176	-0.035	0.002	2.35E-50	4.54E-68
3	98600385	rs9838238	90		unconditional	DCBLD2	missense_variant	T	C	381625	0.0470	0.0470	0.029	0.005	1.23E-07	NA	1.23E-07	251940	0.0507	0.0507	0.027	0.007	5.62E-05	633565	0.0483	0.0483	0.028	0.004	1.68E-12	2.56E-12
3	114511356	rs12490319	92		unconditional	ZBTB20	intron_variant	T	C	374251	0.1610	0.8390	-0.025	0.003	6.47E-15	NA	6.50E-15	223714	0.1537	0.8463	-0.018	0.005	6.51E-05	597965	0.1587	0.8413	-0.023	0.003	6.08E-20	1.51E-14
3	117574822	rs6438424	577	yes	validation	LSAMP	intron_variant	A	C	381625	0.4876	0.5124	0.0106	0.0024	7.56E-06	NA	NA	203334	0.4927	0.4927	0.0166	0.0032	1.54E-07	584959	0.4947	0.5053	0.0128	0.0019	1.71E-11	1.38E-11
3	129050756	rs6439167	93		unconditional	RP13-685P2.8	upstream_gene_variant	T	C	381625	0.2130	0.7870	0.037	0.003	6.73E-38	NA	7.18E-40	252375	0.2233	0.7767	0.037	0.004	2.26E-24	634000	0.2172	0.7828	0.037	0.002	1.35E-57	1.55E-78
3	134233092	rs10935120	94		unconditional	CEP63	intron_variant	A	G	380346	0.3210	0.6790	0.023	0.003	5.53E-20	NA	1.33E-21	252327	0.3189	0.6811	0.020	0.003	2.82E-10	632673	0.32	0.6800	0.022	0.002	3.71E-23	9.44E-27
3	135974216	rs9844666	95		unconditional	PCCB	5_prime_UTR_variant	G	A	381625	0.2420	0.2420	-0.032	0.003	3.91E-29	NA	3.67E-31	252348	0.2499	0.2499	-0.027	0.004	1.01E-14	633973	0.2453	0.2453	-0.030	0.002	1.97E-39	1.20E-50
3	141105570	rs724016	96		unconditional	ZBTB38	5_prime_UTR_variant	A	G	371887	0.4410	0.4410	0.075	0.002	4.99E-208	NA	2.56E-215	252081	0.4474	0.4474	0.083	0.003	3.39E-165	623968	0.4429	0.4429	0.078	0.002	1.17e-469	0.00E+00
3	156862145	rs6809394	98		unconditional	CCNL1	downstream_gene_variant	C	T	372028	0.3480	0.3480	-0.016	0.003	2.17E-10	NA	4.26E-10	223714	0.3412	0.3412	-0.018	0.003	7.83E-08	595742	0.345	0.3450	-0.017	0.002	4.14E-14	1.50E-17
3	157992814	rs7643792	98		unconditional	RSRC1	intron_variant	A	G	381625	0.4320	0.4320	0.017	0.002	5.47E-12	NA	1.07E-11	252323	0.4096	0.4096	0.019	0.003	1.56E-09	633948	0.4253	0.4253	0.018	0.002	2.05E-25	1.79E-19
3	169300219	rs1344555	578	yes	validation	MECOM	intron_variant	C	T	377104	0.1944	0.1944	-0.0143	0.0030	1.98E-06	NA	NA	233035	0.1988	0.1988	#####	0.0038	6.24E-04	610139	0.1961	0.1961	-0.014	0.0024	4.88E-09	9.12E-09
3	171969077	rs7652177	99		unconditional	FNDC3B	missense_variant	C	G	361528	0.4920	0.5080	0.042	0.002	9.52E-68	NA	1.20E-63	237130	0.4890	0.5110	0.035	0.003	5.89E-30	598658	0.4911	0.5089	0.040	0.002	2.56E-125	3.28E-82
3	172165727	rs572169	99		1st conditional round	GHSR	synonymous_variant	C	T	378383	0.3130	0.3130	0.028	0.003	4.90E-27	4.59E-22	5.78E-23	252355	0.3177	0.3177	0.035	0.003	7.76E-27	630738	0.3152	0.3152	0.031	0.002	2.19E-45	2.95E-47
3	183976103	rs11546878	443		unconditional	CAMK2N2	missense_variant	C	T	352338	0.1780	0.1780	-0.022	0.003	6.22E-12	NA	3.35E-12	252413	0.1714	0.1714	-0.017	0.004	1.80E-05	604751	0.1756	0.1756	-0.020	0.002	3.09E-17	1.49E-21
3	185529080	rs1470579	101		1st conditional round	IGF2BP2	intron_variant	A	C	380346	0.3140	0.3140	-0.005	0.003	0.099	4.48E-25	6.73E-28	252259	0.3143	0.3143	0.002	0.003	0.572	632605	0.3141	0.3141	-0.002	0.002	3.83E-01	2.84E-43
3	185548683	rs720390	101		unconditional	-	intergenic_variant	G	A	381625	0.3810	0.3810	0.032	0.002	1.20E-37	NA	6.21E-65	252205	0.3730	0.3730	0.036	0.003	5.08E-30	633830	0.3787	0.3787	0.033	0.002	1.35E-85	1.16E-104
3	185629568	rs2002675	101		2nd conditional rounc	-	intergenic_variant	A	G	297062	0.4170	0.4170	0.014	0.003	5.06E-07	2.67E-11	3.56E-11	216265	0.4269	0.4269	0.022	0.003	3.54E-11	513327	0.4215	0.4215	0.018	0.002	2.74E-15	1.17E-29
3	191114266	rs2293377	103		unconditional	CCDC50	3_prime_UTR_variant	T	C	381625	0.3710	0.3710	0.015	0.003	2.34E-09	NA	1.89E-09	251838	0.3641	0.3641	0.012	0.003	1.64E-04	633463	0.3678	0.3678	0.014	0.002	4.70E-10	9.92E-12
4	1701317	rs2247341	104		unconditional	SLBP	synonymous_variant	G	A	366506	0.3460	0.3460	0.027	0.003	1.58E-25	NA	1.21E-24	252240	0.3477	0.3477	0.028	0.003	2.45E-18	618746	0.3468	0.3468	0.027	0.002	4.51E-36	1.41E-42
4	3473139	rs6831256	444	yes	unconditional	DOK7	intron_variant	A	G	376150	0.4200	0.4200	-0.013	0.002	1.54E-07	NA	NA	252194	0.4177	0.4177	-0.014	0.003	7.69E-06	628344	0.4193	0.4193	-0.013	0.002	3.07E-15	6.68E-11
4	5016883	rs11722554	105		unconditional	CYTL1	missense_variant	G	A	381625	0.0400	0.0400	-0.049	0.006	2.01E-17	NA	3.03E-15	230697	0.0344	0.0344	-0.057	0.009	6.68E-11	612322	0.0382	0.0382	-0.052	0.005	1.86E-25	9.45E-25
4	5035587	rs6446315	105		1st conditional round	-	regulatory_region_variant	G	A	378823	0.1710	0.8290	-0.022	0.003	1.81E-12	7.42E-10	6.13E-10	223714	0.1732	0.8268	-0.018	0.004	1.70E-05	602537	0.1717	0.8283	-0.021	0.003	2.43E-17	6.62E-09
4	8503359	rs1949733	106		unconditional	RP11-689P11.2	intron_variant	A	G	377973	0.3010	0.6990	0.017	0.003	1.90E-10	NA	3.39E-11	252216	0.2884	0.7116	0.017	0.003	4.52E-07	630189	0.2954	0.7046	0.017	0.002	3.26E-14	7.38E-18
4	12963574	rs763318	107		unconditional	-	intergenic_variant	G	A	373208	0.4650	0.4650	-0.026	0.002	2.06E-27	NA	3.65E-29	223714	0.4531	0.4531	-0.027	0.003	1.54E-17	596922	0.4617	0.4617	-0.026	0.002	1.81E-54	7.96E-37
4	17972372	rs2320299	108		1st conditional round	LCORL	intron_variant	G	A	381625	0.2700	0.7300	-0.047	0.003	4.15E-68	1.34E-39	9.78E-42	252070	0.2703	0.7297	-0.055	0.003	1.75E-57	633695	0.2701	0.7299	-0.050	0.002	2.44E-110	3.13E-92
4	18033488	rs6449353	108		unconditional	-	intergenic_variant	T	C	381625	0.1520	0.1520	-0.067	0.004	5.42E-78	NA	6.26E-51	252387	0.1476	0.1476	-0.079	0.004	4.21E-71	634012	0.15	0.1500	-0.072	0.003	2.92E-131	6.84E-80
4	25408838	rs34811474	445	yes	unconditional	ANAPC4	missense_variant	G	A	377876	0.2240	0.2240	0.021	0.003	1.60E-13	NA	4.56E-13	252334	0.2327	0.2327	0.016	0.004	6.74E-06	630210	0.2276	0.2276	0.019	0.002	1.50E-16	1.81E-21
4	40121562	rs794001	446	yes	unconditional	N4BP2	missense_variant	G	A	344724	0.2320	0.7680	0.017	0.003	1.15E-08	NA	8.55E-09	221019	0.2409	0.7591	0.020	0.004	9.25E-08	565743	0.2354	0.7646	0.018	0.002	8.64E-15	2.07E-20
4	48498290	rs10031777	110		unconditional	FRYL	downstream_gene_variant	T	C	298554	0.4940	0.4940	0.018	0.003	1.76E-10	NA	NA	223714	0.4957	0.5043	0.020	0.003	1.11E-09	522268	0.4988	0.4988	0.019	0.002	1.30E-17	1.42E-22
4	57823476	rs17081935	112		unconditional	RP11-738E22.3	downstream_gene_variant	C	T	370749	0.1960	0.1960	0.032	0.003	5.05E-26	NA	1.19E-25	223714	0.1882	0.1882	0.035	0.004	5.12E-18	594463	0.1933	0.1933	0.033	0.002	8.00E-43	2.79E-61
4	73179445	rs141374503	113		2nd conditional rounc	ADAMTS3	missense_variant	C	T	381625	0.0030	0.0030	-0.119	0.021	1.82E-08	1.16E-07	1.70E-07	252411	0.0041	0.0041	-0.089	0.023	1.32E-04	634036	0.0035	0.0035	-0.106	0.016	1.30E-11	3.42E-10
4	73414286	rs788908	113		1st conditional round	ADAMTS3	missense_variant	C	T	381625	0.3800	0.6200	-0.011	0.003	1.02E-05	1.32E-09	5.17E-12	252078	0.3862	0.6138	-0.015	0.003	3.11E-06	633703	0.383	0.6170	-0.013	0.002	4.36E-09	9.20E-15
4	73515313	rs7697556	113		unconditional	-	intergenic_variant	T	C	380346	0.4760	0.5240	-0.033	0.002	1.43E-41	NA	9.96E-47	252311	0.4808	0.5192	-0.036	0.003	1.66E-31	632657	0.4774	0.5226	-0.034	0.002	9.83E-91	1.05E-68
4	82149831	rs710841	114		unconditional	-	intergenic_variant	C	T	378383	0.2530	0.2530	0.047	0.003	1.39E-63	NA	1.99E-62	252340	0.2596	0.2596	0.045	0.003	1.02E-38	630723	0.2559	0.2559	0.046	0.002	3.72E-92	6.22E-118
4	87730980	rs61730641	115		unconditional	PTPN13	missense_variant	C	T	377738	0.0150	0.0150	-0.086	0.010	1.94E-19	NA	7.15E-19	252444	0.0161	0.0161	-0.094	0.012	1.38E-15	630182	0.0155	0.0155	-0.089	0.008	9.43E-32	8.67E-30
4	103188709	rs13107325	447	yes	unconditional	SLC39A8	missense_variant	C	T	381625	0.0620	0.0620	-0.034	0.005	1.96E-12	NA	3.92E-13	252349	0.0714	0.0714	-0.034	0.006	5.27E-08	633974	0.0656	0.0656	-0.034	0.004	3.06E-18	2.46E-16
4	106106353	rs10010325	116		unconditional	TET2	intron_variant	C	A	349669	0.4880	0.4880	0.028	0.003	2.22E-28	NA	2.47E-29	223714	0.4897	0.4897	0.030	0.003	1.77E-20	573383	0.4888	0.4888	0.029	0.002	1.68E-39	1.37E-46
4	109408608	rs1562975	117		unconditional	-	intergenic_variant	G	A	377729	0.2980	0.2980	0.027	0.003	7.40E-26	NA	8.57E-27	223714	0.2917	0.2917	0.026	0.004	9.18E-14	601443	0.2953	0.2953	0.027	0.002	1.56E-31	7.26E-41
4	120422407	rs149385790	448	yes	unconditional	PDE5A	missense_variant	T	G	365908	0.0010	0.0010	0.257	0.031	7.50E-17	NA	1.20E-17	223714	0.0053	0.0053	0.190	0.033	1.28E-08	589622	0.003	0.0030	0.226	0.023	2.65E-23	7.03E-23
4	120716967	rs7699214	448	yes	1st conditional round	LINC01365	downstream_gene_variant	A	G	355718	0.4710	0.5290	0.014	0.002	3.20E-08	1.41E-08	1.78E-08	223714	0.4804	0.5196	0.007	0.003	0.022	579432	0.4737	0.5263	0.012	0.002	9.92E-13	7.33E-10
4	122664323	rs28532673	119		unconditional	-	intergenic_variant	G	A	369655	0.4130	0.4130	0.017	0.002	3.12E-12	NA	3.17E-11	223714	0.3900	0.3900	0.015	0.003	3.23E-06	593369	0.4068	0.4068	0.017	0.002	3.62E-22	3.14E-17
4	123838758	rs12648093	120		unconditional	NUDT6	missense_variant	A	G	370309	0.2570	0.7430	-0.017	0.003	4.88E-10	NA	9.95E-10	230538	0.2608	0.7392	-0.018	0.004	3.65E-07	600847	0.2585	0.7415	-0.018	0.002	2.75E-14	1.44E-18
4	135121721	rs116807401	449	yes	unconditional	PABPC4L	missense_variant	T	C	381625	0.0170	0.0170	0.065	0.009	1.39E-13	NA	1.02E-13	252170	0.0161	0.0161	0.045	0.012	1.33E-04	633795	0.0167	0.0167	0.058	0.007	7.54E-16	4.52E-16
4	140115744	rs11941589	581	yes	validation	-	intergenic_variant	G	A	380102	0.4382	0.5618	-0.0113	0.0024	2.14E-06	NA	NA	205168	0.4450	0.5550	#####	0.0032	3.71E-07	585270	0.4406	0.5594	-0.013	0.0019	8.19E-12	1.29E-11
4	144359490	rs28925904	121		unconditional	GAB1	missense_variant	C	T	381625	0.0190	0.0190	-0.048	0.008	1.04E-08	NA	1.26E-09	252239	0.0233	0.0233	-0.036	0.010	3.24E-04	633864	0.0207	0.0207	-0.043	0.006	4.29E-12	6.49E-17
4	145574844	rs1812175	121		unconditional	HHIP	intron_variant	A	G	378383	0.1630	0.8370	0.075	0.003	4.93E-111	NA	4.61E-79	252402	0.1625	0.8375	0.084	0.004	1.71E-89	630785	0.1628	0.8372	0.078	0.002	8.09E-225	3.02E-281
4	145643079	rs6854783	121		2nd conditional rounc	HHIP	intron_variant	G	A	380346	0.4100	0.5900	0.033	0.003	2.75E-37	2.21E-12	5.79E-18	252434	0.4185	0.5815	0.033	0.003	9.00E-27	632780	0.4141	0.5859	0.033	0.002	3.36E-53	1.92E-24
4	145650021	rs1492820	121		1st conditional round	HHIP	intron_variant	G	A	374731	0.4500	0.5500	0.040	0.003	1.07E-56	6.10E-14	4.23E-28	252397	0.4574	0.5426	0.041	0.003	9.92E-41	627128	0.4536	0.5464	0.041	0.002	1.82E-79	3.93E-41
4	152355268	rs2709828	582		validation	FAM160A1	intron_variant	C	T	358569	0.4521	0.5479	-0.0113	0.0025	5.82E-06	NA	NA	233726	0.4384	0.5616	#####	0.0030	5.76E-04	592295	0.4466	0.5534	-0.011	0.0019	1.28E-08	3.39E-10
4	154557616	rs34343821	450	yes	unconditional	KIAA0922	missense_variant	C	T	361674	0.0110	0.0110	0.059	0.011	7.75E-08	NA	NA	252305	0.0146	0.0146	0.056	0.012	5.75E-06	613979	0.0126	0.0126	0.058	0.008	2.18E-12	3.00E-15
4	184236868	rs4862155	123		unconditional	WWC2	missense_variant	G	A	380102	0.0650	0.0650	-0.038	0.005	2.40E-15	NA	2.41E-15	252408	0.0628	0.0628	-0.040	0.006	2.09E-10	632510	0.0641	0.0641	-0.039	0.004	4.00E-23	1.86E-22
5	31515657	rs55656741	124		unconditional	DROSHA	missense_variant	G	A	381625	0.4930	0.4930	0.014	0.002	1.63E-09	NA	1.80E-08	223714	0.4906	0.4906	0.013	0.003	5.12E-05	605339	0.4923	0.4923	0.014	0.002	6.34E-16	5.36E-12
5	32784907	rs146301345	125		2nd conditional rounc	AC026703.1	missense_variant	G	A	380850	0.0030	0.0030	0.128	0.022	1.05E-08	1.50E-09	8.18E-11	174133	0.0023	0.0023	0.166	0.035	1.78E-06	554983	0.0028	0.0028	0.139	0.019	7.91E-14	3.20E-16
5	32830521	rs1173727	125		unconditional	-	intergenic_variant	T	C	377104	0.4070	0.5930	-0.035	0.002	1.65E-46	NA	2.03E-45	252204	0.3967	0.6033	-0.035	0.003	2.32E-30	629308	0.404	0.5960	-0.035	0.002	4.05E-97	2.58E-67
5	33230034	rs11745439	125		1st conditional round	CTD-2066L21.3	intron_variant	A	G	376860	0.2750	0.7250	0.023	0.003	8.30E-18	1.18E-13	1.13E-13	223714	0.2857	0.7143	0.024	0.004	4.15E-11	600574	0.2794	0.7206	0.023	0.002	4.76E-24	4.19E-24
5	36954812	rs292182	126		unconditional	NIPBL	intron_variant	G	A	378823	0.4320	0.4320	-0.024	0.002	2.62E-22	NA	2.15E-23	223714	0.4371	0.4371	-0.026	0.003	1.85E-15	602537	0.4334	0.4334	-0.025	0.002	6.15E-47	2.65E-35
5	39397132	rs11959928	586		validation	DAB2	intron_variant	T	A	356735	0.4327	0.4327	0.0125	0.0025	6.64E-07	NA	NA	201559	0.4181	0.4181	0.0103	0.0033	0.002	558294	0.4273	0.4273	0.0117	0.002	4.67E-09	3.43E-09
5	42473555	rs13188386	128		1st conditional round	GHR	intron_variant	G	A	377973	0.2680	0.2680	-0.019	0.003	7.11E-12	3.08E-09	4.81E-13	252290	0.2653	0.2653	-0.020	0.003	5.18E-09	630263	0.2668	0.2668	-0.019	0.002	7.10E-18	1.32E-25
5	42782492	rs2973011	128		unconditional	CCDC152	intron_variant	T	C	372028	0.4490	0.4490	-0.021	0.002	8.34E-17	NA	2.06E-18	223714	0.4568	0.4568	-0.028	0.003	5.62E-18	595742	0.4512	0.4512	-0.023	0.002	2.12E-41	1.35E-32
5	54960673	rs4865615	130		unconditional	SLC38A9	missense_variant	C	G	335008	0.3300	0.6700	-0.030	0.003	1.58E-26	NA	6.78E-26	235341	0.3365	0.6635	-0.034	0.003	9.40E-24	570349	0.3329	0.6671	-0.032	0.002	1.83E-45	1.36E-57
5	56031884	rs889312	131		unconditional	-	intergenic_variant	C	A	380346	0.2780	0.7220	0.019	0.003	7.88E-13	NA	2.61E-12	252412	0.2932	0.7068	0.017	0.003	4.56E-07	632758	0.2848	0.7152	0.018	0.002	6.40E-16	2.15E-20
5	64766798	rs61736454	132		unconditional	ADAMTS6	missense_variant	G	A	360412	0.0020	0.0020	-0.152	0.026	7.82E-09	NA	3.26E-08	227487	0.0023	0.0023	-0.182	0.032	1.37E-08	587899	0.0021	0.0021	-0.164	0.020	4.80E-16	3.74E-16
5	67596088	rs3756668	133		unconditional	PIK3R1	3_prime_UTR_variant	G	A	376010	0.4410	0.4410	-0.014	0.002	1.65E-08	NA	1.18E-08	251947	0.4598	0.4598	-0.017	0.003	1.28E-08	627957	0.4467	0.4467	-0.015	0.002	2.86E-19	5.36E-14
5	88354675	rs10037512	138		unconditional	MEF2C-AS1	intron_variant	T	C	381625	0.4580	0.4580	-0.029	0.002	3.99E-32	NA	2.93E-32	252079	0.4587	0.4587	-0.030	0.003	6.65E-22	633704	0.4582	0.4582	-0.029	0.002	8.28E-68	6.32E-49
5	90151589	rs2247870	139		unconditional	ADGRV1	missense_variant	G	A	381625	0.4520	0.5480	0.014	0.002	8.35E-09	NA	8.14E-09	252271	0.4563	0.5437	0.008	0.003	0.009	633896	0.4533	0.5467	0.012	0.002	2.94E-13	6.91E-10
5	95115959	rs41276257	140		1st conditional round	RHOBTB3	missense_variant	C	T	373551	0.0960	0.0960	0.021	0.004	2.02E-07	1.40E-08	3.48E-09	223714	0.0909	0.0909	0.022	0.006	1.21E-04	597265	0.0943	0.0943	0.021	0.003	7.70E-11	3.37E-15
5	95728898	rs6235	140		unconditional	PCSK1	missense_variant	C	G	350404	0.2740	0.2740	0.020	0.003	5.59E-12	NA	5.33E-13	229797	0.2730	0.2730	0.017	0.004	3.03E-06	580201	0.2736	0.2736	0.019	0.002	5.00E-16	2.45E-24
5	102338811	rs35658696	583	yes	validation	PAM	missense_variant	A	G	381625	0.0484	0.0484	-0.0253	0.0055	3.76E-06	NA	NA	233656	0.0530	0.0530	#####	0.0068	8.47E-06	615281	0.05	0.0500	-0.027	0.0043	1.63E-10	1.59E-10
5	108113344	rs13177718	141		unconditional	FER	intron_variant	C	T	353936	0.0730	0.0730	-0.032	0.005	2.13E-11	NA	2.14E-11	251648	0.0764	0.0764	-0.033	0.006	1.02E-08	605584	0.0745	0.0745	-0.032	0.004	8.80E-18	8.92E-16

5	112176756	rs459552	584	yes	recessive	APC	missense_variant	T	A	449259	0.2200	0.7800	-0.020	0.003	4.29E-10	NA	NA	237460	0.2283	0.7717	-0.013	0.005	0.008	686719	0.2225	0.7775	0.018	0.003	2.28E-11	1.06E-09
5	122718736	rs6595440	142		unconditional	CEP120	missense_variant	G	C	151761	0.4330	0.4330	-0.025	0.004	5.02E-11	NA	5.51E-11	229446	0.4354	0.4354	-0.026	0.003	8.66E-16	381207	0.4345	0.4345	-0.026	0.003	2.30E-24	6.09E-17
5	126250812	rs34821177	453	yes	unconditional	MARCH3	missense_variant	C	T	369748	0.0360	0.0360	0.034	0.006	4.25E-08	NA	2.82E-08	252411	0.0289	0.0289	0.027	0.009	0.002	622159	0.0338	0.0338	0.032	0.005	1.67E-10	2.82E-11
5	127668685	rs78727187	143		unconditional	FBN2	missense_variant	G	T	355312	0.0060	0.0060	0.183	0.015	2.47E-33	NA	7.34E-31	252299	0.0060	0.0060	0.181	0.020	5.06E-20	607611	0.006	0.0060	0.182	0.012	1.47E-52	3.00E-44
5	127685135	rs154001	143		1st conditional round	FBN2	missense_variant	C	T	381625	0.3140	0.6860	0.020	0.003	4.73E-15	1.47E-12	1.44E-13	252287	0.3228	0.6772	0.025	0.003	2.97E-14	633912	0.318	0.6820	0.022	0.002	8.74E-24	6.53E-25
5	131663062	rs272893	145		unconditional	SLC22A4	missense_variant	T	C	369664	0.3920	0.6080	0.031	0.003	4.38E-31	NA	7.89E-34	252209	0.3739	0.6261	0.035	0.003	7.77E-27	621873	0.3836	0.6164	0.033	0.002	5.10E-50	2.89E-60
5	134372685	rs31198	146		unconditional	C5orf66	intron_variant	T	C	381625	0.2560	0.2560	-0.030	0.003	6.45E-26	NA	2.44E-26	252421	0.2500	0.2500	-0.038	0.004	2.07E-26	634046	0.2535	0.2535	-0.033	0.002	1.21E-47	5.37E-61
5	135288632	rs62623707	454	yes	unconditional	LECT2	missense_variant	A	G	381625	0.0440	0.0440	-0.030	0.006	1.02E-07	NA	NA	252431	0.0493	0.0493	-0.024	0.007	4.77E-04	634056	0.0463	0.0463	-0.027	0.005	1.36E-09	1.24E-19
5	140562739	rs61743469	585	yes	validation	PCDHB16	missense_variant	G	A	381625	0.0594	0.0594	0.0250	0.0052	1.58E-06	NA	NA	179812	0.0655	0.0655	0.0247	0.0070	4.33E-04	561437	0.0615	0.0615	0.0248	0.0042	2.63E-09	1.14E-08
5	141573265	rs3910203	148		unconditional	-	intergenic_variant	G	A	380102	0.4020	0.5980	0.013	0.002	7.76E-08	NA	3.90E-08	223714	0.4027	0.5973	0.014	0.003	9.36E-06	603816	0.4022	0.5978	0.013	0.002	3.85E-15	6.03E-11
5	168256240	rs4282339	149		unconditional	SLIT3	intron_variant	G	A	377973	0.2030	0.2030	-0.031	0.003	4.05E-26	NA	1.06E-27	252163	0.2036	0.2036	-0.036	0.004	2.91E-22	630136	0.2032	0.2032	-0.033	0.002	2.42E-45	1.52E-58
5	170838791	rs11745536	150		1st conditional round	NPM1	downstream_gene_variant	G	A	372028	0.4450	0.5550	-0.022	0.002	1.71E-19	8.08E-19	1.92E-19	223714	0.4647	0.5353	-0.023	0.003	7.01E-13	595742	0.4506	0.5494	-0.022	0.002	2.12E-39	9.05E-30
5	171281875	rs4868125	150		unconditional	-	intergenic_variant	C	G	371882	0.4090	0.5910	0.032	0.002	6.65E-39	NA	1.99E-41	208811	0.4254	0.5746	0.037	0.003	6.01E-28	580693	0.4132	0.5868	0.033	0.002	2.08E-83	3.87E-61
5	172196752	rs34471628	455	yes	unconditional	DUSP1	missense_variant	A	G	355545	0.0360	0.0360	0.048	0.006	4.00E-14	NA	2.14E-12	252386	0.0423	0.0423	0.036	0.007	1.26E-06	607931	0.0385	0.0385	0.043	0.005	1.93E-20	1.67E-18
5	172755066	rs148833559	151		1st conditional round	STC2	missense_variant	C	A	369802	0.0010	0.0010	0.290	0.037	5.69E-15	1.86E-15	1.60E-14	252362	0.0013	0.0013	0.368	0.043	1.32E-17	622164	0.0011	0.0011	0.323	0.028	1.15E-30	2.34E-30
5	172984114	rs889014	151		unconditional	-	regulatory_region_variant	C	T	380346	0.3540	0.3540	-0.028	0.002	1.34E-28	NA	2.23E-30	252292	0.3480	0.3480	-0.025	0.003	2.69E-15	632638	0.3523	0.3523	-0.027	0.002	5.21E-58	2.10E-42
5	176516631	rs1966265	152		unconditional	FGFR4	missense_variant	G	A	381625	0.2320	0.2320	0.048	0.003	2.63E-64	NA	2.64E-38	252120	0.2450	0.2450	0.048	0.004	3.82E-42	633745	0.2375	0.2375	0.048	0.002	6.39E-98	1.03E-76
5	176517326	rs422421	152		3rd conditional round	FGFR4	intron_variant	T	C	376735	0.2120	0.7880	0.039	0.003	1.14E-38	5.31E-19	1.84E-17	252376	0.2088	0.7912	0.041	0.004	2.53E-28	629111	0.2107	0.7893	0.040	0.002	3.65E-65	1.01E-41
5	176637471	rs28932177	152		1st conditional round	NSD1	missense_variant	G	A	350397	0.0280	0.0280	0.063	0.007	2.38E-17	1.06E-22	NA	252162	0.0272	0.0272	0.065	0.009	2.62E-12	602559	0.0277	0.0277	0.064	0.006	4.27E-30	1.14E-24
5	176722005	rs78247455	152		2nd conditional round	NSD1	missense_variant	G	A	377738	0.0230	0.0230	-0.083	0.008	1.86E-26	7.31E-20	1.63E-41	248028	0.0246	0.0246	-0.085	0.010	8.42E-18	625766	0.0236	0.0236	-0.084	0.006	2.32E-41	1.19E-39
5	178507090	rs1445845	153		unconditional	RP11-281O15.7	missense_variant	G	A	381625	0.3300	0.6700	-0.021	0.003	1.81E-15	NA	3.15E-14	252107	0.3407	0.6593	-0.017	0.003	9.90E-08	633732	0.3349	0.6651	-0.019	0.002	1.98E-18	4.93E-20
5	179731014	rs6879260	154		unconditional	GFPT2	intron_variant	T	C	381625	0.3880	0.6120	0.032	0.002	3.96E-39	NA	4.77E-38	252342	0.3965	0.6035	0.025	0.003	9.34E-16	633967	0.3905	0.6095	0.030	0.002	7.85E-71	9.13E-53
6	1901495	rs1570534	155		unconditional	GMDS	intron_variant	C	T	372028	0.3250	0.6750	0.017	0.003	7.56E-11	NA	4.00E-11	223714	0.3204	0.6796	0.018	0.003	1.60E-07	595742	0.323	0.6770	0.017	0.002	1.21E-14	2.98E-17
6	7231843	rs9379084	156		1st conditional round	RREB1	missense_variant	G	A	294781	0.1140	0.1140	-0.053	0.004	2.23E-36	4.50E-31	2.25E-29	223714	0.1133	0.1133	-0.051	0.005	1.01E-22	518495	0.1138	0.1138	-0.052	0.003	4.82E-61	7.77E-72
6	7720059	rs12198986	156		unconditional	-	intergenic_variant	G	A	381625	0.4660	0.4660	0.038	0.002	5.07E-56	NA	4.63E-53	252310	0.4821	0.4821	0.050	0.003	8.34E-62	633935	0.4709	0.4709	0.042	0.002	5.67E-138	7.29E-103
6	17675246	rs2228375	157		unconditional	NUP153	missense_variant	T	C	381625	0.3130	0.3130	0.015	0.003	6.37E-09	NA	9.51E-09	252129	0.3160	0.3160	0.009	0.003	0.006	633754	0.3143	0.3143	0.012	0.002	2.85E-08	1.44E-10
6	19841493	rs1047014	158		unconditional	ID4	upstream_gene_variant	T	C	377104	0.2480	0.2480	0.029	0.003	1.03E-25	NA	1.34E-25	242670	0.2479	0.2479	0.028	0.004	4.41E-15	619774	0.248	0.2480	0.029	0.002	1.47E-35	9.60E-48
6	26017542	rs16891235	159		2nd conditional round	HIST1H1A	missense_variant	T	C	377738	0.1020	0.1020	-0.020	0.005	1.03E-05	1.32E-21	2.72E-22	252349	0.1177	0.1177	-0.008	0.005	0.106	630087	0.11	0.1100	-0.014	0.004	7.59E-05	5.22E-13
6	26107790	rs198845	159		1st conditional round	HIST1H1T	missense_variant	G	T	356525	0.3790	0.3790	0.035	0.003	1.50E-37	7.13E-14	NA	252318	0.3774	0.3774	0.032	0.003	4.83E-23	608843	0.3782	0.3782	0.034	0.002	1.16E-52	7.54E-14
6	26233387	rs10946808	159		unconditional	HIST1H1D	non_coding_transcript_exon_variant	A	G	375365	0.3020	0.3020	-0.049	0.003	1.48E-71	NA	3.18E-81	244946	0.2774	0.2774	-0.062	0.004	1.00E-69	620311	0.2916	0.2916	-0.054	0.002	4.01E-126	3.83E-96
6	28916252	rs4947339	160		unconditional	LINC01556	downstream_gene_variant	C	T	365143	0.4080	0.4080	-0.022	0.003	2.57E-13	NA	1.49E-08	223083	0.3870	0.3870	-0.027	0.003	4.54E-16	588226	0.3986	0.3986	-0.024	0.002	1.35E-27	7.58E-17
6	30851933	rs7757648	161		unconditional	DDR1	intron_variant	G	A	320859	0.0130	0.0130	-0.075	0.013	1.11E-08	NA	NA	217993	0.0105	0.0105	-0.079	0.018	1.24E-05	538852	0.0121	0.0121	-0.076	0.011	4.64E-13	4.47E-05
6	31380529	rs2256183	162		unconditional	HCP5	intron_variant	A	G	359104	0.4570	0.5430	-0.026	0.003	5.74E-16	NA	NA	245709	0.4922	0.4922	-0.035	0.003	6.28E-27	604813	0.4802	0.5198	-0.030	0.002	2.03E-42	2.54E-23
6	32663851	rs6457617	163		unconditional	-	intergenic_variant	C	T	374936	0.4960	0.5040	-0.026	0.003	4.34E-17	NA	3.76E-11	223714	0.4707	0.4707	-0.034	0.003	2.25E-24	598650	0.4892	0.4892	-0.030	0.002	4.32E-40	5.62E-39
6	33690796	rs4713668	163		1st conditional round	IP6K3	missense_variant	C	T	381625	0.4620	0.4620	0.020	0.003	3.55E-15	3.55E-15	NA	252302	0.4373	0.4373	0.022	0.003	2.71E-12	633927	0.4502	0.4502	0.021	0.002	4.90E-22	2.92E-23
6	34165721	rs7742369	163		4th conditional round	-	regulatory_region_variant	A	G	379252	0.1750	0.1750	0.053	0.003	1.68E-61	5.97E-11	NA	252299	0.1738	0.1738	0.058	0.004	1.48E-47	631551	0.1746	0.1746	0.055	0.002	2.66E-115	3.92E-20
6	34199092	rs2780226	163		unconditional	-	regulatory_region_variant	C	T	378383	0.0840	0.9160	-0.085	0.004	6.12E-83	NA	5.94E-79	252280	0.0847	0.9153	-0.090	0.006	1.54E-59	630663	0.0842	0.9158	-0.087	0.003	1.07E-157	5.66E-55
6	34618893	rs2814993	163		1st conditional round	C6orf106	intron_variant	G	A	379977	0.1530	0.1530	0.056	0.003	2.98E-57	4.13E-38	7.15E-43	252382	0.1355	0.1355	0.065	0.005	2.61E-46	632359	0.1476	0.1476	0.059	0.003	1.23E-121	7.12E-54
6	34730395	rs34427075	163		unconditional	SNRPC	synonymous_variant	C	T	381625	0.0140	0.0140	-0.117	0.010	9.21E-33	NA	6.29E-21	252366	0.0158	0.0158	-0.139	0.012	9.59E-31	633991	0.0147	0.0147	-0.126	0.008	3.45E-60	1.05E-20
6	35402785	rs4713858	163		4th conditional round	-	intergenic_variant	A	G	380346	0.1460	0.8540	0.026	0.003	4.78E-14	1.39E-08	NA	252074	0.1574	0.8426	0.039	0.004	5.91E-20	632420	0.1498	0.8502	0.030	0.002	3.98E-35	7.48E-29
6	36094188	rs6922865	163		2nd conditional round	MAPK13	upstream_gene_variant	T	G	371178	0.3610	0.6390	-0.014	0.003	4.09E-08	1.30E-09	NA	252230	0.3608	0.6392	-0.008	0.003	0.015	623408	0.3609	0.6391	-0.011	0.002	3.94E-07	1.67E-05
6	41650736	rs2842643	164		1st conditional round	TFEB	downstream_gene_variant	C	T	374731	0.2740	0.7260	-0.015	0.003	2.24E-08	1.10E-07	9.81E-08	252321	0.2899	0.7101	-0.008	0.003	0.017	627052	0.281	0.7190	-0.012	0.002	1.01E-07	2.25E-10
6	41903798	rs33966734	164		unconditional	CCND3	stop_gained	C	A	135421	0.0130	0.0130	-0.140	0.017	5.51E-17	NA	1.88E-16	194563	0.0107	0.0107	-0.101	0.018	3.41E-08	329984	0.0119	0.0119	-0.122	0.012	1.28E-22	8.74E-25
6	43273604	rs2242416	589	yes	validation	CRIP3	missense_variant	A	G	379977	0.3996	0.6004	0.0127	0.0025	4.34E-07	NA	NA	233722	0.3887	0.6113	0.0160	0.0031	2.22E-07	613699	0.3953	0.6047	0.014	0.0019	6.55E-13	1.88E-13
6	44946506	rs9472414	165		1st conditional round	SUPT3H	intron_variant	T	A	374724	0.2130	0.2130	-0.026	0.003	8.81E-19	1.41E-08	2.17E-08	229512	0.2018	0.2018	-0.026	0.004	4.23E-11	604236	0.2089	0.2089	-0.026	0.002	1.27E-27	3.04E-24
6	45095163	rs9395066	165		unconditional	SUPT3H	intron_variant	A	C	369748	0.4080	0.4080	0.022	0.002	3.66E-19	NA	1.02E-08	252338	0.4165	0.4165	0.019	0.003	3.56E-10	622086	0.4105	0.4105	0.021	0.002	1.22E-36	3.85E-10
6	47649574	rs10807372	166		unconditional	ADGRF2	missense_variant	A	G	381625	0.3650	0.6350	0.016	0.003	3.07E-09	NA	3.71E-09	251162	0.3691	0.6309	0.019	0.003	1.17E-08	632787	0.3668	0.6332	0.017	0.002	7.00E-15	1.02E-18
6	56919443	rs61740375	590	yes	validation	KIAA1586	missense_variant	A	G	368149	0.0863	0.0863	0.0217	0.0044	8.52E-07	NA	NA	233756	0.0839	0.0839	0.0129	0.0055	0.020	601905	0.0853	0.0853	0.0183	0.0034	1.15E-07	3.18E-08
6	76173832	rs6903448	168		1st conditional round	RP11-415D17.1	intron_variant	C	T	380102	0.1470	0.1470	-0.032	0.003	1.88E-21	1.95E-14	1.54E-16	223714	0.1584	0.1584	-0.036	0.004	5.39E-16	603816	0.1506	0.1506	-0.033	0.003	8.27E-41	6.72E-21
6	76265642	rs9360921	168		unconditional	-	regulatory_region_variant	T	G	376597	0.1080	0.1080	0.048	0.004	5.90E-34	NA	8.45E-28	252200	0.1029	0.1029	0.048	0.005	7.21E-22	628797	0.106	0.1060	0.048	0.003	2.44E-53	2.25E-54
6	80196848	rs1875845	591		recessive	LCA5	missense_variant	C	T	445497	0.3225	0.3225	0.028	0.005	1.35E-08	NA	NA	223714	0.3148	0.3148	0.025	0.007	4.27E-04	669211	0.32	0.3200	-0.027	0.004	2.54E-11	2.15E-16
6	80956208	rs648831	169		unconditional	BCKDHB	intron_variant	C	T	376860	0.4770	0.5230	0.034	0.002	7.20E-47	NA	2.83E-46	223714	0.4846	0.5154	0.029	0.003	1.68E-19	600574	0.4791	0.5209	0.033	0.002	3.43E-82	2.85E-60
6	81315597	rs9443804	169		1st conditional round	-	regulatory_region_variant	A	G	380102	0.4370	0.4370	0.020	0.002	1.11E-16	2.78E-16	2.33E-20	223714	0.4450	0.4450	0.015	0.003	2.22E-06	603816	0.4392	0.4392	0.019	0.002	3.96E-28	1.27E-31
6	81913895	rs2323150	169		1st conditional round	-	intergenic_variant	G	A	345730	0.4840	0.5160	-0.025	0.003	2.56E-23	NA	NA	223714	0.4736	0.5264	-0.034	0.003	5.27E-26	569444	0.4792	0.5208	-0.029	0.002	3.05E-40	2.75E-39
6	83838673	rs4706980	458	yes	unconditional	DOPEY1	missense_variant	G	A	368874	0.1300	0.1300	0.020	0.004	3.07E-08	NA	NA	252342	0.1372	0.1372	0.016	0.004	2.09E-04	621216	0.1333	0.1333	0.018	0.003	5.96E-10	8.69E-09
6	105378954	rs7759938	171		unconditional	-	intergenic_variant	C	T	381625	0.3220	0.6780	-0.044	0.003	2.78E-59	NA	4.54E-59	222180	0.3244	0.6756	-0.049	0.004	2.60E-45	603805	0.323	0.6770	-0.046	0.002	6.47E-92	2.57E-116
6	108996963	rs3800229	172		1st conditional round	FOXO3	intron_variant	G	T	372972	0.2950	0.7050	0.022	0.003	1.30E-15	1.64E-14	2.72E-15	223714	0.2784	0.7216	0.022	0.004	1.03E-09	596686	0.2882	0.7118	0.022	0.002	1.40E-21	4.98E-28
6	109764535	rs1476387	172		unconditional	PPIL6	missense_variant	G	T	359848	0.4150	0.4150	-0.026	0.003	2.07E-22	NA	7.14E-22	252198	0.4007	0.4007	-0.027	0.003	1.23E-16	612046	0.4083	0.4083	-0.026	0.002	4.24E-33	5.83E-39
6	116387134	rs1999930	173		unconditional	-	intergenic_variant	C	T	377104	0.2720	0.2720	0.018	0.003	3.08E-10	NA	2.38E-10	252174	0.2975	0.2975	0.016	0.003	1.15E-06	629278	0.2833	0.2833	0.017	0.002	1.21E-14	2.51E-19
6	117522156	rs961764	174		unconditional	-	intergenic_variant	C	G	199891	0.4210	0.5790	0.026	0.003	6.72E-16	NA	1.73E-16	208537	0.4328	0.5672	0.020	0.003	3.66E-09	408428	0.4262	0.5738	0.023	0.002	2.61E-25	6.79E-33
6	126835655	rs1490388	175		unconditional	-	intergenic_variant	C	T	379016	0.4630	0.4630	0.042	0.003	4.30E-58	NA	8.69E-58	252354	0.4504	0.4504	0.046	0.003	1.06E-47	631370	0.457	0.4570	0.044	0.002	2.92E-90	1.15E-109
6	130322179	rs2876066	176		1st conditional round	-	regulatory_region_variant	C	A	375581	0.0790	0.0790	-0.034	0.004	2.94E-14	1.48E-07	NA	223714	0.0819	0.0819	-0.038	0.006	1.22E-10	599295	0.0799	0.0799	-0.035	0.003	1.74E-26	3.13E-16
6	130349119	rs6569648	176		unconditional	L3MBTL3	intron_variant	C	T	369748	0.2310	0.7690	-0.049	0.003	2.45E-60	NA	7.95E-61	252258	0.2438	0.7562	-0.050	0.004	2.94E-45	622006	0.2363	0.7637	-0.050	0.002	2.35E-103	1.40E-125
6	136227558	rs7752169	587	yes	validation	PDE7B	intron_variant	T	C	380102	0.4598	0.5402	0.0120	0.0024	4.31E-07	NA	NA	205168	0.4699	0.5301	0.0114	0.0032	3.71E-04	585270	0.4634	0.5366	0.0118	0.0019	6.40E-10	9.78E-10
6	140273647	rs642858	459	yes	unconditional	-	intergenic_variant	G	A	373217	0.2300	0.2300	-0.016	0.003	5.40E-08	NA	NA	221633	0.2342	0.2342	-0.021	0.004	3.34E-08	594850	0.2316	0.2316	-0.018	0.002	2.78E-14	1.97E-11
6	141443540	rs2931796	460	yes	unconditional	-	intergenic_variant	C	T	372973	0.3670	0.6330	-0.013	0.002	7.23E-08	NA	NA	223714	0.3646	0.6354	-0.015	0.003	8.37E-06	596687	0.3664	0.6336	-0.014	0.002	3.70E-15	7.79E-05
6	142548099	rs225717	178		1st conditional round	VTA1	downstream_gene_variant	C	T	381625	0.2290	0.7710	0.024	0.003	9.73E-17	1.99E-15	1.11E-16	252303	0.2313	0.7687	0.023	0.004	3.41E-10	633928	0.23	0.7700	0.023	0.002	2.86E-24	2.15E-26
6	142679572	rs6570507	178		unconditional	ADGRG6	intron_variant	G	A	375774	0.2870	0.2870	-0.054	0.003	2.68E-79	NA	2.36E-78	252415	0.2778	0.2778	-0.062	0.004	5.10E-71	628189	0.2831	0.2831	-0.057	0.002	7.38E-141	1.64E-167
6	146125793	rs3811102	588		validation	RP11-545I5.3	missense_variant	A	T	375498	0.4218	0.4218	-0.0128	0.0025	3.71E-07	NA	NA	232672	0.4204	0.4204	#####	0.0031	1.28E-05	608170	0.4212	0.4212	-0.013	0.002	2.15E-11	1.32E-11
6	152110943	rs543650	181		unconditional	ESR1	intron_variant	T	G	367628	0.4040	0.5960	0.025	0.002	6.24E-25	NA	8.31E-25	223714	0.3973	0.6027	0.030	0.003	9.86E-20	591342	0.4022	0.5978	0.026	0.002	1.61E-53	3.13E-40
6	155450779	rs148543891	461	yes	unconditional	TIAM2	missense_variant	A	G	376353	0.0030	0.0030	-0.124	0.022	1.45E-08	NA	1.77E-08	151101	0.0012	0.0012	-0.016	0.082	0.850	527454	0.0029	0.0029	-0.117	0.021	3.96E-08	4.39E-08
6	158743188	rs1539312	183		1st conditional round	TULP4	intron_variant	G	A	380102	0.4900	0.5100	-0.017	0.002	3.29E-13	2.39E-08	1.76E-08	223714	0.4856	0.5144	-0.022	0.003	3.77E-12	603816	0.4887	0.5113	-0.018	0.002	1.25E-27	5.48E-14
6	158910698	rs12206717	183		unconditional	TULP4	missense_variant	G	A	377738	0.0510	0.0510	-0.050	0.005	4.78E-20	NA	4.59E-15	252403	0.0560	0.0560	-0.033	0.007	4.11E-07	630141	0.0528	0.0528	-0.044	0.004	2.94E-28	4.62E-23
6	168810725	rs2147457	186		unconditional	-	intergenic_variant	A	G	380102	0.4140	0.4140	-0.022	0.002	1.51E-20	NA	6.63E-20	223714	0.4034	0.4034	-0.025	0.003	4.00E-14	603816	0.4111	0.4111	-0.023	0.002	1.59E-40	7.62E-31
7	1854263	rs6948971	462		unconditional	MAD1L1	downstream_gene_variant	A	G	375774	0.2070	0.2070	0.015	0.003	1.99E-07	NA	NA	252171	0.1928	0.1928	0.006	0.004	0.097	627945	0.2016	0.2016	0.012	0.002	6.94E-07	4.14E-08
7	2795957	rs798497	187		unconditional	GNA12	intron_variant	A	G	377104	0.3000	0.3000	-0.049	0.003	1.49E-68	NA	1.74E-68	252097	0.2950	0.2950	-0.057	0.003	1.18E-61	629201	0.2978	0.2978	-0.052	0.002	4.09E-119	1.35E-147
7	19616522	rs4470914	190		unconditional	AC007091.1	intron_variant	C	T	196538	0.1750	0.1750	0.035	0.004	1.20E-16	NA	6.44E-17	245558	0.1848	0.1848	0.032	0.004	1.32E-16	442096	0.18	0.1800	0.034	0.003	2.44E-33	1.55E-30
7	23502974	rs12534093	191		unconditional	IGF2BP3	intron_variant	T	A	344325	0.2260	0.2260	-0.037	0.003	3.61E-34	NA	4.92E-34	252258	0.2406	0.2406	-0.040	0.004	5.91E-30	596583	0.2322	0.2322	-0.038	0.002	4.66E-63	6.54E-81
7	25871109	rs1055144	192		unconditional	-	intergenic_variant	C	T	377104	0.1900	0.1900	0.024	0.003	2.02E-15	NA	1.02E-16	252394	0.1884	0.1884	0.032	0.004	1.30E-16	629498	0.1894	0.1894	0.027	0.002	4.82E-30	9.58E-44
7	28185091	rs849141	193		unconditional	JAZF1	intron_variant	A	G	381625	0.2890	0.7110	-0.045	0.003	7.91E-62	NA	1.72E-62	252332	0.3008	0.6992	-0.048	0.003	1.88E-47	633957	0.2943	0.7057	-0.047	0.002	2.36E-96	4.16E-120
7	37947103	rs1802074	195		unconditional	SFRP4	missense_variant	C	T	381625	0.2070	0.2070	0.018	0.003	1.13E-09	NA	5.30E-12	252389	0.2066	0.2066	0.019	0.004	6.19E-07	634014	0.2068	0.2068	0.018	0.002	6.21E-15	1.58E-21
7	38128326	rs6959212	195		1st conditional round	-	intergenic_variant	T	C	285694	0.3300	0.6700	0.018	0.003	1.19E-09	2.65E-10	2.23E-11	217993	0.3446	0.6554	0.024	0.003	1.60E-12	503687	0.3364	0.6636	0.021	0.002	4.68E-20	1.01E-27
7	41470093	rs1079866	593	yes	validation	-	intergenic_variant	C	G	366654	0.1407	0.1407	0.0164	0.0035	2.29E-06	NA	NA	233700	0.1358	0.1358	0.0112	0.0044	0.011	600354	0.1388	0.1388	0.0144	0.0027	1.24E-07	1.14E-07
7	46201355	rs1007358	196		1st conditional round	-	regulatory_region_variant	A	G	376860	0.2230	0.2230	0.019	0.003	1.80E-11	1.12E-09	1.65E-10	223714	0.2185	0.2185	0.026	0.004	2.38E-11	600574	0.2213	0.2213	0.022	0.002	9.38E-20	5.00E-25
7	46437154	rs17172694	196		unconditional	-	intergenic_variant	G	T	380102	0.0740	0.0740	-0.041	0.005	5.10E-19	NA	5.01E-18	223714	0.0858	0.0858	-0.032	0.006	2.05E-08	603816	0.0791	0.0791	-0.037	0.004	5.89E-23	6.57E-18
7	50751090	rs10248619	197		unconditional	GRB10	intron_variant	T	C	377973	0.2220	0.7780	-0.017	0.003	6.28E-09	NA	4.17E-09	252268	0.2192	0.7808	-0.014	0.004	1.05E-04	630241	0.2209	0.7791	-0.016	0.002	7.62E-12	1.72E-15
7	55855180	rs11982736	198		unconditional	RNU6-1126P	upstream_gene_variant	G	A	367090	0.1630	0.1630	-0.018	0.003	5.88E-08	NA	9.22E-09	252295	0.1472	0.1472	-0.024	0.004	1.06E-08	619385	0.1577	0.1577	-0.020	0.003	2.39E-16	2.90E-11
7	72904810	rs17145713	594		validation	BAZ1B	intron_variant	C	T	381625	0.1859	0.1859	0.0166	0.0033	3.68E-07	NA	NA	233772	0.1944	0.1944	0.0155	0.0040	9.45E-05	615397	0.1893	0.1893	0.0162	0.0025	1.48E-10	6.51E-11
7	73482987	rs41511151	595		validation	ELN	missense_variant	G	A	343448	0.0042	0.0042	-0.0861	0.0183	2.63E-06	NA	NA	218793	0.0070	0.0070	#####	0.0191	0.002	562241	0.0055	0.0055	-0.074	0.0132	2.31E-08	1.53E-08
7	92248076	rs42235	201		unconditional	CDK6	intron_variant	C	T	372272	0.3080	0.3080	0.057	0.003	2.53E-102	NA	2.82E-102	251765	0.2940	0.2940	0.058	0.003	2.38E-68	624037	0.3017	0.3017	0.058	0.002	6.89E-147	2.91E-186
7	99489571	rs17277546	203		unconditional	TRIM4	3_prime_UTR_variant	G	A	380113	0.0490	0.0490	0.034	0.005	3.28E-10	NA	7.94E-10	223714	0.0524	0.0524	0.038	0.007	2.26E-07	603827	0.0501	0.0501	0.035	0.004	1.40E-17	2.57E-19
7	100490077	rs7636	463	yes	unconditional	ACHE	synonymous_variant	G	A	356606	0.0430	0.0430	-0.037	0.006	8.59E-10	NA	1.37E-08	252406	0.0346	0.0346	-0.019	0.009	0.029	609012	0.0402	0.0402	-0.031	0.005	2.98E-10	1.81E-09
7	128573967	rs4728142	592	yes	recessive	IRF5	upstream_gene_variant	G	A	380346	0.4390	0.4390	-0.022	0.004	2.06E-07	NA	NA	252281	0.4556	0.4556	-0.010	0.005	0.039	632627	0.4459	0.4459	-0.017	0.003	1.30E-07	3.20E-08
7	129663496	rs11556924	464	yes	unconditional	RP11-306G20.1	missense_variant	C	T	381625	0.3790	0.3790	0.014	0.002	7.90E-09	NA	2.48E-09	252389	0.3800	0.3800	0.015	0.003	2.98E-06	634014	0.3793	0.3793	0.014	0.002	3.95E-17	4.52E-11
7	132526350	rs4731907	465	yes	unconditional	CHCHD3	intron_variant	T	C	369655	0.4520	0.5480	-0.013	0.002	9.36E-08	NA	1.85E-07	223714	0.4342	0.5658	-0.011	0.003	9.85E-04	593369	0.447	0.5530	-0.012	0.002	3.89E-13	2.31E-09
7	135082953	rs77841106	205		1st conditional round	CNOT4	missense_variant	G	C	374724	0.1040	0.1040	0.023	0.004	3.43E-09	1.80E-09	1.93E-12	251955	0.1090	0.1090	0.021	0.005	2.20E-05	626679	0.106	0.1060	0.022	0.003	9.53E-13	7.30E-15
7	135123060	rs17480616	205		unconditional	CNOT4	missense_variant	G	C	366650	0.0280	0.0280	0.060	0.007	2.31E-17	NA	1.52E-12	252216	0.0299	0.0299	0.054	0.009	5.04E-10	618866	0.0287	0.0287	0.058	0.005	3.90E-26	1.02E-33
7	137600690	rs273957	206		unconditional	CREB3L2	missense_variant	C	T	381625	0.3910	0.6090	0.020	0.002	5.23E-17	NA	3.44E-16	251778	0.3836	0.6164	0.018	0.003	4.85E-09	633403	0.3888	0.6112	0.020	0.002	5.46E-31	7.34E-23
7	140244560	rs2293177	466	yes	unconditional	DENND2A	missense_variant	C	T	379252	0.3240	0.3240	0.015	0.003	7.97E-09	NA	4.30E-09	252062	0.3068	0.3068	0.020	0.003	1.18E-09	631314	0.3161	0.3161	0.017	0.002	6.32E-15	7.92E-19
7	148650634	rs822552	207		unconditional	-	intergenic_variant	C	G	374724	0.2680	0.2680	0.031	0.003	1.49E-31	NA	2.38E-31	252250	0.2590	0.2590	0.042	0.003	2.16E-34	626974	0.2641	0.2641	0.036	0.002	1.89E-56	1.35E-72
7	150667210	rs3807375	208		unconditional	KCNH2	intron_variant	C	T	376010	0.3680	0.3680	0.017	0.003	7.00E-12	NA	8.32E-12	252262	0.3578	0.3578	0.021	0.003	3.80E-11	628272	0.3632	0.3632	0.019	0.002	4.73E-18	2.20E-21
8	13273477	rs7834383	211		unconditional	DLC1	intron_variant	G	T	378823	0.3400	0.3400	0.019	0.002	5.49E-15	NA	3.92E-15	223714	0.3538	0.3538	0.012	0.003	5.87E-04	602537	0.3436	0.3436	0.017	0.002	3.19E-23	3.89E-18
8	23167353	rs1063582	212		1st conditional round	LOXL2	missense_variant	T	G	374783	0.2270	0.7730	-0.026	0.003	1.55E-19	1.51E-18	4.13E-14	252387	0.2408	0.7592	-0.030	0.004	8.45E-18	627170	0.2328	0.7672	-0.028	0.002	4.49E-34	2.25E-36
8	23418444	rs2942202	212		2nd conditional round	SLC25A37	intron_variant	A	C	338374	0.5000	0.5000	-0.019	0.003	3.26E-14	7.71E-09	6.13E-09	223714	0.4972	0.5028	-0.019	0.003	1.05E-08	562088	0.4987	0.5013	-0.019	0.002	1.39E-17	2.07E-12
8	24116304	rs1013209	212		unconditional	-	intergenic_variant	C	T	380346	0.2480	0.2480	-0.028	0.003	3.02E-25	NA	4.63E-24	231003	0.2361	0.2361	-0.029	0.004	1.03E-14	611349	0.2433	0.2433	-0.028	0.002	8.06E-34	5.38E-44
8	30383013	rs2979531	467	yes	unconditional	RBPMS	intron_variant	A	G	372028	0.4900	0.4900	-0.013	0.002	5.24E-08	NA	7.99E-08	223714	0.4853	0.4853	-0.014	0.003	1.64E-05	595742	0.4887	0.4887	-0.013	0.002	6.45E-15	8.03E-11
8	42226805	rs3136797	597	yes	validation	POLB	missense_variant	C	G	332909	0.0178	0.0178	0.0437	0.0092	1.95E-06	NA	NA	233757	0.0210	0.0210	0.0259	0.0104	0.013	566666	0.0192	0.0192	0.0359	0.0069	1.88E-07	1.96E-07
8	57095808	rs10958476	216		1st conditional round	PLAG1	intron_variant	T	C	381625	0.2150	0.2150	0.045	0.003	4.00E-54	1.34E-36	3.82E-37	252082	0.2163	0.2163	0.048	0.004	7.07E-40	633707	0.2155	0.2155	0.046	0.002	8.38E-89	2.76E-89
8	57155598	rs9650315	216		unconditional	-	intergenic_variant	G	T	357882	0.1310	0.1310	-0.061	0.004	2.02E-58	NA	1.96E-41	246566	0.1250	0.1250	-0.064	0.005	3.44E-41	604448	0.1285	0.1285	-0.062	0.003	7.89E-92	4.23E-67
8	78160179	rs7846385	218		unconditional	-	intergenic_variant	T	C	380346	0.2830	0.2830	0.035	0.003	4.99E-38	NA	2.28E-38	252400	0.2814	0.2814	0.043	0.003	1.50E-35	632746	0.2823	0.2823	0.038	0.002	1.18E-64	1.35E-80
8	87568644	rs2304787	468	yes	unconditional	CPNE3	intron_variant	T	G	377104	0.2620	0.7380	0.017	0.003	3.88E-10	NA	1.68E-10	252032	0.2536	0.7464	0.011	0.003	9.06E-04	629136	0.2584	0.7416	0.015	0.002	1.10E-10	4.57E-14
8	116599199	rs2293889	220		unconditional	TRPS1	intron_variant	T	G	380346	0.4150	0.5850	-0.014	0.002	2.26E-09	NA	2.24E-09	251285	0.4298	0.5702	-0.011	0.003	2.73E-04	631631	0.4195	0.5805	-0.013	0.002	4.22E-15	7.71E-12
8	120353267	rs2469997	221		unconditional	-	intergenic_variant	G	C	372631	0.1750	0.8250	0.020	0.003	2.07E-10	NA	1.87E-10	237482	0.1929	0.8071	0.017	0.004	1.26E-05	610113	0.1815	0.8185	0.019	0.002	1.86E-15	3.74E-22
8	120744399	rs956749	221		1st conditional round	TAF2	missense_variant	C	T	381625	0.0660	0.0660	0.026	0.005	1.34E-07	1.50E-07	6.24E-08	252436	0.0671	0.0671	0.021	0.006	5.53E-04	634061	0.0664	0.0664	0.024	0.004	5.35E-10	1.02E-09
8	126490972	rs2954029	223		unconditional	RP11-136O12.2	intron_variant	A	T	367424	0.4650	0.4650	0.014	0.002	2.78E-08	NA	3.68E-08	223714	0.4717	0.4717	0.012	0.003	9.44E-05	591138	0.4669	0.4669	0.014	0.002	1.20E-15	5.72E-12
8	129192271	rs2019960	596	yes	validation	-	intergenic_variant	T	C	379252	0.2086	0.2086	-0.0134	0.0029	4.36E-06	NA	NA	233747	0.2208	0.2208	#####	0.0035	8.03E-09	612999	0.2135	0.2135	-0.016	0.0023	5.45E-13	2.71E-12
8	130760850	rs4144738	224		unconditional	GSDMC	missense_variant	A	G	381625	0.4520	0.4520	-0.031	0.002	4.67E-38	NA	1.39E-37	244760	0.4732	0.4732	-0.036	0.003	9.95E-33	626385	0.4584	0.4584	-0.033	0.002	1.22E-84	2.51E-59
8	135614553	rs112892337	225		1st conditional round	ZFAT	missense_variant	G	C	360530	0.0040	0.0040	0.196	0.019	4.42E-26	2.43E-23	1.12E-23	252151	0.0040	0.0040	0.184	0.024	1.20E-14	612681	0.004	0.0040	0.191	0.015	6.12E-38	1.57E-31
8	135622851	rs75596750	225		2nd conditional round	ZFAT	missense_variant	G	A	377876	0.0010	0.0010	0.255	0.036	1.54E-12	4.42E-14	1.65E-12	252434	0.0023	0.0023	0.339	0.039	5.94E-18	630310	0.0016	0.0016	0.293	0.027	2.05E-28	5.09E-29
8	135637337	rs12680655	225		unconditional	ZFAT	intron_variant	C	G	375498	0.4000	0.4000	-0.031	0.002	3.76E-35	NA	5.12E-21	252327	0.3881	0.3881	-0.035	0.003	3.20E-29	627825	0.3965	0.3965	-0.032	0.002	2.13E-81	4.45E-32
8	135649848	rs12541381	225		4th conditional round	ZFAT	missense_variant	G	A	381625	0.2520	0.2520	-0.027	0.003	8.80E-24	1.45E-10	6.46E-10	252358	0.2515	0.2515	-0.038	0.004	6.75E-28	633983	0.2518	0.2518	-0.032	0.002	2.37E-44	5.85E-29
8	145059425	rs11136344	226		unconditional	PARP10	missense_variant	T	C	381625	0.4210	0.4210	-0.020	0.003	9.29E-15	NA	1.16E-14	251887	0.4242	0.4242	-0.026	0.003	3.29E-16	633512	0.4225	0.4225	-0.023	0.002	1.32E-25	1.25E-29
9	34660864	rs11575580	469	yes	unconditional	IL11RA	missense_variant	C	T	381625	0.0160	0.0160	-0.064	0.009	5.20E-13	NA	5.22E-13	252411	0.0203	0.0203	-0.030	0.011	0.004	634036	0.0178	0.0178	-0.050	0.007	4.01E-13	9.16E-13
9	78542286	rs11144688	231		unconditional	PCSK5	intron_variant	G	A	376901	0.1270	0.1270	-0.043	0.004	1.09E-32	NA	2.61E-33	252342	0.1151	0.1151	-0.049	0.005	2.51E-25	629243	0.122	0.1220	-0.046	0.003	2.33E-50	1.09E-52
9	85126163	rs7866939	470	yes	unconditional	RP11-15B24.5	intron_variant	T	C	364374	0.3250	0.3250	0.014	0.003	1.05E-07	NA	3.61E-08	223714	0.3213	0.3213	0.015	0.003	7.69E-06	588088	0.3234	0.3234	0.015	0.002	1.06E-10	1.59E-15
9	86617265	rs1982151	232		unconditional	RMI1	missense_variant	A	G	381625	0.2650	0.7350	-0.026	0.003	1.19E-21	NA	2.76E-21	252363	0.2615	0.7385	-0.028	0.003	1.45E-16	633988	0.2635	0.7365	-0.027	0.002	5.65E-33	2.14E-41
9	89099362	rs353785	233		unconditional	-	intergenic_variant	T	C	375581	0.4850	0.5150	0.022	0.002	1.84E-19	NA	1.25E-20	223714	0.4911	0.5089	0.033	0.003	2.92E-25	599295	0.4867	0.5133	0.025	0.002	7.84E-50	1.69E-32
9	90883630	rs10746839	234		unconditional	-	intergenic_variant	A	G	378823	0.4230	0.5770	-0.022	0.002	2.37E-20	NA	6.82E-22	223714	0.4282	0.5718	-0.027	0.003	3.82E-16	602537	0.4244	0.5756	-0.023	0.002	2.80E-42	2.14E-28
9	94486321	rs10761129	235		unconditional	ROR2	missense_variant	C	T	363055	0.3260	0.6740	-0.016	0.003	4.39E-10	NA	NA	157150	0.3290	0.6710	-0.019	0.004	1.37E-06	520205	0.3271	0.6729	-0.017	0.002	7.24E-13	5.50E-14
9	95063947	rs921122	235		1st conditional round	NOL8	missense_variant	C	T	189795	0.0390	0.0390	0.041	0.009	2.56E-06	1.60E-08	NA	216647	0.0402	0.0402	0.018	0.008	0.035	406442	0.0397	0.0397	0.029	0.006	3.33E-06	1.40E-07
9	95429120	rs9969804	236		unconditional	IPPK	intron_variant	A	C	381625	0.4400	0.5600	-0.020	0.002	6.22E-16	NA	1.03E-19	252371	0.4380	0.5620	-0.017	0.003	3.92E-08	633996	0.4394	0.5606	-0.019	0.002	5.15E-30	8.49E-17
9	96893945	rs1257763	237		unconditional	-	intergenic_variant	A	G	381625	0.0430	0.9570	-0.047	0.006	2.22E-17	NA	2.86E-14	252362	0.0426	0.9574	-0.060	0.007	3.33E-16	633987	0.0428	0.9572	-0.052	0.005	2.88E-29	3.74E-17
9	98209594	rs357564	237		unconditional	PTCH1	missense_variant	G	A	369802	0.3420	0.3420	-0.037	0.003	1.05E-47	NA	6.84E-21	252185	0.3316	0.3316	-0.037	0.003	1.70E-31	621987	0.3371	0.3371	-0.037	0.002	1.10E-64	3.27E-67
9	98410405	rs10990303	237		1st conditional round	RP11-180I4.1	upstream_gene_variant	C	T	380102	0.2250	0.2250	0.036	0.003	6.78E-36	2.60E-33	2.26E-28	223714	0.2266	0.2266	0.041	0.004	1.08E-25	603816	0.2256	0.2256	0.038	0.002	6.04E-57	3.08E-69
9	101748356	rs2075663	239		unconditional	COL15A1	missense_variant	A	G	381625	0.3860	0.3860	-0.019	0.002	1.22E-14	NA	1.53E-12	251876	0.3697	0.3697	-0.017	0.003	6.17E-08	633501	0.3813	0.3813	-0.019	0.002	8.96E-28	2.46E-18
9	108967088	rs2090409	240		unconditional	-	intergenic_variant	C	A	374496	0.3270	0.3270	-0.023	0.003	2.95E-18	NA	5.45E-17	216759	0.3029	0.3029	-0.020	0.004	1.78E-08	591255	0.317	0.3170	-0.022	0.002	2.28E-21	5.74E-28
9	109599046	rs7027110	240		unconditional	-	intergenic_variant	G	A	380346	0.2280	0.2280	0.029	0.003	1.35E-23	NA	NA	252211	0.2351	0.2351	0.031	0.004	7.99E-18	632557	0.2309	0.2309	0.030	0.002	2.95E-38	1.57E-47
9	111660851	rs2230792	471	yes	unconditional	IKBKAP	missense_variant	C	T	372028	0.1900	0.1900	0.017	0.003	6.35E-08	NA	NA	223714	0.1928	0.1928	0.011	0.004	0.006	595742	0.191	0.1910	0.015	0.002	5.52E-10	5.61E-13
9	113807082	rs1468758	241		unconditional	-	intergenic_variant	C	T	380346	0.2410	0.2410	-0.022	0.003	3.63E-15	NA	2.82E-15	252257	0.2455	0.2455	-0.025	0.004	5.06E-13	632603	0.2429	0.2429	-0.023	0.002	9.55E-25	2.82E-30
9	117050998	rs10982134	242		unconditional	COL27A1	missense_variant	G	A	381625	0.3200	0.3200	-0.014	0.003	1.24E-07	NA	NA	252386	0.3181	0.3181	-0.013	0.003	5.50E-05	634011	0.3191	0.3191	-0.014	0.002	7.10E-10	4.13E-13
9	119134796	rs7869550	243		unconditional	PAPPA	intron_variant	A	G	381625	0.2020	0.2020	-0.033	0.003	2.88E-29	NA	6.67E-31	252320	0.2086	0.2086	-0.036	0.004	2.95E-21	633945	0.2046	0.2046	-0.034	0.002	1.17E-47	3.90E-62
9	119232655	rs10817896	243		1st conditional round	ASTN2	intron_variant	C	T	380102	0.2730	0.2730	-0.018	0.003	1.73E-11	1.31E-11	1.68E-12	223714	0.2781	0.2781	-0.008	0.004	0.038	603816	0.2751	0.2751	-0.014	0.002	2.71E-09	2.00E-10
9	124422403	rs7025486	472	yes	unconditional	DAB2IP	intron_variant	G	A	380346	0.2630	0.2630	0.017	0.003	2.57E-10	NA	3.42E-10	252264	0.2684	0.2684	0.021	0.003	1.37E-09	632610	0.2654	0.2654	0.019	0.002	1.48E-16	8.15E-22
9	133464084	rs7466269	244		unconditional	FUBP3	intron_variant	A	G	372272	0.3570	0.3570	-0.030	0.003	1.46E-32	NA	2.11E-32	252301	0.3522	0.3522	-0.036	0.003	1.02E-29	624573	0.3547	0.3547	-0.033	0.002	3.35E-51	3.59E-61
9	136996067	rs28473627	598		validation	WDR5	upstream_gene_variant	A	G	372028	0.3955	0.6045	-0.0126	0.0025	3.27E-07	NA	NA	205168	0.3744	0.6256	#####	0.0033	9.19E-04	577196	0.3881	0.6119	-0.012	0.002	1.22E-09	1.83E-09
9	139110654	rs12684650	246		unconditional	QSOX2	splice_region_variant	C	T	381625	0.3050	0.3050	-0.030	0.003	8.62E-32	NA	2.86E-14	252325	0.3257	0.3257	-0.030	0.003	3.06E-21	633950	0.3146	0.3146	-0.030	0.002	4.10E-43	3.87E-17
9	139121740	rs12338076	246		2nd conditional round	QSOX2	intron_variant	A	C	356606	0.3330	0.3330	0.027	0.003	2.68E-25	2.34E-08	6.50E-09	252323	0.3380	0.3380	0.032	0.003	5.23E-24	608929	0.3354	0.3354	0.030	0.002	2.08E-41	1.45E-20
9	139368953	rs3812594	246		1st conditional round	SEC16A	missense_variant	G	A	370561	0.2720	0.2720	0.021	0.003	8.92E-14	2.77E-11	5.06E-13	246468	0.2668	0.2668	0.031	0.004	1.55E-18	617029	0.2698	0.2698	0.025	0.002	2.80E-28	1.51E-32
10	4963327	rs12774134	247		unconditional	AKR1C2	downstream_gene_variant	C	T	299046	0.1210	0.1210	-0.036	0.004	6.48E-19	NA	6.55E-19	252378	0.1178	0.1178	-0.045	0.005	1.36E-21	551424	0.1196	0.1196	-0.040	0.003	7.07E-39	5.28E-40
10	12918764	rs7909670	248		unconditional	-	intergenic_variant	C	T	292460	0.4540	0.4540	-0.022	0.003	1.14E-15	NA	NA	244354	0.4339	0.4339	-0.027	0.003	1.08E-17	536814	0.4443	0.4443	-0.024	0.002	2.98E-29	2.52E-32
10	22839628	rs2230469	473	yes	unconditional	PIP4K2A	missense_variant	T	C	367429	0.3170	0.3170	0.014	0.003	5.23E-08	NA	8.66E-08	252204	0.3352	0.3352	0.015	0.003	1.67E-06	619633	0.3255	0.3255	0.015	0.002	2.39E-11	9.53E-14
10	25244392	rs274312	249		unconditional	RP11-165A20.3	upstream_gene_variant	C	T	372028	0.3790	0.3790	0.014	0.002	4.50E-08	NA	7.45E-08	223714	0.3957	0.3957	0.011	0.003	5.43E-04	595742	0.3835	0.3835	0.013	0.002	7.29E-15	6.00E-11
10	63723577	rs10821936	474	yes	unconditional	ARID5B	intron_variant	C	T	380346	0.3190	0.6810	-0.014	0.003	7.33E-08	NA	5.75E-08	252274	0.3292	0.6708	-0.015	0.003	6.63E-06	632620	0.3237	0.6763	-0.014	0.002	8.91E-11	1.84E-08
10	69933921	rs10997975	253		unconditional	MYPN	missense_variant	G	A	381625	0.4950	0.4950	0.021	0.003	3.13E-16	NA	3.68E-15	252097	0.4987	0.5013	0.024	0.003	3.95E-14	633722	0.498	0.4980	0.022	0.002	8.12E-25	3.13E-28
10	70332862	rs12221107	253		1st conditional round	TET1	missense_variant	C	T	334827	0.0930	0.0930	-0.036	0.005	2.60E-15	2.03E-14	2.21E-11	223330	0.0719	0.0719	-0.047	0.006	6.03E-14	558157	0.0848	0.0848	-0.040	0.004	6.27E-25	1.07E-23
10	79580976	rs41274586	475	yes	unconditional	DLG5	missense_variant	G	A	373551	0.0170	0.0170	-0.058	0.009	2.72E-11	NA	5.12E-11	252432	0.0173	0.0173	-0.076	0.012	5.15E-11	625983	0.0171	0.0171	-0.065	0.007	7.66E-20	2.35E-19
10	79616605	rs1248696	542		recessive	DLG5	missense_variant	T	C	457279	0.0881	0.9119	-0.021	0.004	2.59E-07	NA	NA	252310	0.1085	0.8915	-0.016	0.006	0.006	709589	0.0948	0.9052	-0.020	0.003	6.51E-09	5.34E-11
10	93032943	rs2631681	255		unconditional	PCGF5	intron_variant	C	T	380102	0.3250	0.3250	0.025	0.003	8.51E-23	NA	5.33E-23	223714	0.3180	0.3180	0.026	0.003	3.83E-14	603816	0.322	0.3220	0.025	0.002	2.21E-29	1.73E-36
10	97919011	rs41291604	256		unconditional	ZNF518A	missense_variant	A	G	381625	0.0400	0.0400	0.031	0.006	9.94E-08	NA	1.18E-07	252326	0.0396	0.0396	0.022	0.008	0.003	633951	0.0398	0.0398	0.028	0.005	3.91E-09	2.55E-07
10	100017453	rs1983864	476	yes	unconditional	RP11-34A14.3	missense_variant	T	G	381625	0.3420	0.3420	0.017	0.003	7.11E-12	NA	6.88E-12	252368	0.3405	0.3405	0.017	0.003	6.79E-08	633993	0.3413	0.3413	0.017	0.002	5.08E-15	2.53E-20
10	101805442	rs11599750	257		unconditional	CPN1	intron_variant	C	T	381625	0.3810	0.3810	-0.017	0.003	5.65E-12	NA	8.35E-11	251910	0.4018	0.4018	-0.014	0.003	1.13E-05	633535	0.391	0.3910	-0.016	0.002	1.01E-12	3.98E-16
10	102744331	rs11591349	257		unconditional	MRPL43	missense_variant	A	T	341990	0.4520	0.4520	0.018	0.003	4.88E-13	NA	8.50E-13	246525	0.4365	0.4365	0.020	0.003	1.69E-10	588515	0.4444	0.4444	0.019	0.002	2.04E-18	3.01E-21
10	104269217	rs2281880	258		unconditional	SUFU	intron_variant	G	A	380346	0.4620	0.5380	0.025	0.002	4.02E-25	NA	7.76E-26	251940	0.4725	0.5275	0.032	0.003	5.33E-26	632286	0.4652	0.5348	0.027	0.002	2.68E-59	3.04E-42
10	105659826	rs2487999	259		unconditional	OBFC1	missense_variant	T	C	381625	0.0970	0.9030	-0.022	0.004	1.01E-07	NA	NA	252349	0.0944	0.9056	-0.029	0.005	2.75E-08	633974	0.096	0.9040	-0.025	0.003	9.47E-15	1.47E-16
10	114169276	rs3736946	477	yes	unconditional	RP11-324O2.3	missense_variant	A	G	381625	0.1080	0.1080	-0.020	0.004	8.73E-08	NA	1.46E-07	251952	0.1130	0.1130	-0.005	0.005	0.310	633577	0.1101	0.1101	-0.014	0.003	7.35E-06	4.70E-06
10	121429633	rs2234962	260		unconditional	BAG3	missense_variant	T	C	381625	0.2170	0.2170	-0.015	0.003	7.95E-08	NA	8.14E-08	252206	0.2220	0.2220	-0.022	0.004	1.14E-09	633831	0.219	0.2190	-0.018	0.002	1.02E-14	6.95E-19
10	124165615	rs6585827	261		unconditional	PLEKHA1	intron_variant	G	A	381625	0.4910	0.4910	0.016	0.002	3.06E-11	NA	3.00E-11	252264	0.4795	0.4795	0.021	0.003	4.60E-12	633889	0.4876	0.4876	0.018	0.002	1.06E-25	6.13E-19
11	1977552	rs12812	264		1st conditional round	MRPL23	missense_variant	G	A	381625	0.1510	0.1510	0.021	0.003	4.77E-10	6.57E-10	1.62E-11	179620	0.1436	0.1436	0.031	0.005	1.95E-10	561245	0.149	0.1490	0.024	0.003	1.36E-20	8.84E-19
11	2169014	rs10770125	264		unconditional	IGF2-AS	missense_variant	A	G	381625	0.4940	0.4940	0.022	0.002	3.56E-19	NA	1.09E-25	252337	0.4902	0.4902	0.020	0.003	9.19E-11	633962	0.4929	0.4929	0.021	0.002	3.10E-37	2.24E-35
11	2170143	rs1004446	264		2nd conditional round	IGF2	intron_variant	G	A	378383	0.3730	0.3730	0.011	0.002	1.68E-05	5.58E-09	1.95E-10	252422	0.3891	0.3891	0.011	0.003	4.28E-04	630805	0.3777	0.3777	0.011	0.002	6.53E-11	2.82E-14
11	2810731	rs2237886	264		unconditional	KCNQ1	intron_variant	C	T	354682	0.1010	0.1010	0.050	0.004	2.64E-35	NA	1.90E-33	252337	0.1117	0.1117	0.047	0.005	8.69E-23	607019	0.1054	0.1054	0.049	0.003	6.99E-57	4.56E-59
11	8252853	rs110419	478	yes	unconditional	LMO1	intron_variant	A	G	351774	0.4990	0.5010	-0.016	0.002	2.25E-11	NA	1.90E-10	150549	0.4731	0.5269	-0.011	0.004	0.003	502323	0.4929	0.5071	-0.015	0.002	3.39E-17	3.64E-13
11	11986061	rs3206824	479	yes	unconditional	DKK3	missense_variant	T	C	359266	0.2660	0.7340	0.016	0.003	8.77E-09	NA	8.07E-10	252417	0.2617	0.7383	0.013	0.003	1.29E-04	611683	0.2641	0.7359	0.015	0.002	6.37E-11	2.83E-10
11	12698040	rs7926971	265		unconditional	TEAD1	intron_variant	A	G	381625	0.4530	0.4530	0.021	0.002	2.41E-19	NA	4.82E-18	252278	0.4642	0.4642	0.022	0.003	1.63E-13	633903	0.4564	0.4564	0.021	0.002	1.14E-37	1.72E-24
11	17351683	rs757081	266		unconditional	NUCB2	missense_variant	C	G	345647	0.3380	0.3380	0.019	0.003	7.48E-12	NA	4.28E-12	251742	0.3445	0.3445	0.019	0.003	4.43E-09	597389	0.341	0.3410	0.019	0.002	5.96E-18	2.04E-21
11	18645843	rs11024739	480	yes	unconditional	SPTY2D1	intron_variant	C	A	374251	0.2730	0.7270	-0.020	0.003	8.53E-14	NA	1.61E-14	223714	0.2730	0.7270	-0.019	0.004	1.72E-07	597965	0.273	0.7270	-0.020	0.002	2.51E-17	2.25E-23
11	27016360	rs138273386	481	yes	unconditional	FIBIN	missense_variant	G	A	377738	0.0040	0.0040	-0.120	0.017	5.79E-12	NA	7.43E-12	252447	0.0046	0.0046	-0.076	0.024	0.002	630185	0.0042	0.0042	-0.105	0.014	3.26E-14	1.91E-13
11	30394734	rs2183848	543		validation	RP4-710M3.1	downstream_gene_variant	G	A	380102	0.2831	0.2831	-0.0130	0.0026	7.47E-07	NA	NA	205168	0.2788	0.2788	#####	0.0036	6.09E-07	585270	0.2816	0.2816	-0.015	0.0021	3.84E-12	2.27E-12
11	46052575	rs16938437	268		unconditional	PHF21A	intron_variant	C	T	376459	0.0920	0.0920	-0.033	0.004	5.96E-15	NA	5.26E-12	252362	0.0874	0.0874	-0.028	0.005	1.98E-07	628821	0.0904	0.0904	-0.031	0.003	2.37E-22	5.62E-19
11	47663049	rs10838738	269		unconditional	MTCH2	intron_variant	A	G	376105	0.3520	0.3520	-0.026	0.003	8.61E-21	NA	7.37E-18	252262	0.3523	0.3523	-0.029	0.003	9.32E-18	628367	0.3521	0.3521	-0.027	0.002	3.77E-34	1.68E-35
11	61557803	rs102275	482	yes	unconditional	FEN1	non_coding_transcript_exon_variant	T	C	378383	0.3480	0.3480	-0.016	0.003	3.47E-09	NA	2.42E-09	252210	0.3630	0.3630	-0.013	0.003	3.71E-05	630593	0.355	0.3550	-0.015	0.002	1.92E-11	7.10E-15
11	64990041	rs514076	271		unconditional	SLC22A20	non_coding_transcript_exon_variant	G	C	369389	0.2170	0.7830	0.020	0.003	7.36E-11	NA	NA	236803	0.2342	0.7658	0.023	0.004	5.84E-10	606192	0.2237	0.7763	0.021	0.002	1.12E-19	5.05E-19
11	65715204	rs71455793	271		unconditional	TSGA10IP	missense_variant	G	A	381625	0.0390	0.0390	-0.058	0.006	1.82E-21	NA	4.13E-16	252432	0.0459	0.0459	-0.072	0.007	1.41E-23	634057	0.0418	0.0418	-0.064	0.005	1.52E-43	3.30E-19
11	66826160	rs7112925	272		unconditional	RHOD	intron_variant	C	T	380346	0.3500	0.3500	-0.025	0.003	9.92E-22	NA	4.86E-16	252330	0.3607	0.3607	-0.031	0.003	7.89E-23	632676	0.355	0.3550	-0.028	0.002	1.44E-37	2.25E-31
11	68201295	rs3736228	273		unconditional	LRP5	missense_variant	C	T	361382	0.1350	0.1350	-0.028	0.004	4.27E-15	NA	8.15E-15	252399	0.1553	0.1553	-0.034	0.004	2.18E-16	613781	0.1447	0.1447	-0.031	0.003	7.06E-27	1.84E-23
11	68855363	rs3829241	273		unconditional	MIR3164	missense_variant	G	A	381625	0.3920	0.3920	-0.016	0.002	8.64E-11	NA	2.23E-09	252230	0.4121	0.4121	-0.016	0.003	8.03E-08	633855	0.398	0.3980	-0.016	0.002	5.83E-22	8.82E-17
11	75282052	rs634552	274		unconditional	SERPINH1	intron_variant	T	G	380346	0.1390	0.8610	-0.050	0.003	9.97E-49	NA	4.54E-49	252426	0.1374	0.8626	-0.057	0.004	5.07E-39	632772	0.1385	0.8615	-0.052	0.003	3.60E-99	2.68E-64
11	77909014	rs2510044	484	yes	unconditional	USP35	missense_variant	G	A	381625	0.1440	0.1440	0.019	0.004	9.54E-08	NA	NA	252262	0.1341	0.1341	0.011	0.005	0.019	633887	0.1397	0.1397	0.015	0.003	3.25E-07	2.34E-05
11	85436352	rs641393	545	yes	validation	SYTL2	missense_variant	G	A	381625	0.3581	0.6419	0.0125	0.0026	1.23E-06	NA	NA	233289	0.3625	0.6375	0.0177	0.0032	4.03E-08	614914	0.3598	0.6402	0.0145	0.002	5.42E-13	1.60E-13
11	94533444	rs138059525	485	yes	unconditional	AMOTL1	missense_variant	G	A	373551	0.0090	0.0090	-0.096	0.012	9.01E-16	NA	9.06E-16	252470	0.0072	0.0072	-0.089	0.017	3.84E-07	626021	0.0084	0.0084	-0.094	0.010	2.84E-21	2.55E-21
11	116973929	rs12269901	486	yes	unconditional	AP000936.4	intron_variant	G	C	374724	0.2990	0.2990	-0.015	0.003	2.93E-08	NA	4.89E-08	252322	0.2803	0.2803	-0.013	0.003	1.53E-04	627046	0.2908	0.2908	-0.014	0.002	3.99E-10	4.30E-12
11	118574675	rs494459	275		unconditional	-	intergenic_variant	C	T	378383	0.4140	0.4140	0.020	0.002	1.98E-16	NA	3.30E-16	252185	0.4056	0.4056	0.020	0.003	1.54E-10	630568	0.4115	0.4115	0.020	0.002	1.63E-32	2.56E-23
11	128586155	rs654723	278		unconditional	FLI1	intron_variant	C	A	328329	0.3760	0.6240	0.017	0.003	1.76E-10	NA	1.77E-10	252339	0.3815	0.6185	0.016	0.003	5.64E-07	580668	0.3787	0.6213	0.016	0.002	4.28E-14	1.25E-15
12	371410	rs527118	279		unconditional	RP11-283I3.4	intron_variant	T	C	380102	0.1710	0.8290	-0.017	0.003	4.70E-08	NA	7.18E-08	223714	0.1546	0.8454	-0.027	0.005	2.75E-09	603816	0.1659	0.8341	-0.020	0.003	1.07E-15	2.07E-11
12	4374373	rs11063069	487	yes	unconditional	CCND2-AS2	intron_variant	A	G	377876	0.2140	0.2140	-0.015	0.003	1.88E-07	NA	NA	245898	0.2076	0.2076	-0.016	0.004	2.03E-05	623774	0.2115	0.2115	-0.015	0.002	5.15E-11	2.59E-14
12	7548996	rs4072796	488	yes	unconditional	CD163L1	missense_variant	C	G	375498	0.0350	0.0350	0.034	0.006	4.11E-08	NA	2.84E-08	252299	0.0368	0.0368	0.015	0.008	0.067	627797	0.0357	0.0357	0.027	0.005	1.87E-08	2.56E-07
12	11855773	rs2856321	280		unconditional	ETV6	intron_variant	G	A	375774	0.3530	0.6470	-0.026	0.003	6.75E-25	NA	1.87E-25	252369	0.3678	0.6322	-0.028	0.003	8.14E-19	628143	0.36	0.6400	-0.027	0.002	3.16E-35	1.64E-43
12	14587301	rs3213764	282		unconditional	ATF7IP	missense_variant	A	G	381625	0.4870	0.4870	0.015	0.002	4.32E-10	NA	3.69E-11	252070	0.4529	0.4529	0.020	0.003	2.72E-10	633695	0.4769	0.4769	0.016	0.002	2.28E-22	3.17E-16
12	20857467	rs10770705	283		unconditional	SLCO1C1	intron_variant	A	C	359199	0.3220	0.6780	-0.025	0.003	1.70E-22	NA	3.29E-24	251650	0.3504	0.6496	-0.022	0.003	1.48E-12	610849	0.3355	0.6645	-0.024	0.002	9.83E-28	2.62E-33
12	28412372	rs11049488	285		unconditional	CCDC91	missense_variant	G	A	372028	0.2980	0.2980	-0.033	0.003	1.34E-33	NA	2.61E-34	223714	0.3044	0.3044	-0.042	0.004	2.59E-33	595742	0.3007	0.3007	-0.037	0.002	6.73E-59	1.87E-75

12	50901882	rs10876041	489	yes	unconditional	*DIP2B*	intron_variant	T	C	369899	0.3730	0.6270	-0.015	0.003	4.28E-09	NA	6.61E-10	222929	0.3529	0.6471	-0.018	0.003	1.69E-07	592828	0.3642	0.6358	-0.016	0.002	5.56E-13	1.87E-15
12	56636975	rs59626664	287		unconditional	*ANKRD52*	missense_variant	C	G	269461	0.0670	0.0670	0.036	0.006	3.63E-09	NA	NA	243327	0.0733	0.0733	0.043	0.006	3.05E-12	512788	0.0701	0.0701	0.039	0.004	4.84E-20	6.40E-24
12	57146069	rs2277339	287		unconditional	*PRIM1*	missense_variant	T	G	381625	0.1050	0.1050	-0.031	0.004	4.22E-16	NA	4.30E-20	252327	0.1012	0.1012	-0.030	0.005	2.31E-09	633952	0.1035	0.1035	-0.031	0.003	1.32E-22	6.36E-27
12	58138971	rs147996581	288		1st conditional round	*TSPAN31*	missense_variant	G	A	368141	0.0030	0.0030	-0.116	0.022	8.26E-08	3.13E-08	1.23E-08	151101	0.0009	0.0009	-0.268	0.090	0.003	519242	0.0029	0.0029	-0.125	0.021	5.50E-09	9.49E-11
12	58222672	rs4760332	288		unconditional	*CTDSP2*	intron_variant	C	A	376214	0.3220	0.3220	-0.019	0.003	6.55E-13	NA	2.34E-16	223714	0.3321	0.3321	-0.027	0.003	5.05E-15	599928	0.3264	0.3264	-0.022	0.002	3.56E-23	3.19E-34
12	66359752	rs8756	290		unconditional	*HMGA2*	3_prime_UTR_variant	C	A	381625	0.4900	0.5100	-0.052	0.002	2.50E-98	NA	4.72E-46	221612	0.4958	0.5042	-0.055	0.003	1.15E-63	603237	0.4916	0.5084	-0.053	0.002	1.25E-210	1.77E-63
12	66364509	rs12424086	290		1st conditional round	*HMGA2*	downstream_gene_variant	T	C	381625	0.2070	0.2070	-0.048	0.003	1.31E-59	6.92E-13	4.49E-11	252362	0.1971	0.1971	-0.049	0.004	4.67E-37	633987	0.2032	0.2032	-0.048	0.002	7.54E-93	4.82E-49
12	66394664	rs4026608	290		2nd conditional rounc	-	intergenic_variant	C	T	381625	0.3730	0.6270	0.025	0.002	2.73E-24	3.24E-12	2.72E-13	252376	0.3865	0.6135	0.027	0.003	1.95E-18	634001	0.377	0.6230	0.026	0.002	1.57E-52	1.08E-25
12	66546100	rs8793	290		3rd conditional round	*TMBIM4*	missense_variant	A	G	381625	0.4290	0.4290	0.015	0.002	6.34E-11	2.98E-11	7.59E-14	252288	0.4335	0.4335	0.016	0.003	7.01E-08	633913	0.4304	0.4304	0.015	0.002	2.75E-20	2.24E-19
12	69140339	rs61743810	490	yes	unconditional	*SLC35E3*	missense_variant	G	C	375498	0.0220	0.0220	-0.047	0.008	1.13E-09	NA	5.90E-09	241154	0.0229	0.0229	-0.036	0.010	5.11E-04	616652	0.0224	0.0224	-0.043	0.006	1.29E-11	2.63E-11
12	69827658	rs10748128	291		unconditional	-	intergenic_variant	G	T	381625	0.3490	0.3490	0.036	0.003	2.46E-46	NA	3.37E-46	252257	0.3544	0.3544	0.029	0.003	3.26E-19	633882	0.3515	0.3515	0.033	0.002	4.47E-50	1.53E-58
12	90231386	rs17783015	292		unconditional	-	intergenic_variant	C	T	377973	0.1580	0.1580	-0.019	0.003	5.18E-09	NA	4.30E-10	251896	0.1516	0.1516	-0.016	0.004	1.74E-04	629869	0.1558	0.1558	-0.018	0.002	2.18E-13	1.02E-18
12	93976954	rs3825199	293		unconditional	*SOCS2*	3_prime_UTR_variant	A	G	370309	0.2210	0.2210	0.047	0.003	1.75E-58	NA	8.55E-60	251591	0.2234	0.2234	0.059	0.004	2.67E-59	621900	0.222	0.2220	0.052	0.002	2.64E-111	2.05E-148
12	95927762	rs3812813	491	yes	unconditional	*USP44*	missense_variant	T	C	381625	0.4660	0.5340	-0.014	0.002	6.78E-09	NA	4.95E-09	252134	0.4575	0.5425	-0.010	0.003	0.001	633759	0.4634	0.5366	-0.013	0.002	2.09E-14	4.77E-13
12	102368065	rs7978999	294		unconditional	*DRAM1*	intron_variant	T	C	380102	0.4630	0.4630	-0.024	0.002	1.05E-23	NA	9.72E-26	223714	0.4825	0.4825	-0.025	0.003	7.47E-15	603816	0.4685	0.4685	-0.024	0.002	2.26E-46	3.62E-33
12	103077198	rs7296248	294		unconditional	-	intergenic_variant	C	T	350251	0.4930	0.5070	0.016	0.002	1.36E-10	NA	8.22E-10	223714	0.4832	0.5168	0.022	0.003	8.45E-12	573965	0.4902	0.5098	0.018	0.002	2.37E-25	5.15E-17
12	104354173	rs11612024	295		unconditional	*C12orf73*	intron_variant	C	T	372028	0.3070	0.3070	0.018	0.003	2.98E-11	NA	1.66E-13	223714	0.2930	0.2930	0.020	0.004	1.76E-08	595742	0.3011	0.3011	0.019	0.002	2.02E-16	4.32E-25
12	104408832	rs117801489	295		1st conditional round	*GLT8D2*	missense_variant	T	C	381625	0.0170	0.0170	0.053	0.009	8.72E-10	3.00E-11	1.76E-12	252373	0.0276	0.0276	0.062	0.010	5.82E-10	633998	0.0217	0.0217	0.057	0.007	1.60E-17	1.52E-19
12	105606172	rs1196761	492	yes	unconditional	*APPL2*	intron_variant	G	A	369655	0.4780	0.5220	0.013	0.002	4.32E-08	NA	5.67E-08	223714	0.4797	0.5203	0.011	0.003	4.45E-04	593369	0.4785	0.5215	0.013	0.002	1.64E-13	5.03E-12
12	107174646	rs10861661	296		unconditional	*RIC8B*	intron_variant	A	C	346158	0.2300	0.2300	-0.020	0.003	2.58E-11	NA	9.48E-12	251284	0.2353	0.2353	-0.019	0.004	1.19E-07	597442	0.2322	0.2322	-0.020	0.002	1.73E-17	1.32E-25
12	117383320	rs4076700	297		unconditional	*FBXW8*	missense_variant	G	A	375774	0.1540	0.8460	0.018	0.003	6.41E-08	NA	3.86E-08	252128	0.1466	0.8534	0.024	0.004	1.69E-08	627902	0.1515	0.8485	0.020	0.002	3.39E-16	2.63E-24
12	121756084	rs13141	493	yes	unconditional	*ANAPC5*	missense_variant	G	A	381625	0.0090	0.0090	-0.082	0.012	1.09E-11	NA	2.18E-10	248595	0.0107	0.0107	-0.105	0.016	1.44E-11	630220	0.0096	0.0096	-0.091	0.010	1.45E-21	2.88E-17
12	122494809	rs11835818	299		unconditional	*BCL7A*	intron_variant	T	C	370749	0.4740	0.4740	0.018	0.002	6.71E-13	NA	NA	223714	0.4967	0.4967	0.016	0.003	4.30E-07	594463	0.4802	0.4802	0.018	0.002	6.10E-25	1.95E-09
12	123806219	rs1060105	300		unconditional	*SBNO1*	missense_variant	C	T	381625	0.2050	0.2050	0.036	0.003	7.73E-32	NA	1.31E-27	252299	0.2132	0.2132	0.039	0.004	1.53E-24	633924	0.2082	0.2082	0.037	0.002	6.15E-56	8.88E-67
12	124801226	rs1809889	300		unconditional	*FAM101A*	downstream_gene_variant	T	C	353804	0.2790	0.7210	-0.027	0.003	4.90E-22	NA	3.02E-11	223714	0.2771	0.7229	-0.029	0.004	8.06E-16	577518	0.2782	0.7218	-0.028	0.002	1.50E-33	9.45E-40
13	21189941	rs2442455	301		1st conditional round	*RNU2-7P*	missense_variant	G	A	381625	0.1480	0.1480	0.020	0.003	2.88E-09	1.95E-08	5.04E-09	251823	0.1436	0.1436	0.015	0.005	1.03E-03	633448	0.1467	0.1467	0.019	0.003	1.51E-13	3.23E-10
13	21562832	rs2770928	301		unconditional	*LATS2*	missense_variant	C	T	381625	0.1250	0.8750	0.025	0.004	3.42E-12	NA	5.97E-12	251886	0.1132	0.8868	0.037	0.005	1.28E-14	633511	0.1201	0.8799	0.030	0.003	1.88E-22	2.06E-23
13	33147548	rs7332115	303		unconditional	-	intergenic_variant	T	G	377973	0.3790	0.3790	0.016	0.002	3.96E-11	NA	1.35E-11	251508	0.3687	0.3687	0.022	0.003	3.83E-12	629481	0.376	0.3760	0.018	0.002	1.08E-25	3.46E-20
13	33693837	rs9315204	303		unconditional	*STARD13*	intron_variant	C	T	368469	0.2270	0.2270	-0.018	0.003	2.19E-09	NA	7.40E-10	252353	0.2248	0.2248	-0.017	0.004	3.50E-06	620822	0.2261	0.2261	-0.018	0.002	3.40E-14	4.75E-20
13	41109429	rs2755237	550	yes	validation	*AL133318.1*	downstream_gene_variant	A	C	369748	0.1497	0.1497	-0.0161	0.0034	2.76E-06	NA	NA	233775	0.1450	0.1450	#####	0.0043	2.73E-05	603523	0.1479	0.1479	-0.017	0.0027	3.35E-10	7.13E-10
13	50842259	rs2066674	306		1st conditional round	*DLEU1*	intron_variant	G	A	380102	0.0440	0.0440	0.073	0.006	2.33E-37	2.35E-31	3.74E-37	223714	0.0406	0.0406	0.084	0.008	7.02E-25	603816	0.0428	0.0428	0.077	0.005	5.66E-57	1.53E-51
13	51116901	rs3118914	306		unconditional	*DLEU1*	intron_variant	G	T	380346	0.2180	0.2180	-0.051	0.003	1.09E-64	NA	3.16E-70	251989	0.2140	0.2140	-0.055	0.004	1.09E-48	632335	0.2164	0.2164	-0.053	0.002	1.80E-111	6.30E-160
13	51133655	rs279070	306		2nd conditional rounc	*BCMS*	intron_variant	A	G	372028	0.4150	0.4150	0.006	0.002	0.0185	1.57E-11	9.67E-14	223714	0.4127	0.4127	0.009	0.003	0.004	595742	0.4144	0.4144	0.007	0.002	5.12E-05	8.90E-18
13	80717156	rs1359790	309		unconditional	-	intergenic_variant	G	A	377104	0.2760	0.2760	0.017	0.003	4.38E-10	NA	4.39E-10	252357	0.2871	0.2871	0.014	0.003	3.39E-05	629461	0.281	0.2810	0.016	0.002	2.85E-12	1.25E-15
13	92024574	rs7319045	310		unconditional	-	intergenic_variant	A	G	380346	0.3910	0.6090	-0.024	0.002	2.39E-22	NA	2.43E-22	252322	0.3752	0.6248	-0.030	0.003	2.97E-21	632668	0.3864	0.6136	-0.026	0.002	3.19E-52	2.44E-38
13	101708310	rs2044117	549	yes	validation	*NALCN*	intron_variant	G	A	377104	0.2306	0.2306	-0.0142	0.0028	5.06E-07	NA	NA	233743	0.2339	0.2339	#####	0.0037	0.004	610847	0.2319	0.2319	-0.013	0.0022	1.05E-08	1.18E-08
14	23313633	rs17880989	313		1st conditional round	*MMP14*	missense_variant	G	A	373551	0.0270	0.0270	0.041	0.007	1.72E-08	4.60E-08	7.15E-08	247993	0.0292	0.0292	0.052	0.009	7.81E-09	621544	0.0278	0.0278	0.045	0.006	3.27E-16	8.21E-13
14	23761094	rs12050260	313		unconditional	*PPP1R3E*	intron_variant	T	C	360151	0.3510	0.6490	0.016	0.003	1.78E-10	NA	2.24E-10	223714	0.3555	0.6445	0.016	0.003	1.29E-06	583865	0.3531	0.6469	0.016	0.002	5.89E-13	5.36E-14
14	24707479	rs34354104	314		1st conditional round	*GMPR2*	missense_variant	G	A	381625	0.0480	0.0480	0.045	0.005	3.67E-16	3.64E-09	4.89E-09	252386	0.0503	0.0503	0.047	0.007	1.34E-11	634011	0.0488	0.0488	0.046	0.004	2.13E-29	2.45E-19
14	24830850	rs1950500	314		unconditional	*NFATC4*	upstream_gene_variant	T	C	378383	0.2880	0.7120	-0.030	0.003	6.25E-30	NA	1.41E-22	251117	0.2990	0.7010	-0.029	0.003	7.59E-18	629500	0.2929	0.7071	-0.029	0.002	1.00E-39	7.79E-37
14	45403699	rs117295933	551	yes	validation	*KLHL28*	missense_variant	C	A	348676	0.0161	0.0161	-0.0451	0.0094	1.55E-06	NA	NA	233879	0.0246	0.0246	#####	0.0103	4.13E-04	582555	0.02	0.0200	-0.041	0.0069	3.05E-09	3.89E-09
14	55265828	rs8022503	317		unconditional	-	intergenic_variant	T	C	380102	0.4500	0.5500	0.018	0.002	4.96E-14	NA	1.39E-13	223714	0.4362	0.5638	0.018	0.003	4.35E-08	603816	0.4462	0.5538	0.018	0.002	5.98E-26	8.83E-19
14	61072875	rs10483727	319		unconditional	*RP11-1042B17.2*	upstream_gene_variant	T	C	375774	0.3900	0.6100	-0.036	0.003	2.39E-43	NA	1.37E-42	252120	0.3955	0.6045	-0.042	0.003	2.32E-40	627894	0.3926	0.6074	-0.039	0.002	2.34E-71	1.78E-86
14	63855760	rs6573513	552	yes	validation	*PPP2R5E*	intron_variant	C	T	376860	0.0881	0.0881	-0.0185	0.0042	1.09E-05	NA	NA	205168	0.0850	0.0850	#####	0.0060	9.77E-04	582028	0.0871	0.0871	-0.019	0.0034	3.92E-08	7.18E-08
14	65475540	rs4466998	320		unconditional	*FNTB*	intron_variant	C	A	381625	0.4900	0.5100	-0.013	0.002	1.77E-07	NA	NA	252167	0.4772	0.5228	-0.017	0.003	1.05E-08	633792	0.4861	0.5139	-0.014	0.002	9.18E-18	1.95E-12
14	68785077	rs8017304	553		validation	*RAD51B*	intron_variant	G	A	380102	0.3710	0.6290	0.0125	0.0025	7.01E-07	NA	NA	205168	0.3572	0.6428	0.0078	0.0034	0.022	585270	0.3661	0.6339	0.0108	0.002	8.89E-08	4.35E-08
14	70633411	rs41286548	495	yes	unconditional	*SLC8A3*	missense_variant	C	T	373551	0.0210	0.0210	-0.054	0.008	2.49E-11	NA	2.19E-11	252367	0.0261	0.0261	-0.045	0.009	2.02E-06	625918	0.0231	0.0231	-0.050	0.006	2.03E-16	6.69E-15
14	74990746	rs862034	323		unconditional	*LTBP2*	intron_variant	A	G	378383	0.3670	0.6330	0.026	0.002	1.05E-26	NA	2.16E-28	252207	0.3628	0.6372	0.025	0.003	3.67E-15	630590	0.3658	0.6342	0.026	0.002	4.08E-52	1.86E-42
14	75347585	rs10083386	323		1st conditional round	*DLST*	upstream_gene_variant	C	A	380102	0.4640	0.4640	0.015	0.002	7.34E-10	2.56E-10	4.22E-11	223714	0.4436	0.4436	0.019	0.003	3.83E-09	603816	0.4584	0.4584	0.016	0.002	2.61E-21	1.02E-18
14	76156609	rs2303345	496	yes	unconditional	*TTLL5*	missense_variant	C	T	292029	0.3300	0.6700	-0.017	0.003	1.60E-08	NA	NA	243903	0.3486	0.6514	-0.021	0.003	1.63E-10	535932	0.3386	0.6614	-0.019	0.002	1.85E-17	1.24E-21
14	79945162	rs10146997	497	yes	unconditional	*NRXN3*	intron_variant	A	G	380346	0.2160	0.2160	0.016	0.003	4.07E-08	NA	4.84E-08	252371	0.2189	0.2189	0.012	0.004	0.001	632717	0.2172	0.2172	0.014	0.002	7.24E-10	1.09E-12
14	92427222	rs7153027	324		unconditional	-	intergenic_variant	A	C	356196	0.4240	0.4240	-0.031	0.003	1.49E-32	NA	9.31E-33	252232	0.4362	0.4362	-0.028	0.003	2.24E-19	608428	0.4299	0.4299	-0.030	0.002	1.22E-42	4.01E-49
14	94844947	rs28929474	498	yes	unconditional	*SERPINA1*	missense_variant	C	T	365451	0.0180	0.0180	0.124	0.009	1.39E-45	NA	1.98E-45	245144	0.0193	0.0193	0.139	0.011	2.50E-34	610595	0.0185	0.0185	0.130	0.007	1.72E-75	3.13E-76
14	101349454	rs41286560	499	yes	unconditional	*MIR432*	missense_variant	G	T	381625	0.0240	0.0240	-0.050	0.007	1.17E-11	NA	1.50E-11	252363	0.0279	0.0279	-0.033	0.009	2.12E-04	633988	0.0255	0.0255	-0.044	0.006	2.50E-15	4.72E-13
14	102792631	rs7158139	325		unconditional	*ZNF839*	missense_variant	G	A	376860	0.1760	0.1760	-0.020	0.003	2.90E-10	NA	3.35E-10	252423	0.1754	0.1754	-0.017	0.004	1.72E-05	629283	0.1758	0.1758	-0.019	0.002	2.47E-15	9.41E-22
15	34520687	rs116858574	554	yes	validation	*EMC4*	missense_variant	T	C	381625	0.0138	0.0138	0.0470	0.0097	1.16E-06	NA	NA	229869	0.0144	0.0144	0.0283	0.0124	0.022	611494	0.014	0.0140	0.0399	0.0076	1.60E-07	1.58E-07
15	41689232	rs1899	327		unconditional	*NDUFAF1*	missense_variant	C	T	369748	0.2610	0.2610	-0.018	0.003	3.07E-10	NA	2.47E-10	222018	0.2581	0.2581	-0.018	0.004	2.39E-06	591766	0.2598	0.2598	-0.018	0.002	2.31E-14	1.55E-15
15	44153571	rs150494621	556	yes	validation	*Y_RNA*	missense_variant	C	T	381625	0.0075	0.0075	0.0630	0.0131	1.56E-06	NA	NA	227404	0.0143	0.0143	0.0538	0.0150	3.42E-04	609029	0.0105	0.0105	0.059	0.0099	2.32E-09	9.03E-09
15	50932357	rs56170748	329		unconditional	*TRPM7*	intron_variant	C	T	380102	0.4890	0.5110	0.013	0.002	6.55E-08	NA	NA	223714	0.4926	0.5074	0.016	0.003	7.55E-07	603816	0.49	0.5100	0.014	0.002	4.23E-16	7.11E-12
15	51530495	rs16964211	329		unconditional	*CYP19A1*	intron_variant	G	A	260475	0.0540	0.0540	-0.052	0.006	1.58E-16	NA	4.72E-14	246319	0.0418	0.0418	-0.046	0.008	2.33E-09	506794	0.0495	0.0495	-0.050	0.005	7.76E-26	NA
15	60781513	rs3743266	500	yes	unconditional	*RORA*	3_prime_UTR_variant	T	C	377104	0.3170	0.3170	-0.015	0.003	5.76E-09	NA	2.36E-09	252160	0.3234	0.3234	-0.015	0.003	3.27E-06	629264	0.32	0.3200	-0.015	0.002	8.50E-12	1.25E-12
15	62380259	rs7178424	330		unconditional	*NPM1P47*	upstream_gene_variant	C	T	375505	0.4560	0.4560	-0.020	0.003	1.52E-14	NA	7.75E-15	252255	0.4559	0.4559	-0.024	0.003	4.59E-15	627760	0.456	0.4560	-0.022	0.002	1.26E-24	7.20E-31
15	65916527	rs3743171	501	yes	unconditional	*SLC24A1*	missense_variant	A	T	375498	0.1880	0.1880	0.020	0.003	4.95E-11	NA	4.42E-11	252165	0.1844	0.1844	0.020	0.004	5.46E-07	627663	0.1867	0.1867	0.020	0.002	7.53E-17	3.61E-23
15	67528374	rs7173826	332		unconditional	*AAGAB*	missense_variant	T	G	381625	0.3320	0.3320	-0.013	0.003	1.36E-07	NA	NA	252164	0.3314	0.3314	-0.011	0.003	4.78E-04	633789	0.3317	0.3317	-0.012	0.002	2.90E-08	1.02E-08
15	70048157	rs10152591	333		1st conditional round	-	regulatory_region_variant	A	C	347130	0.0920	0.0920	-0.047	0.004	2.25E-27	1.92E-25	6.48E-28	252144	0.1003	0.1003	-0.045	0.005	2.87E-19	599274	0.0952	0.0952	-0.046	0.003	1.92E-49	2.14E-52
15	70364352	rs975210	333		unconditional	*TLE3*	intron_variant	G	A	375581	0.1740	0.1740	0.037	0.003	1.63E-31	NA	3.34E-30	223714	0.1880	0.1880	0.034	0.004	8.72E-17	599295	0.1789	0.1789	0.036	0.002	5.51E-50	1.15E-71
15	72462255	rs34815962	334		unconditional	*GRAMD2*	missense_variant	C	T	359848	0.0190	0.0190	0.073	0.009	8.72E-17	NA	4.62E-17	252351	0.0227	0.0227	0.074	0.010	3.66E-13	612199	0.0207	0.0207	0.073	0.007	1.28E-27	3.76E-27
15	74229065	rs893817	335		1st conditional round	*LOXL1*	intron_variant	G	A	381625	0.3480	0.6520	-0.023	0.002	1.29E-19	1.10E-16	5.07E-19	252330	0.3639	0.6361	-0.025	0.003	2.96E-15	633955	0.3526	0.6474	-0.024	0.002	3.59E-44	4.82E-32
15	74336633	rs5742915	335		unconditional	*PML*	missense_variant	T	C	381625	0.4510	0.4510	0.031	0.002	7.35E-38	NA	3.14E-35	252302	0.4621	0.4621	0.037	0.003	6.53E-34	633927	0.4543	0.4543	0.033	0.002	1.02E-85	1.33E-55
15	75755467	rs4886707	502	yes	unconditional	*PTPN9*	downstream_gene_variant	C	T	368469	0.2490	0.2490	0.017	0.003	2.07E-09	NA	6.04E-09	252329	0.2430	0.2430	0.022	0.004	2.72E-10	620798	0.2465	0.2465	0.019	0.002	4.33E-17	3.17E-20
15	77335891	rs11636648	503	yes	unconditional	*TSPAN3*	3_prime_UTR_variant	C	T	376860	0.3360	0.6640	-0.017	0.003	2.27E-10	NA	1.22E-07	223714	0.3368	0.6632	-0.015	0.003	1.93E-05	600574	0.3363	0.6637	-0.016	0.002	1.49E-12	3.30E-16
15	84573041	rs7183263	338		unconditional	*ADAMTSL3*	intron_variant	T	G	380346	0.4820	0.5180	0.049	0.003	3.78E-80	NA	2.50E-73	252302	0.4896	0.5104	0.049	0.003	1.67E-55	632648	0.4857	0.5143	0.049	0.002	1.36E-113	4.74E-140
15	85635890	rs8032301	339		unconditional	*PDE8A*	intron_variant	T	C	380102	0.4380	0.4380	0.014	0.002	2.55E-09	NA	NA	223714	0.4190	0.4190	0.013	0.003	5.02E-05	603816	0.4327	0.4327	0.014	0.002	6.15E-16	1.40E-07
15	86278479	rs16943741	504		unconditional	*AKAP13*	intron_variant	A	G	373551	0.4870	0.5130	-0.016	0.002	1.65E-10	NA	NA	252264	0.4699	0.5301	-0.019	0.003	4.16E-10	625815	0.4819	0.5181	-0.017	0.002	4.88E-24	2.53E-21
15	89345947	rs8028537	340		2nd conditional rounc	*ACAN*	upstream_gene_variant	A	G	380102	0.4880	0.4880	0.030	0.002	1.92E-34	1.05E-28	5.60E-32	223714	0.4850	0.4850	0.036	0.003	3.22E-28	603816	0.4872	0.4872	0.032	0.002	7.94E-77	7.44E-54
15	89386652	rs34949187	430		4th conditional round	*ACAN*	missense_variant	G	A	372272	0.1740	0.1740	-0.029	0.003	1.67E-19	2.59E-19	7.47E-21	252181	0.1828	0.1828	-0.033	0.004	1.70E-17	624453	0.1773	0.1773	-0.031	0.002	8.53E-38	1.09E-53
15	89388905	rs16942341	340		unconditional	*ACAN*	synonymous_variant	C	T	379977	0.0260	0.0260	-0.129	0.007	4.30E-72	NA	1.35E-66	252436	0.0275	0.0275	-0.146	0.009	1.08E-56	632413	0.0266	0.0266	-0.135	0.006	3.79E-130	1.73E-98
15	89398605	rs938608	340		1st conditional round	*ACAN*	missense_variant	G	T	348325	0.3620	0.6380	-0.026	0.003	6.57E-21	2.89E-37	9.97E-08	248131	0.3499	0.6501	-0.023	0.003	1.93E-12	596456	0.3565	0.6435	-0.025	0.002	7.36E-29	2.20E-15
15	89415247	rs3817428	340		3rd conditional round	*ACAN*	missense_variant	C	G	374724	0.2740	0.2740	-0.039	0.003	4.05E-47	9.61E-14	7.03E-25	252164	0.2708	0.2708	-0.041	0.003	3.08E-33	626888	0.2726	0.2726	-0.040	0.002	4.66E-70	7.47E-43
15	89424870	rs141308595	340		5th conditional round	*HAPLN3*	missense_variant	G	T	377055	0.0010	0.0010	-0.267	0.037	2.84E-13	1.18E-11	2.79E-12	252428	0.0021	0.0021	-0.234	0.035	2.43E-11	629483	0.0016	0.0016	-0.250	0.025	1.02E-22	1.06E-20
15	90903311	rs2589957	505	yes	unconditional	*ZNF774*	missense_variant	A	G	381625	0.4680	0.4680	0.013	0.002	7.33E-08	NA	3.13E-09	252231	0.4623	0.4623	0.015	0.003	5.84E-07	633856	0.4663	0.4663	0.014	0.002	2.91E-16	1.96E-07
15	94570578	rs899609	341		unconditional	*LINC01581*	intron_variant	T	C	380102	0.4110	0.5890	0.015	0.002	3.16E-10	NA	1.68E-09	223714	0.4079	0.5921	0.010	0.003	3.35E-03	603816	0.4102	0.5898	0.014	0.002	2.20E-15	1.02E-10
15	99194896	rs2871865	342		unconditional	*IGF1R*	intron_variant	C	G	375498	0.1050	0.1050	-0.057	0.004	1.27E-47	NA	3.48E-48	252379	0.1127	0.1127	-0.061	0.005	1.93E-37	627877	0.1082	0.1082	-0.059	0.003	1.30E-81	3.76E-84
15	100516472	rs11634977	343		2nd conditional rounc	*ADAMTS17*	non_coding_transcript_exon_variant	G	A	327132	0.3240	0.6760	0.027	0.003	1.68E-20	2.77E-29	NA	223714	0.3321	0.6679	0.024	0.003	2.92E-12	550846	0.3275	0.6725	0.026	0.002	5.93E-30	6.09E-69
15	100692953	rs72755233	343		unconditional	*ADAMTS17*	missense_variant	G	A	377876	0.1100	0.1100	-0.092	0.004	7.09E-130	NA	1.38E-143	252354	0.1187	0.1187	-0.092	0.005	5.65E-86	630230	0.1137	0.1137	-0.092	0.003	4.96E-201	1.91E-234
15	100786271	rs4533267	343		1st conditional round	*ADAMTS17*	intron_variant	A	G	369899	0.2810	0.7190	-0.032	0.003	3.00E-32	8.43E-35	4.75E-37	252361	0.2861	0.7139	-0.034	0.003	2.63E-24	622260	0.2833	0.7167	-0.033	0.002	3.96E-49	1.88E-70
15	101717888	rs62621399	343		1st conditional round	*CHSY1*	missense_variant	C	T	381625	0.1470	0.1470	0.025	0.003	9.94E-14	7.45E-10	4.33E-10	252358	0.1440	0.1440	0.024	0.004	2.67E-08	633983	0.146	0.1460	0.025	0.003	1.28E-23	1.94E-11
15	101718239	rs62621400	343		unconditional	*CHSY1*	missense_variant	C	G	375498	0.0600	0.0600	-0.062	0.005	2.52E-35	NA	1.19E-30	252328	0.0553	0.0553	-0.066	0.007	7.54E-24	627826	0.0583	0.0583	-0.064	0.004	2.23E-57	2.57E-56
16	624114	rs2071979	344		unconditional	*PIGQ*	missense_variant	A	G	360151	0.4310	0.4310	0.022	0.003	5.17E-17	NA	1.52E-16	223714	0.4495	0.4495	0.020	0.003	7.16E-10	583865	0.4394	0.4394	0.021	0.002	1.06E-21	3.58E-09
16	774692	rs2071950	344		1st conditional round	*CCDC78*	missense_variant	A	G	313052	0.4880	0.4880	0.022	0.003	3.08E-16	1.37E-07	NA	246190	0.4817	0.4817	0.023	0.003	1.85E-13	559242	0.4849	0.4849	0.022	0.002	2.81E-25	5.20E-13
16	2140680	rs10960	345		unconditional	*PKD1*	missense_variant	T	C	372384	0.1820	0.1820	-0.024	0.003	1.90E-14	NA	5.11E-14	246544	0.1681	0.1681	-0.035	0.004	7.84E-17	618928	0.1772	0.1772	-0.028	0.002	6.07E-30	3.41E-44
16	2260567	rs26857	345		1st conditional round	*MLST8*	missense_variant	C	T	269592	0.4950	0.5050	0.017	0.003	4.88E-09	1.05E-08	NA	203511	0.4709	0.4709	0.018	0.003	1.36E-07	473103	0.4902	0.4902	0.018	0.002	1.03E-14	2.59E-20
16	4812705	rs61733564	345		unconditional	*ZNF500*	missense_variant	A	G	357633	0.0320	0.0320	0.056	0.007	8.61E-17	NA	2.11E-16	252328	0.0316	0.0316	0.044	0.009	2.34E-07	609961	0.0318	0.0318	0.051	0.005	2.89E-21	1.12E-23
16	14388305	rs1659127	346		unconditional	-	intergenic_variant	G	A	314333	0.3460	0.3460	0.025	0.003	1.21E-18	NA	NA	244751	0.3345	0.3345	0.027	0.003	2.68E-16	559084	0.3407	0.3407	0.026	0.002	1.69E-31	2.53E-40
16	15131974	rs1136001	506	yes	unconditional	*NTAN1*	missense_variant	G	T	359848	0.3030	0.3030	-0.015	0.003	8.23E-08	NA	1.05E-07	252056	0.2870	0.2870	-0.015	0.003	1.01E-05	611904	0.296	0.2960	-0.015	0.002	2.55E-11	4.91E-16
16	20748331	rs11074471	347		unconditional	*THUMPD1*	missense_variant	C	A	381625	0.1390	0.1390	-0.019	0.004	1.83E-07	NA	1.82E-07	252053	0.1288	0.1288	-0.018	0.005	2.26E-04	633678	0.1348	0.1348	-0.019	0.003	1.85E-09	1.58E-10
16	24804954	rs113388806	507	yes	unconditional	*TNRC6A*	missense_variant	A	T	367424	0.0400	0.0400	0.036	0.006	1.08E-09	NA	1.56E-09	221673	0.0471	0.0471	0.041	0.008	1.65E-07	589097	0.0426	0.0426	0.038	0.005	1.90E-15	2.65E-13
16	30072530	rs9928448	348		unconditional	*ALDOA*	intron_variant	T	C	381625	0.4610	0.4610	0.016	0.002	1.58E-11	NA	8.35E-12	252314	0.4614	0.4614	0.017	0.003	2.53E-08	633939	0.4611	0.4611	0.016	0.002	1.94E-22	6.49E-16
16	31474091	rs141923065	509	yes	unconditional	*ARMC5*	splice_acceptor_variant	A	G	373551	0.0060	0.0060	0.104	0.015	5.88E-12	NA	3.68E-12	244737	0.0133	0.0133	0.057	0.018	0.001	618288	0.0091	0.0091	0.084	0.011	1.62E-13	7.35E-09
16	47684830	rs34667348	510	yes	unconditional	*PHKB*	missense_variant	C	A	381625	0.0050	0.0050	0.121	0.016	3.96E-14	NA	3.97E-14	252421	0.0053	0.0053	0.033	0.020	0.104	634046	0.0051	0.0051	0.088	0.013	3.43E-12	1.30E-11
16	67409180	rs8052655	351		unconditional	*LRRC36*	missense_variant	G	A	365995	0.0430	0.0430	-0.054	0.006	1.08E-18	NA	2.56E-17	252362	0.0432	0.0432	-0.055	0.008	3.91E-13	618357	0.0431	0.0431	-0.054	0.005	6.40E-31	1.24E-28
16	67470505	rs140385822	351		2nd conditional rounc	*ATP6V0D1*	missense_variant	G	A	366511	0.0020	0.0020	-0.148	0.028	1.27E-07	9.35E-08	5.71E-08	252413	0.0022	0.0022	-0.124	0.035	3.38E-04	618924	0.0021	0.0021	-0.139	0.022	1.97E-10	4.47E-11
16	69547741	rs4783718	352		unconditional	-	regulatory_region_variant	T	C	377729	0.3970	0.6030	0.027	0.003	3.58E-26	NA	1.20E-25	223714	0.4091	0.5909	0.023	0.003	7.84E-12	601443	0.4024	0.5976	0.025	0.002	1.86E-29	8.53E-31
16	70548297	rs3931036	512	yes	unconditional	*COG4*	missense_variant	G	A	381625	0.0630	0.9370	-0.029	0.005	4.72E-09	NA	NA	252345	0.0833	0.9167	-0.031	0.006	3.82E-08	633970	0.072	0.9280	-0.030	0.004	1.37E-15	1.04E-06
16	71988106	rs9921412	353		unconditional	*PKD1L3*	missense_variant	C	T	351178	0.2620	0.7380	-0.020	0.003	9.26E-11	NA	5.34E-11	229960	0.2615	0.7385	-0.012	0.004	0.001	581138	0.2618	0.7382	-0.017	0.002	4.91E-13	3.84E-15
16	73793552	rs2063506	557	yes	validation	-	intergenic_variant	A	G	380893	0.4549	0.5451	-0.0105	0.0024	9.27E-06	NA	NA	232437	0.4765	0.5235	#####	0.0030	8.66E-05	613330	0.4633	0.5367	-0.011	0.0019	3.34E-09	3.54E-08
16	78343690	rs9927661	558	yes	recessive	*WWOX*	intron_variant	G	A	443983	0.3537	0.3537	-0.023	0.005	3.01E-07	NA	NA	217993	0.3423	0.3423	-0.017	0.007	0.013	661976	0.3501	0.3501	0.021	0.004	1.37E-08	7.49E-08
16	82203758	rs2303262	355		unconditional	*MPHOSPH6*	missense_variant	C	T	381625	0.2150	0.7850	-0.019	0.003	1.80E-11	NA	9.72E-12	252441	0.2273	0.7727	-0.019	0.004	1.14E-07	634066	0.22	0.7800	-0.019	0.002	1.45E-16	1.49E-21
16	84900645	rs149615348	356		2nd conditional rounc	*CRISPLD2*	missense_variant	G	A	381625	0.0070	0.0070	-0.095	0.014	9.13E-12	2.67E-11	6.00E-12	248440	0.0083	0.0083	-0.098	0.017	4.34E-09	630065	0.0076	0.0076	-0.096	0.011	2.92E-19	4.61E-18
16	84902472	rs148934412	356		1st conditional round	*CRISPLD2*	missense_variant	G	A	381625	0.0010	0.0010	-0.297	0.040	7.75E-14	1.86E-14	3.45E-14	164882	0.0009	0.0009	-0.317	0.058	3.49E-08	546507	0.001	0.0010	-0.304	0.033	2.36E-20	1.16E-21
16	84987679	rs2326458	356		unconditional	-	intergenic_variant	C	A	380346	0.2640	0.7360	-0.021	0.003	2.68E-15	NA	1.81E-15	252431	0.2559	0.7441	-0.026	0.004	2.70E-14	632777	0.2605	0.7395	-0.023	0.002	9.02E-25	7.72E-33
16	88798919	rs201226914	358		unconditional	*PIEZO1*	missense_variant	G	T	369776	0.0020	0.0020	-0.187	0.027	5.27E-12	NA	1.95E-10	174051	0.0015	0.0015	-0.241	0.043	1.99E-08	543827	0.0019	0.0019	-0.202	0.023	8.68E-19	2.09E-16
16	88804734	rs7184427	358		1st conditional round	*RP5-1142A6.7*	missense_variant	A	G	302165	0.1480	0.8520	0.024	0.004	1.57E-10	5.73E-08	NA	239331	0.1490	0.8510	0.033	0.005	2.12E-13	541496	0.1484	0.8516	0.028	0.003	7.74E-21	2.73E-22
16	88853729	rs837763	358		2nd conditional rounc	-	intergenic_variant	C	T	365261	0.4370	0.5630	-0.009	0.002	1.68E-04	5.84E-09	4.98E-08	244717	0.4447	0.5553	-0.008	0.003	0.006	609978	0.4393	0.5607	-0.009	0.002	1.44E-07	7.71E-11
16	89704365	rs1126464	358		unconditional	*DPEP1*	missense_variant	G	C	347585	0.2410	0.2410	0.023	0.003	4.85E-15	NA	1.70E-14	238336	0.2423	0.2423	0.026	0.004	3.46E-12	585921	0.2415	0.2415	0.024	0.002	4.74E-25	5.46E-30
17	1673276	rs1136287	513	yes	unconditional	*SERPINF1*	missense_variant	C	T	381625	0.3580	0.6420	-0.014	0.003	3.13E-08	NA	1.48E-08	246253	0.3529	0.6471	-0.021	0.003	6.47E-11	627878	0.3556	0.6444	-0.017	0.002	3.79E-15	1.16E-17
17	7363088	rs9217	360		unconditional	*CHRNB1*	3_prime_UTR_variant	T	C	378383	0.3680	0.3680	0.030	0.003	7.64E-32	NA	3.78E-32	250184	0.3631	0.3631	0.038	0.003	2.65E-32	628567	0.3657	0.3657	0.034	0.002	2.33E-53	5.39E-65
17	17409560	rs7946	559	yes	recessive	*PEMT*	missense_variant	C	T	369280	0.2692	0.7308	0.019	0.003	2.77E-08	NA	NA	221787	0.2491	0.7509	0.012	0.005	0.013	591067	0.2627	0.7373	0.017	0.003	1.67E-09	2.24E-08
17	21284223	rs4640244	362		unconditional	*KCNJ12*	intron_variant	A	G	380346	0.3980	0.3980	-0.020	0.002	8.81E-17	NA	2.14E-15	252314	0.3980	0.3980	-0.029	0.003	3.61E-21	632660	0.398	0.3980	-0.023	0.002	1.08E-41	2.73E-30
17	27889986	rs542939	363		unconditional	*TP53I13*	missense_variant	C	T	372789	0.3430	0.6570	0.025	0.003	3.72E-23	NA	4.77E-14	252344	0.3509	0.6491	0.031	0.003	1.51E-22	625133	0.3467	0.6533	0.028	0.002	2.42E-37	6.76E-29
17	29161358	rs3816780	364		1st conditional round	*ATAD5*	missense_variant	C	T	359266	0.1060	0.1060	0.003	0.004	0.424	1.38E-19	NA	252378	0.1076	0.1076	0.003	0.005	0.488	611644	0.1066	0.1066	0.003	0.003	3.08E-01	1.89E-40
17	29247715	rs3760318	364		unconditional	*ADAP2*	intron_variant	G	A	378383	0.3730	0.3730	-0.045	0.003	2.72E-71	NA	1.78E-78	252278	0.3728	0.3728	-0.053	0.003	2.26E-62	630661	0.3729	0.3729	-0.049	0.002	1.13E-110	1.05E-156
17	36922196	rs1043515	365		unconditional	*PIP4K2B*	3_prime_UTR_variant	A	G	326741	0.4430	0.5570	0.025	0.003	4.06E-22	NA	2.78E-24	246482	0.4446	0.5554	0.023	0.003	2.46E-14	573223	0.4438	0.5562	0.024	0.002	1.51E-29	4.74E-36
17	38545193	rs13695	366		unconditional	*TOP2A*	3_prime_UTR_variant	C	T	369030	0.2560	0.2560	0.018	0.003	8.35E-11	NA	2.14E-11	250911	0.2646	0.2646	0.020	0.004	1.84E-08	619941	0.2597	0.2597	0.019	0.002	2.05E-16	1.88E-23
17	38640744	rs2290207	366		1st conditional round	*TNS4*	missense_variant	C	T	379252	0.2510	0.2510	0.015	0.003	1.37E-07	1.70E-07	1.13E-07	252317	0.2586	0.2586	0.007	0.003	0.040	631569	0.2543	0.2543	0.012	0.002	3.15E-07	1.13E-12
17	40725799	rs2292751	367		unconditional	*PSMC3IP*	non_coding_transcript_exon_variant	C	T	372028	0.4480	0.5520	0.017	0.003	1.30E-11	NA	2.34E-13	223714	0.4140	0.5860	0.009	0.003	0.006	595742	0.4326	0.5674	0.013	0.002	1.49E-09	5.32E-11
17	43216281	rs4986172	368		unconditional	*ACBD4*	intron_variant	C	T	381625	0.3480	0.3480	-0.032	0.003	3.90E-35	NA	3.48E-39	252258	0.3381	0.3381	-0.027	0.003	9.12E-17	633883	0.3434	0.3434	-0.030	0.002	2.15E-41	4.44E-52
17	44081064	rs8070723	515		unconditional	*MAPT*	intron_variant	A	G	381625	0.2040	0.2040	-0.021	0.004	2.04E-08	NA	2.81E-13	252338	0.2176	0.2176	-0.016	0.004	3.89E-05	633963	0.2109	0.2109	-0.019	0.003	3.64E-11	1.77E-17
17	45786621	rs80267077	370		unconditional	*TBKBP1*	missense_variant	G	A	309280	0.1130	0.1130	-0.026	0.004	3.78E-10	NA	9.09E-13	216265	0.1186	0.1186	-0.031	0.005	1.76E-08	525545	0.115	0.1150	-0.028	0.003	9.86E-18	4.63E-30
17	47005193	rs15563	370		unconditional	*UBE2Z*	3_prime_UTR_variant	A	G	378383	0.4670	0.5330	-0.027	0.003	2.20E-24	NA	2.40E-23	252261	0.4685	0.5315	-0.030	0.003	2.93E-21	630644	0.4677	0.5323	-0.028	0.002	6.77E-39	5.70E-45
17	47390014	rs2072153	370		1st conditional round	*ZNF652*	intron_variant	G	C	364247	0.3060	0.3060	0.025	0.003	1.49E-21	5.02E-19	1.10E-19	236293	0.3135	0.3135	0.026	0.003	2.89E-14	600540	0.3093	0.3093	0.025	0.002	1.65E-29	5.51E-32
17	54778817	rs227724	372		1st conditional round	-	intergenic_variant	A	T	366654	0.3450	0.3450	0.024	0.003	4.39E-21	5.63E-18	8.81E-20	207293	0.3438	0.3438	0.024	0.004	5.82E-12	573947	0.3445	0.3445	0.024	0.002	4.86E-26	4.64E-32
17	54850329	rs4794665	372		unconditional	-	intergenic_variant	A	G	379252	0.4920	0.5080	-0.026	0.002	9.65E-28	NA	1.44E-27	251525	0.4946	0.5054	-0.030	0.003	1.98E-23	630777	0.4928	0.5072	-0.027	0.002	4.52E-60	1.69E-40
17	59497277	rs757608	373		unconditional	-	intergenic_variant	A	G	378383	0.3250	0.6750	-0.045	0.003	8.65E-70	NA	6.26E-69	252411	0.3370	0.6630	-0.049	0.003	6.18E-53	630794	0.3306	0.6694	-0.047	0.002	9.41E-102	4.86E-122
17	59638769	rs2378871	373		1st conditional round	-	intergenic_variant	A	C	378823	0.3850	0.6150	-0.025	0.002	1.46E-25	7.95E-22	9.50E-28	223714	0.3671	0.6329	-0.029	0.003	1.01E-17	602537	0.3803	0.6197	-0.026	0.002	1.02E-51	4.68E-37
17	61712964	rs7209435	374		unconditional	*MAP3K3*	intron_variant	T	C	334293	0.2790	0.2790	0.041	0.003	1.20E-46	NA	6.65E-19	244979	0.2756	0.2756	0.049	0.004	1.22E-44	579272	0.2775	0.2775	0.044	0.002	9.48E-85	1.75E-64
17	61908556	rs13030	374		1st conditional round	*SMARCD2*	synonymous_variant	C	T	377973	0.3340	0.3340	-0.034	0.003	1.44E-40	3.82E-15	4.07E-21	252310	0.3298	0.3298	-0.038	0.003	2.38E-32	630283	0.3321	0.3321	-0.036	0.002	3.54E-60	5.00E-20
17	62050528	rs3760238	374		2nd conditional rounc	*CTC-264K15.6*	non_coding_transcript_exon_variant	T	C	380102	0.4890	0.4890	-0.013	0.002	1.10E-08	4.99E-09	1.36E-08	223714	0.4813	0.4813	-0.018	0.003	2.23E-08	603816	0.4868	0.4868	-0.014	0.002	2.28E-17	1.00E-13
17	63554591	rs2240308	375		unconditional	*AXIN2*	missense_variant	G	A	369663	0.4730	0.5270	0.016	0.002	5.33E-12	NA	1.22E-10	251919	0.4569	0.5431	0.020	0.003	5.92E-11	621582	0.4682	0.5318	0.017	0.002	8.78E-25	4.36E-15
17	64318357	rs9912468	516	yes	unconditional	*PRKCA*	intron_variant	G	C	373405	0.4210	0.5790	0.014	0.002	2.22E-08	NA	1.71E-07	237120	0.4134	0.5866	0.010	0.003	0.002	610525	0.4189	0.5811	0.013	0.002	3.43E-14	2.03E-10
17	65870073	rs12602912	376		unconditional	*BPTF*	intron_variant	C	T	378823	0.2050	0.2050	0.016	0.003	9.72E-08	NA	8.47E-08	223714	0.1939	0.1939	0.011	0.004	0.010	602537	0.2012	0.2012	0.014	0.002	5.75E-09	2.56E-14
17	67081278	rs77542162	560	yes	validation	*ABCA6*	missense_variant	A	G	280300	0.0169	0.0169	0.0493	0.0104	2.17E-06	NA	NA	226061	0.0229	0.0229	0.0509	0.0102	5.58E-07	506361	0.02	0.0200	0.0501	0.0073	5.57E-12	2.22E-10
17	68090207	rs11867479	377		unconditional	*AC002539.1*	intron_variant	C	T	380346	0.3490	0.3490	0.025	0.002	2.06E-23	NA	5.67E-24	252313	0.3555	0.3555	0.026	0.003	2.56E-16	632659	0.3509	0.3509	0.025	0.002	1.70E-50	2.18E-32
17	69926109	rs2158917	378		unconditional	-	intergenic_variant	C	T	364983	0.2670	0.2670	0.021	0.003	4.78E-14	NA	6.91E-14	223714	0.2420	0.2420	0.023	0.004	1.10E-09	588697	0.2572	0.2572	0.022	0.002	1.80E-20	1.72E-26
17	76799795	rs1057040	380		unconditional	*USP36*	missense_variant	G	A	350042	0.4630	0.5370	-0.017	0.003	1.04E-11	NA	3.53E-12	252082	0.4807	0.5193	-0.020	0.003	1.44E-10	602124	0.4717	0.5283	-0.018	0.002	1.40E-17	2.27E-20
17	80176641	rs4239020	381		unconditional	*RP13-516M14.2*	downstream_gene_variant	C	T	314970	0.3210	0.6790	-0.016	0.003	1.32E-08	NA	1.08E-08	221515	0.3438	0.6562	-0.016	0.003	3.25E-06	536485	0.331	0.6690	-0.016	0.002	1.46E-12	1.24E-15
18	166819	rs563155	518	yes	unconditional	*USP14*	splice_region_variant	T	C	359848	0.2220	0.2220	0.017	0.003	7.29E-09	NA	7.30E-09	251587	0.2274	0.2274	0.014	0.004	1.58E-04	611435	0.2242	0.2242	0.016	0.002	1.28E-11	1.25E-15
18	13069782	rs6505780	561		validation	*CEP192*	missense_variant	C	T	381625	0.3861	0.6139	-0.0127	0.0027	1.92E-06	NA	NA	233650	0.3961	0.6039	#####	0.0032	2.58E-06	615275	0.3901	0.6099	-0.014	0.002	2.63E-11	2.69E-11
18	20720973	rs11082304	385		1st conditional round	*CABLES1*	intron_variant	G	T	381625	0.4940	0.5060	0.035	0.002	9.69E-47	1.51E-07	NA	252238	0.4858	0.5142	0.044	0.003	1.62E-46	633863	0.4915	0.5085	0.038	0.002	4.95E-112	1.43E-08
18	20735408	rs4369779	385		unconditional	*CABLES1*	intron_variant	T	C	380346	0.2050	0.7950	0.063	0.003	9.29E-93	NA	1.22E-92	252411	0.2103	0.7897	0.070	0.004	4.16E-75	632757	0.207	0.7930	0.066	0.002	1.18E-170	4.82E-167
18	46959500	rs9967417	386		1st conditional round	*DYM*	intron_variant	G	C	372631	0.4210	0.5790	-0.030	0.002	3.98E-34	9.50E-10	2.11E-09	237289	0.4342	0.5658	-0.036	0.003	1.48E-30	609920	0.4248	0.5752	-0.032	0.002	5.09E-79	3.91E-16
18	46991160	rs8099594	386		unconditional	*DYM*	upstream_gene_variant	A	G	380346	0.3440	0.3440	-0.031	0.003	1.32E-34	NA	1.25E-09	252314	0.3399	0.3399	-0.033	0.003	2.69E-25	632660	0.3421	0.3421	-0.032	0.002	1.45E-48	3.89E-16
18	57851097	rs17782313	387		unconditional	-	intergenic_variant	T	C	380346	0.2350	0.2350	0.031	0.003	2.13E-24	NA	2.17E-24	252220	0.2388	0.2388	0.033	0.004	1.61E-19	632566	0.2365	0.2365	0.032	0.002	7.81E-43	1.33E-57
18	74980601	rs77169818	388		unconditional	*GALR1*	missense_variant	A	T	374724	0.0470	0.0470	-0.048	0.006	3.60E-18	NA	3.63E-18	221160	0.0384	0.0384	-0.035	0.008	3.64E-05	595884	0.0441	0.0441	-0.044	0.005	5.11E-19	1.38E-18
19	2177193	rs12982744	390		unconditional	*DOT1L*	intron_variant	C	G	365127	0.3880	0.3880	0.029	0.003	1.23E-29	NA	9.53E-28	223714	0.3870	0.3870	0.034	0.003	3.41E-24	588841	0.3875	0.3875	0.031	0.002	2.14E-44	1.64E-55
19	4910889	rs2261988	392		unconditional	*UHRF1*	missense_variant	G	T	341234	0.3300	0.3300	0.020	0.003	2.82E-14	NA	3.84E-15	242673	0.3205	0.3205	0.025	0.003	3.91E-14	583907	0.3257	0.3257	0.022	0.002	1.25E-23	3.77E-28
19	7184762	rs891088	393		unconditional	*INSR*	intron_variant	A	G	377973	0.2630	0.2630	0.029	0.003	6.31E-26	NA	3.12E-18	251972	0.2592	0.2592	0.027	0.003	3.67E-15	629945	0.2614	0.2614	0.028	0.002	1.31E-35	1.06E-37
19	7224431	rs7248104	393		1st conditional round	*INSR*	intron_variant	G	A	380346	0.4110	0.4110	0.018	0.002	2.54E-14	1.65E-08	5.10E-11	252240	0.4213	0.4213	0.012	0.003	6.40E-05	632586	0.4141	0.4141	0.016	0.002	2.38E-22	1.81E-08
19	8644031	rs4072910	394		unconditional	*AC130469.2*	upstream_gene_variant	G	C	375498	0.4710	0.4710	-0.031	0.002	2.77E-39	NA	9.83E-49	252363	0.4470	0.4470	-0.031	0.003	5.08E-25	627861	0.4637	0.4637	-0.031	0.002	1.93E-77	2.72E-61
19	8669931	rs7255721	394		1st conditional round	*ADAMTS10*	missense_variant	G	C	333237	0.2970	0.7030	-0.019	0.003	6.22E-12	2.31E-19	3.73E-20	201362	0.2947	0.7053	-0.021	0.004	1.19E-08	534599	0.2961	0.7039	-0.020	0.002	1.76E-17	7.83E-16
19	8672000	rs7249094	394		2nd conditional rounc	*ADAMTS10*	intron_variant	G	A	380346	0.3870	0.3870	-0.022	0.002	4.24E-19	3.31E-08	NA	252356	0.3835	0.3835	-0.025	0.003	9.64E-16	632702	0.386	0.3860	-0.023	0.002	4.14E-42	2.71E-10
19	10273372	rs2228612	395		unconditional	*DNMT1*	missense_variant	T	C	381625	0.0640	0.0640	0.037	0.005	5.98E-14	NA	5.56E-16	252302	0.0620	0.0620	0.027	0.006	1.87E-05	633927	0.0632	0.0632	0.033	0.004	2.90E-17	2.36E-16
19	10801185	rs8102380	395		unconditional	*ILF3*	3_prime_UTR_variant	G	A	380102	0.3130	0.6870	-0.020	0.003	3.47E-14	NA	9.23E-12	223714	0.3215	0.6785	-0.022	0.004	1.88E-10	603816	0.3166	0.6834	-0.021	0.002	3.26E-20	5.28E-23
19	11275139	rs7188	395		1st conditional round	*KANK2*	3_prime_UTR_variant	A	C	376010	0.3260	0.3260	-0.018	0.003	9.28E-13	1.90E-10	5.74E-12	252329	0.3175	0.3175	-0.024	0.003	1.53E-13	628339	0.3221	0.3221	-0.021	0.002	4.55E-21	9.93E-24
19	12154799	rs67102109	396		unconditional	*ZNF878*	missense_variant	G	C	371611	0.0720	0.0720	0.036	0.005	7.20E-14	NA	1.22E-14	252400	0.0707	0.0707	0.046	0.006	1.31E-14	624011	0.0714	0.0714	0.040	0.004	1.20E-25	8.39E-24
19	13001547	rs11085824	562	yes	validation	*GCDH*	upstream_gene_variant	A	G	373551	0.3635	0.3635	0.0109	0.0025	1.50E-05	NA	NA	233699	0.3813	0.3813	0.0120	0.0031	1.32E-04	607250	0.3705	0.3705	0.0114	0.002	7.96E-09	1.01E-08
19	17283303	rs2279008	397		unconditional	*MYO9B*	intron_variant	T	C	364133	0.2580	0.2580	-0.016	0.003	1.47E-08	NA	1.66E-11	252373	0.2457	0.2457	-0.026	0.004	4.03E-14	616506	0.2528	0.2528	-0.020	0.002	2.87E-19	2.66E-22
19	18123738	rs7259041	563	yes	validation	*ARRDC2*	missense_variant	T	C	381625	0.2327	0.2327	-0.0134	0.0028	1.60E-06	NA	NA	233205	0.2188	0.2188	#####	0.0036	5.34E-06	614830	0.2275	0.2275	-0.015	0.0022	4.75E-11	1.22E-12
19	19361735	rs1064395	398		unconditional	*AC138430.4*	3_prime_UTR_variant	G	A	379252	0.1570	0.1570	0.026	0.003	4.49E-15	NA	1.90E-14	252447	0.1573	0.1573	0.017	0.004	7.03E-05	631699	0.1571	0.1571	0.023	0.002	8.18E-21	2.75E-29
19	37441365	rs547483	564		validation	*ZNF568*	missense_variant	T	C	381625	0.3589	0.3589	-0.0125	0.0028	6.72E-06	NA	NA	233676	0.3752	0.3752	#####	0.0032	3.90E-04	615301	0.3658	0.3658	-0.012	0.0021	1.03E-08	1.31E-08
19	41944237	rs2231940	401		unconditional	*ATP5SL*	missense_variant	T	C	381625	0.3960	0.3960	0.024	0.003	2.76E-21	NA	1.09E-21	252331	0.4066	0.4066	0.031	0.003	2.80E-22	633956	0.401	0.4010	0.027	0.002	8.92E-36	2.81E-42
19	42863035	rs1206038	401		unconditional	*MEGF8*	missense_variant	A	G	359848	0.0510	0.0510	-0.035	0.006	1.39E-10	NA	6.22E-11	252382	0.0509	0.0509	-0.033	0.007	9.13E-07	612230	0.051	0.0510	-0.034	0.005	2.49E-14	1.25E-11
19	45296806	rs3208856	521	yes	unconditional	*CBLC*	missense_variant	C	T	330127	0.0340	0.0340	0.036	0.007	1.48E-07	NA	NA	252354	0.0342	0.0342	0.021	0.008	0.012	582481	0.0341	0.0341	0.030	0.005	2.96E-08	3.63E-08
19	46914927	rs75175362	522	yes	unconditional	*CCDC8*	missense_variant	C	T	373551	0.0540	0.0540	0.032	0.005	8.77E-10	NA	2.33E-08	223211	0.0473	0.0473	0.028	0.008	2.63E-04	596762	0.052	0.0520	0.031	0.004	1.93E-13	4.76E-14
19	48198675	rs13346368	403		unconditional	*GLTSCR1*	missense_variant	A	G	381625	0.2630	0.2630	0.015	0.003	9.97E-08	NA	1.39E-07	252164	0.2510	0.2510	0.012	0.004	0.001	633789	0.258	0.2580	0.014	0.002	3.37E-09	9.00E-11
19	49116359	rs447802	523	yes	unconditional	*RPL18*	missense_variant	T	C	377104	0.2700	0.2700	0.015	0.003	2.27E-08	NA	2.06E-09	251917	0.2463	0.2463	0.012	0.004	7.12E-04	629021	0.2601	0.2601	0.014	0.002	1.95E-09	5.29E-11
19	55879672	rs4252548	424		unconditional	*IL11*	missense_variant	C	T	381625	0.0260	0.0260	-0.114	0.007	1.02E-57	NA	4.02E-60	252366	0.0217	0.0217	-0.101	0.010	2.28E-23	633991	0.0246	0.0246	-0.110	0.006	5.32E-81	1.01E-77
19	55993436	rs147110934	424		1st conditional round	*NAT14*	missense_variant	G	T	266399	0.0210	0.0210	-0.084	0.010	2.28E-18	1.05E-19	8.02E-20	232650	0.0224	0.0224	-0.098	0.011	1.17E-18	499049	0.0216	0.0216	-0.090	0.007	6.33E-34	2.90E-33
20	4101800	rs1741344	404		unconditional	*SMOX*	non_coding_transcript_exon_variant	C	T	380346	0.3610	0.6390	-0.024	0.002	5.10E-22	NA	1.61E-23	252331	0.3572	0.6428	-0.033	0.003	1.44E-25	632677	0.3599	0.6401	-0.027	0.002	8.51E-56	2.51E-41
20	6620893	rs967417	405		1st conditional round	-	intergenic_variant	G	A	377104	0.4720	0.4720	-0.041	0.002	4.57E-64	2.51E-13	7.51E-13	252333	0.4581	0.4581	-0.037	0.003	1.15E-33	629437	0.4678	0.4678	-0.040	0.002	6.52E-125	1.18E-13
20	6621685	rs2145270	405		unconditional	-	intergenic_variant	C	T	381625	0.3650	0.6350	-0.044	0.002	2.09E-68	NA	1.41E-17	252264	0.3788	0.6212	-0.047	0.003	2.32E-50	633889	0.369	0.6310	-0.045	0.002	1.35E-155	2.09E-37
20	21142523	rs4815025	407		unconditional	*KIZ*	missense_variant	C	G	359880	0.3230	0.6770	-0.021	0.003	4.95E-14	NA	4.98E-14	237045	0.3322	0.6678	-0.019	0.003	1.53E-08	596925	0.3271	0.6729	-0.020	0.002	2.47E-19	1.54E-23
20	32333181	rs7274811	408		unconditional	*ZNF341*	intron_variant	G	T	368384	0.2390	0.2390	-0.039	0.003	2.77E-40	NA	3.29E-35	252382	0.2471	0.2471	-0.038	0.004	6.22E-27	620766	0.2424	0.2424	-0.039	0.002	8.16E-64	1.67E-63
20	33411871	rs6088619	409		unconditional	*NCOA6*	intron_variant	A	G	374936	0.1310	0.1310	0.041	0.004	1.36E-29	NA	NA	223714	0.1330	0.1330	0.054	0.005	5.93E-30	598650	0.1318	0.1318	0.047	0.003	6.63E-52	2.47E-19
20	34025756	rs143384	409		unconditional	*GDF5*	5_prime_UTR_variant	A	G	373217	0.4250	0.4250	0.074	0.003	5.90E-167	NA	1.02E-120	252272	0.3958	0.3958	0.084	0.003	7.31E-151	625489	0.4115	0.4115	0.079	0.002	6.61E-282	1.17E-213
20	34596371	rs6060750	409		unconditional	*CNBD2*	missense_variant	C	T	377006	0.1940	0.1940	0.041	0.003	3.99E-37	NA	7.81E-08	252390	0.1735	0.1735	0.051	0.004	8.84E-35	629396	0.1869	0.1869	0.044	0.002	9.93E-75	8.37E-40
20	35865054	rs4608	410		unconditional	*RPN2*	synonymous_variant	C	T	381625	0.2040	0.7960	0.022	0.003	3.78E-13	NA	5.46E-20	252386	0.1966	0.8034	0.020	0.004	3.97E-07	634011	0.2012	0.7988	0.021	0.002	5.48E-19	2.09E-33
20	47253150	rs2664521	524		unconditional	*PREX1*	missense_variant	T	C	325105	0.0360	0.9640	0.045	0.007	2.59E-11	NA	3.14E-09	230464	0.0313	0.9687	0.033	0.009	1.40E-04	555569	0.0341	0.9659	0.040	0.006	1.40E-13	1.23E-08
20	47865784	rs6512577	412		unconditional	*ZNFX1*	missense_variant	C	T	379252	0.2170	0.2170	0.040	0.003	1.58E-39	NA	1.42E-35	251854	0.2125	0.2125	0.038	0.004	1.20E-23	631106	0.2153	0.2153	0.039	0.002	1.91E-62	1.22E-78
20	48600631	rs4647958	412		unconditional	*SNAI1*	missense_variant	T	C	378383	0.1220	0.1220	-0.025	0.004	1.39E-11	NA	1.18E-11	252216	0.1197	0.1197	-0.033	0.005	8.78E-13	630599	0.121	0.1210	-0.029	0.003	5.31E-21	3.78E-22
20	57475191	rs13831	414		1st conditional round	*GNAS*	3_prime_UTR_variant	A	G	374634	0.2950	0.7050	-0.016	0.003	1.47E-09	1.76E-09	2.03E-09	252314	0.3025	0.6975	-0.013	0.003	7.47E-05	626948	0.2984	0.7016	-0.015	0.002	3.91E-11	1.56E-13
20	57758720	rs16982520	414		unconditional	-	intergenic_variant	A	G	381625	0.1320	0.1320	0.028	0.004	1.11E-14	NA	1.87E-14	252288	0.1235	0.1235	0.023	0.005	4.19E-07	633913	0.1283	0.1283	0.026	0.003	7.73E-18	5.17E-18
20	60986019	rs2236200	415		unconditional	*CABLES2*	missense_variant	A	C	376655	0.2420	0.2420	-0.017	0.003	2.91E-09	NA	2.63E-09	252350	0.2517	0.2517	-0.012	0.004	5.37E-04	629005	0.2461	0.2461	-0.015	0.002	5.50E-11	1.81E-13
21	28305212	rs2830585	572	yes	validation	*ADAMTS5*	missense_variant	C	T	381625	0.1551	0.1551	-0.0169	0.0033	2.31E-07	NA	NA	233624	0.1503	0.1503	#####	0.0040	0.002	615249	0.1532	0.1532	-0.015	0.0025	3.27E-09	5.46E-09
21	35690786	rs2834442	417		unconditional	*AP000318.2*	intron_variant	T	A	314611	0.3390	0.6610	0.022	0.003	8.78E-16	NA	1.95E-16	237452	0.3594	0.6406	0.022	0.003	4.15E-11	552063	0.3484	0.6516	0.022	0.002	5.94E-23	6.21E-28
21	38491095	rs1003719	525	yes	unconditional	*TTC3*	intron_variant	A	G	381625	0.4460	0.5540	-0.013	0.002	1.18E-07	NA	NA	251359	0.4329	0.5671	-0.014	0.003	1.53E-05	632984	0.4422	0.5578	-0.013	0.002	5.92E-15	2.33E-10
21	39671476	rs2230033	418		unconditional	*KCNJ15*	missense_variant	G	A	377651	0.4580	0.5420	-0.022	0.002	4.73E-20	NA	6.21E-21	252277	0.4314	0.5686	-0.031	0.003	1.63E-25	629928	0.4499	0.5501	-0.025	0.002	1.83E-50	4.78E-36
22	17625915	rs35665085	526	yes	unconditional	*CECR5*	missense_variant	G	A	381625	0.0580	0.0580	-0.028	0.005	2.68E-08	NA	4.75E-08	252293	0.0624	0.0624	-0.031	0.006	8.65E-07	633918	0.0597	0.0597	-0.029	0.004	9.66E-14	5.05E-13
22	20789074	rs1005640	527	yes	unconditional	*XXbac-B562F10.12*	intron_variant	T	C	379252	0.4330	0.4330	0.015	0.002	8.00E-10	NA	1.60E-09	252130	0.4237	0.4237	0.013	0.003	1.04E-05	631382	0.4302	0.4302	0.015	0.002	3.69E-18	9.59E-14
22	24255296	rs4822455	573	yes	validation	-	intergenic_variant	C	T	381625	0.4092	0.5908	0.0117	0.0024	1.43E-06	NA	NA	233390	0.4247	0.5753	0.0112	0.0031	2.73E-04	615015	0.4151	0.5849	0.0115	0.0019	1.55E-09	6.14E-10

22	28501414	rs77885044	528	yes	unconditional	*TTC28*	missense_variant	C	T	373551	0.0120	0.0120	-0.067	0.010	9.47E-11	NA	1.26E-10	252395	0.0170	0.0170	-0.069	0.012	3.24E-09	625946	0.0141	0.0141	-0.068	0.008	3.93E-19	6.68E-18
22	35663523	rs2413338	529	yes	unconditional	*HMGXB4*	intron_variant	C	T	374251	0.3750	0.6250	0.014	0.003	5.85E-08	NA	9.32E-08	223714	0.3827	0.6173	0.010	0.003	0.003	597965	0.3784	0.6216	0.012	0.002	4.80E-08	2.40E-09
22	38121152	rs9610841	421		1st conditional round	*RP1-37E16.12*	missense_variant	C	A	359848	0.4360	0.4360	0.014	0.003	3.72E-08	2.10E-08	1.15E-08	252394	0.4593	0.4593	0.014	0.003	1.20E-05	612242	0.4473	0.4473	0.014	0.002	1.58E-10	2.18E-13
22	38544298	rs2284063	421		unconditional	*PLA2G6*	non_coding_transcript_exon_variant	A	G	380346	0.3540	0.3540	0.016	0.003	1.94E-10	NA	7.31E-11	252306	0.3509	0.3509	0.012	0.003	3.10E-04	632652	0.3526	0.3526	0.014	0.002	2.02E-10	5.70E-14
22	42095658	rs147348682	530	yes	unconditional	*MEI1*	missense_variant	T	G	377832	0.0250	0.0250	0.041	0.007	2.25E-08	NA	3.16E-08	252114	0.0341	0.0341	0.024	0.009	0.007	629946	0.0286	0.0286	0.034	0.006	3.70E-10	1.72E-08
22	45749983	rs5764698	423		unconditional	*SMC1B*	missense_variant	G	T	360183	0.4830	0.5170	-0.019	0.003	1.33E-13	NA	2.47E-13	245357	0.4578	0.5422	-0.012	0.003	2.07E-04	605540	0.4708	0.5292	-0.015	0.002	9.99E-13	1.76E-13
23	38009121	rs35318931	531	yes	unconditional	*SRPX*	missense_variant	G	A	262032	0.0760	0.0760	-0.029	0.005	3.97E-10	NA	NA	224258	0.0797	0.0797	-0.036	0.006	2.58E-09	486290	0.0775	0.0775	-0.032	0.004	1.41E-16	1.25E-15
23	56889389	rs1930983	533	yes	unconditional	-	intergenic_variant	C	T	260509	0.2230	0.7770	0.023	0.003	4.66E-13	NA	NA	75557	0.1797	0.8203	0.012	0.007	0.082	336066	0.2157	0.7843	0.021	0.003	1.31E-14	1.30E-04
23	66941751	rs137852591	599	yes	recessive	*AR*	missense variant	C	G	280075	0.0021	0.0021	-0.304	0.061	7.05E-07	NA	NA	110065	0.0080	0.0080	-0.333	0.058	7.12E-09	390140	0.0052	0.0052	-0.319	0.042	2.67E-14	4.10E-14
23	77268502	rs2227291	425		unconditional	*ATP7A*	missense_variant	G	C	255905	0.2130	0.2130	0.018	0.003	1.43E-08	NA	NA	224266	0.1955	0.1955	0.020	0.004	1.20E-06	480171	0.2069	0.2069	0.019	0.002	1.26E-14	6.43E-23
23	77913569	rs4077512	535	yes	unconditional	*ZCCHC5*	missense_variant	G	A	210715	0.1440	0.1440	-0.023	0.004	2.76E-09	NA	NA	224239	0.1412	0.1412	-0.021	0.005	5.48E-06	434954	0.1428	0.1428	-0.022	0.003	2.44E-13	1.42E-09
23	78649193	rs1474563	426		unconditional	-	intergenic_variant	C	T	217091	0.4150	0.5850	0.031	0.003	5.74E-31	NA	NA	224267	0.4354	0.5646	0.050	0.003	2.63E-52	441358	0.4244	0.5756	0.040	0.002	8.75E-72	1.72E-88
23	99890204	rs1802288	536	yes	unconditional	*TSPAN6*	missense_variant	C	T	240255	0.1760	0.1760	-0.018	0.003	3.99E-08	NA	NA	224196	0.1968	0.1968	-0.020	0.004	1.09E-06	464451	0.1834	0.1834	-0.019	0.002	1.14E-14	1.19E-20
23	105152282	rs209373	574	yes	validation	*NRK*	missense_variant	G	A	259423	0.2184	0.2184	-0.0109	0.0030	2.79E-04	NA	NA	205718	0.2260	0.2260	#####	0.0038	2.03E-07	465141	0.2213	0.2213	-0.014	0.0024	1.27E-09	1.48E-08
23	118587003	rs3810755	575	yes	validation	*SLC25A43*	missense_variant	C	T	240566	0.4195	0.5805	0.0127	0.0026	1.01E-06	NA	NA	205692	0.4377	0.5623	0.0199	0.0033	1.10E-09	446258	0.4265	0.5735	0.0155	0.002	2.52E-14	9.22E-15

Supplementary Table 12. Unconditional and conditional results in in the UK Biobank (N=120,084) and using SSimp (summary statistics from discovery studies)

					UK Biobank					SSimp				
rsID	Chr	Pos (hg19)	Other allele	Effect allele	standardized effect size (unconditiona	P-value (unconditional	standardized effect size (conditiona	P-value (conditional	Other allele	Effect allele	standardized effect size (unconditiona	standardized effect size (conditional)
rs425277	1	2069172	C	T	0.013728343	1.90E-06	2.70E-05	0.99	C	T	0.015354007	-0.005417837
rs34305100	1	7913029	A	G	0.011004152	0.00014	0.012073944	2.80E-05	A	G	0.013236263	0.012617391
rs2239560	1	9304731	G	A	0.012377007	1.80E-05	-0.00130065	0.65	G	A	0.012802946	-0.001459479
rs6541085	1	10285709	A	G	0.016149713	2.10E-08	0.014691708	3.50E-07	A	G	0.002805261	0.003278733
rs2284746	1	17306675	C	G	0.029352454	2.40E-24	-0.000380947	0.89	C	G	0.027007717	1.09E-05
rs12045440	1	19765518	T	G	-0.013026287	6.20E-06	-0.004509285	0.12	T	G	-0.007491397	-0.001611355
rs213060	1	21629447	A	C	0.013329826	3.80E-06	0.00373859	0.19	A	C	0.012071954	0.004836929
rs2501279	1	22368342	C	T	-0.012261758	2.10E-05	-0.008114952	0.0049	C	T	-0.007351395	-0.003574096
rs1738475	1	23536891	C	G	-0.011833453	4.10E-05	0.002344741	0.42	C	G	-0.014715853	0.001769813
rs3091242	1	25674785	C	T	0.011390605	7.80E-05	-0.000606129	0.83	C	T	0.005211407	-0.004621587
rs17163588	1	26450009	C	T	0.013411071	3.30E-06	-0.002731152	0.34	C	T	0.014503101	0.001170156
rs7532866	1	26741544	A	G	-0.019241413	2.50E-11	-0.006604738	0.022	A	G	-0.011925476	-0.005250206
rs12748152	1	27138393	C	T	0.007678043	0.0077	0.005103953	0.077	C	T	0.008108175	0.006953386
rs2271933	1	32092525	A	G	0.010286833	0.00036	0.009615626	0.00085	A	G	0.007012503	0.006504328
rs3903683	1	32672908	T	G	0.013537685	2.70E-06	0.007214263	0.012	T	G	0.007780461	0.006726838
rs150341307	1	32673514	G	C	-0.011497845	6.70E-05	-0.011097245	0.00012	G	C	-0.003702261	-0.01122769
rs11488569	1	38338795	A	G	-0.010298461	0.00035	-0.007828198	0.0066	A	G	-0.007679899	-0.003825908
rs2228564	1	40773149	T	C	-0.011462849	7.00E-05	-0.001359188	0.64	T	C	-0.010970005	0.000190565
rs143365597	1	41540902	G	A	0.015099164	1.60E-07	0.01282377	8.70E-06	G	A	0.002105279	0.016274333
rs114233776	1	41618297	G	A	-0.012854245	8.30E-06	-0.012058058	2.90E-05	G	A	-0.009155781	-0.012006757
rs2154319	1	41745770	T	C	0.028997046	8.60E-24	0.014632512	3.90E-07	T	C	0.019692413	0.011160625
rs1707336	1	46493460	T	G	-0.013100011	5.50E-06	-0.000924376	0.75	T	G	-0.011172604	-0.011548636
rs517384	1	47952663	T	G	-0.013031949	6.20E-06	-0.009641169	0.00083	T	G	-0.009957896	-0.006740944
rs41292521	1	51873967	G	A	0.015719059	5.00E-08	0.0052182	0.07	G	A	0.008656181	0.002398273
rs1886686	1	67390468	C	G	0.009858546	0.00063	0.003658702	0.2	C	G	0.0092601	0.003154478
rs17391694	1	78623626	C	T	0.018470545	1.50E-10	-0.000958542	0.74	C	T	0.013629767	-0.001681176
rs6699417	1	89123443	C	T	0.022561144	5.10E-15	-0.001692166	0.56	C	T	0.016456679	-0.001236994
rs10874746	1	93323971	T	C	0.014504891	4.90E-07	0.003433586	0.23	T	C	0.013913541	-0.000826656
rs713162	1	103216881	G	A	0.014911175	2.30E-07	0.003761615	0.19	G	A	0.011949601	0.006506973
rs12755987	1	103432657	A	G	-0.021847459	3.50E-14	-0.003222812	0.26	A	G	-0.011272614	-0.003433856
rs17030613	1	113190807	A	C	-0.015292118	1.10E-07	-0.000767954	0.79	A	C	-0.012979711	-0.000572814
rs17038182	1	118868405	G	C	-0.033485729	3.50E-31	0.004155342	0.15	G	C	-0.025522868	0.002851573
rs61730011	1	119427467	A	C	-0.017017441	3.60E-09	-0.009407554	0.0011	A	C	-0.012715962	-0.012548684
rs11239931	1	146568955	G	A	0.000604406	0.83	-0.005728748	0.047	G	A	0.009987243	0.001999483
rs145659444	1	149902342	C	T	0.011996145	3.20E-05	0.013631796	2.30E-06	C	T	0.001332686	0.008759191
rs11205303	1	149906413	T	C	0.03859022	7.50E-41	0.02333132	5.90E-16	T	C	0.030207814	0.014604068
rs11580946	1	150551327	G	A	0.019746235	7.50E-12	0.019136525	3.20E-11	G	A	0.009681719	0.008971514
rs11204697	1	150658971	C	T	0.006848321	0.018	0.007204808	0.012	C	T	0.000837688	0.001477087
rs3748545	1	151259543	G	A	-0.00890716	0.002	-0.001754888	0.54	G	A	-0.011818721	0.000124896
rs141845046	1	154987704	C	T	0.013551787	2.60E-06	0.008238146	0.0043	C	T	0.001238339	0.016508214
rs17346452	1	172053287	T	C	0.023592599	2.80E-16	-0.00026898	0.93	T	C	0.022994783	-0.002430729
rs678962	1	172189889	T	G	0.034219189	1.70E-32	0.010120903	0.00045	T	G	0.022496861	0.003856807
rs4916245	1	172206026	G	A	-0.012611286	1.20E-05	-0.00751206	0.0092	G	A	-0.00364027	-0.002692556
rs1129942	1	172437592	G	A	-0.017536081	1.20E-09	-0.002215625	0.44	G	A	-0.011922703	2.01E-05
rs1553770	1	176219438	C	T	-0.011307923	8.80E-05	-0.013710046	2.00E-06	C	T	-0.007021052	-0.012452121
rs11583447	1	176521349	T	G	0.01086534	0.00016	0.015558714	6.80E-08	T	G	0.001602005	0.011384728
rs1325598	1	176792249	A	G	0.022400561	7.90E-15	-0.000818808	0.78	A	G	0.016259738	-0.000226586
rs79485039	1	180886140	C	T	0.007112375	0.014	0.007404269	0.01	C	T	-0.000285807	0.008142124
rs20558	1	183094547	T	C	-0.009689185	0.00078	0.003188947	0.27	T	C	-0.015075958	-0.001184602
rs144712473	1	183495812	A	G	-0.008091991	0.005	-0.009031632	0.0017	A	G	0.002392069	-0.011101783
rs2274432	1	184020945	G	A	0.033930731	5.70E-32	0.002892484	0.32	G	A	0.03023903	0.000861354
rs2294851	1	210577884	G	A	0.005584295	0.053	0.006958397	0.016	G	A	0.008261216	0.01006689
rs2647116	1	219009835	G	A	-0.014651235	3.70E-07	-0.001788402	0.54	G	A	-0.01395773	0.000254152
rs11118346	1	219743719	C	T	-0.011428959	7.40E-05	0.000758388	0.79	C	T	-0.014208509	0.001043992
rs144673025	1	223178026	T	C	-0.007058786	0.014	-0.01050579	0.00027	T	C	-0.008331507	-0.010198699
rs2236359	1	227935444	A	G	-0.021005105	3.20E-13	-0.005310183	0.066	A	G	-0.012542031	-0.001502636
rs2290911	2	224919	A	G	0.018296252	2.20E-10	0.019326863	2.00E-11	A	G	0.009635609	0.008157982
rs12615742	2	224919	T	C	-0.015915676	3.40E-08	0.002016261	0.48	NA	NA	NA	NA
rs142036701	2	224919	T	G	-0.000674897	0.81	-0.000575526	0.84	NA	NA	NA	NA
rs6726313	2	1756908	C	T	0.010228118	0.00039	0.005264179	0.068	C	T	0.008429737	0.000104088
rs10495563	2	9662210	G	A	0.009419812	0.0011	0.009337263	0.0012	G	A	0.007242207	0.008076377
rs978906	2	11323276	T	C	-0.010624584	0.00023	-0.010459215	0.00029	T	C	-0.008698246	-0.010418317
rs52826764	2	20205541	C	T	-0.018468204	1.50E-10	-0.020938628	3.80E-13	C	T	-0.011402177	-0.014947889
rs7561273	2	24247514	A	G	0.023431227	4.40E-16	0.001634134	0.57	A	G	0.015594563	-0.002045283
rs4665736	2	25187599	C	T	0.02738064	2.20E-21	0.007455016	0.0097	C	T	0.02281596	0.006499184
rs7594432	2	25482883	T	C	0.032432769	2.40E-29	-0.001553402	0.59	T	C	0.024075809	-0.000615668
rs1260326	2	27730940	T	C	0.015201666	1.30E-07	-4.69E-05	0.99	T	C	0.013629706	0.000408682
rs6714546	2	33361425	A	G	0.022835647	2.40E-15	-0.002305361	0.42	A	G	0.01618764	-0.003578674
rs6751657	2	33405151	T	C	0.018659064	9.70E-11	0.000475947	0.87	T	C	0.015582065	8.14E-05
rs848642	2	36782886	G	A	-0.01758229	1.10E-09	-0.001335036	0.64	G	A	-0.012944309	0.001166136
rs1800440	2	38298139	T	C	-0.015743093	4.80E-08	-0.01632817	1.50E-08	T	C	-0.006825681	-0.006280033
rs7578597	2	43732823	T	C	0.00555407	0.054	0.00042784	0.88	T	C	0.010432116	0.002961712
rs2341459	2	44768202	T	C	-0.017349222	1.80E-09	-0.003526801	0.22	T	C	-0.014169592	0.003110929
rs3755073	2	45640374	C	A	-0.011238461	9.70E-05	-0.011090562	0.00012	C	A	-0.006476611	-0.005439857
rs12474201	2	46921285	G	A	0.026390976	5.50E-20	0.001779461	0.54	G	A	0.017309142	-0.001162766
rs3791679	2	56096892	A	G	-0.049552697	3.40E-66	0.002050598	0.48	A	G	-0.032721789	-0.003147029
rs68148245	2	65777628	C	T	-0.012792221	9.10E-06	-0.013127496	5.30E-06	C	T	-0.003296274	-0.00395155
rs6714975	2	71633389	C	T	-0.023304531	6.30E-16	-0.00147117	0.61	C	T	-0.015354821	-0.000372029
rs13045	2	88895123	T	C	-0.026464728	4.40E-20	0.00159282	0.58	T	C	-0.020785393	0.000364359
rs2166898	2	121612659	G	A	-0.022216156	1.30E-14	-0.000936563	0.75	G	A	-0.012361024	-1.44E-05
rs744265	2	128944424	T	C	0.010559021	0.00025	0.009619798	0.00085	T	C	0.007677262	0.007956967
rs7567288	2	134434824	T	C	0.007966051	0.0057	-0.000707163	0.81	T	C	0.01576611	-0.000420185
rs59900519	2	135988127	T	A	-0.009759637	0.00071	-0.0001291	0.96	T	A	-0.01304112	0.000904118
rs7567851	2	178684720	G	C	0.011306378	8.80E-05	-4.22E-05	0.99	G	C/A	0.01035998	-0.000941508
rs16866412	2	179474668	G	A	-0.006012239	0.037	-0.005904544	0.041	G	A	-0.003604768	-0.002775722
rs288326	2	183703336	G	A	0.012368649	1.80E-05	0.012458815	1.60E-05	G	A	0.008687159	0.00812498
rs1813849	2	200142847	T	C	0.006705818	0.02	0.007940937	0.0059	T	C	0.010409537	0.010989794
rs13022398	2	216577567	C	A	0.007354104	0.011	0.008427449	0.0035	C	A	0.009412519	0.008645565
rs6435957	2	217878209	T	C	0.013903015	1.40E-06	0.012253489	2.10E-05	T	C	0.011529669	0.009217605
rs1351164	2	218271898	T	C	-0.014210231	8.30E-07	-0.001511595	0.6	T	C	-0.015658411	-0.003040949
rs10932775	2	219195799	G	A	0.017986595	4.40E-10	0.000928561	0.75	G	A	0.011254366	-0.000981321
rs1344642	2	219555262	G	A	-0.021856845	3.40E-14	-0.000749142	0.8	G	A	-0.017455897	-0.00013443
rs6724465	2	219943846	G	A	-0.021017887	3.10E-13	2.07E-05	0.99	G	A	-0.016809638	0.001946705
rs16859517	2	219949184	C	T	0.016494359	1.10E-08	-0.000606208	0.83	C	T	0.01514666	-0.000881666
rs147445258	2	220078652	C	T	-0.006582792	0.022	-0.006371171	0.027	C	T	-0.003499593	-0.009926619
rs2629046	2	225047744	T	C	-0.019002919	4.40E-11	-0.000242642	0.93	T	C	-0.014383277	0.000389815
rs2290130	2	232263127	G	A	-0.006306229	0.029	-0.00027977	0.92	G	A	-0.013723424	-0.002703131
rs4973417	2	232349636	G	T	-0.017520502	1.20E-09	-0.002547914	0.38	G	T	-0.019338298	-0.006925201
rs749052	2	232796610	T	C	-0.026201405	1.00E-19	-0.000679097	0.81	T	C	-0.018730863	0.00193008
rs2580816	2	232797966	C	T	-0.024919243	5.50E-18	0.000443152	0.88	C	T	-0.020559169	-0.000430138
rs11677466	2	232982257	A	T	0.023015055	1.40E-15	-0.000683339	0.81	A	T	0.017933054	0.000261694
rs7571816	2	233077064	A	G	-0.019203574	2.70E-11	0.00239961	0.41	A	G	-0.015523361	-6.49E-05
rs1801251	2	233633460	G	A	-0.019609789	1.00E-11	-0.018526812	1.30E-10	G	A	-0.00764322	-0.01130545
rs6719451	2	238336802	T	C	-0.008321261	0.0039	-0.008134246	0.0048	T	C	-0.008597861	-0.007680441
rs4675801	2	242493511	C	T	-0.018453504	1.60E-10	-0.015373	9.70E-08	C	T	-0.015123404	-0.011165064
rs6772112	3	11641535	C	T	0.010948547	0.00015	0.001428632	0.62	C	T	0.011912244	-0.002303749
rs2229089	3	14214524	G	A	-0.006194886	0.032	-0.005931543	0.04	G	A	-0.007718374	-0.007706652
rs6810039	3	33194990	C	A	-0.009874498	0.00062	-0.009842907	0.00064	C	A	-0.006377005	-0.010043412
rs9816693	3	38047954	G	C	0.013516979	2.80E-06	-0.000769573	0.79	G	C	0.015534468	-0.000326064
rs10490823	3	41123735	C	T	0.007250985	0.012	0.002602498	0.37	C	T	0.00958977	0.007237583
rs3732858	3	43097765	G	A	-0.013290419	4.00E-06	-0.013755204	1.80E-06	G	A	-0.009173643	-0.006684059
rs121434601	3	46939587	C	T	0.011551792	6.20E-05	0.011415253	7.50E-05	C	T	0.002290488	0.011721858
rs76208147	3	47162886	C	T	0.013533444	2.70E-06	0.006778084	0.019	C	T	0.005075621	0.009540297
rs34759087	3	49162284	C	T	0.015890565	3.60E-08	0.014583164	4.20E-07	C	T	0.006110984	0.006298901
rs35713889	3	49162583	C	T	0.020206621	2.40E-12	0.005480478	0.057	C	T	0.010788768	0.001673256
rs13088462	3	51071713	T	C	0.016780807	5.90E-09	-0.002645423	0.36	T	C	0.016571888	-8.48E-05
rs79979130	3	52551010	C	T	0.015298867	1.10E-07	0.01283415	8.50E-06	C	T	0.00449679	-0.000559061
rs2336725	3	53118739	C	T	-0.023629259	2.50E-16	-0.003408031	0.24	C	T	-0.019917901	-0.002135271
rs1392224	3	55474073	A	G	0.013711515	2.00E-06	0.01327184	4.20E-06	A	G	0.008117045	0.004224317
rs7637449	3	56628031	G	A	0.016359468	1.40E-08	-0.002911451	0.31	G	A	0.018712999	0.000272247
rs9311651	3	57528503	A	G	0.008304368	0.004	0.000518875	0.86	A	G	0.008750502	0.002262585
rs17806888	3	67416322	T	C	-0.013344137	3.70E-06	0.001569825	0.59	T	C	-0.014068899	-1.51E-05
rs9863706	3	72437413	C	T	-0.023176528	9.10E-16	-0.0007334	0.8	C	T	-0.017873703	-0.001487785
rs9838238	3	98600385	T	C	0.012032654	3.00E-05	0.012823894	8.70E-06	T	C	0.005595148	0.003767162
rs12490319	3	114511356	T	C	-0.009661218	0.00081	-0.004648817	0.11	T	C	-0.00980491	-0.004994233
rs6438424	3	117574822	A	C	0.013689756	2.10E-06	0.014423418	5.70E-07	A	C	0.0081475	0.007842255
rs6439167	3	129050756	T	C	0.025140269	2.80E-18	-0.002739552	0.34	T	C	0.019331287	0.00066733

rs10935120	3	134233092	A	G	0.017482632	1.30E-09	0.000543995	0.85	A	G	0.01385336	-0.003070341
rs9844666	3	135974216	G	A	-0.017587769	1.10E-09	-0.000870733	0.76	G	A	-0.016471703	0.003143866
rs724016	3	141105570	A	G	0.063744443	2.60E-108	-0.003721157	0.2	A	G	0.050486086	-0.000934997
rs6809394	3	156862145	C	T	-0.015529294	7.20E-08	-0.006713404	0.02	C	T	-0.009551362	-0.004532359
rs7643792	3	157992814	A	G	0.019282853	2.30E-11	0.005178924	0.072	A	G	0.010226049	5.36E-05
rs1344555	3	169300219	C	T	-0.008354712	0.0038	-0.008965124	0.0019	C	T	-0.008298609	-0.009684004
rs7652177	3	171969077	C	G	0.024561205	1.60E-17	-6.78E-06	1	C	G	0.026557695	0.001174791
rs572169	3	172165727	C	T	0.025780784	3.80E-19	0.000115269	0.97	C	T	0.014121389	-0.006371434
rs11546878	3	183976103	C	T	-0.009856352	0.00063	-0.011315888	8.70E-05	C	T	-0.007168843	-0.006616274
rs1470579	3	185529080	A	C	0.00016867	0.95	-0.000105385	0.97	A	C	-0.000674766	-0.002882002
rs720390	3	185548683	G	A	0.023947165	9.90E-17	-0.001534198	0.59	G	A	0.020664752	-0.001309225
rs2002675	3	185629568	A	G	0.011351454	8.30E-05	-0.001343038	0.64	A	G	0.011085273	-0.000585511
rs2293377	3	191114266	T	C	0.008096756	0.005	0.000443971	0.88	T	C	0.010198577	-0.000818271
rs2247341	4	1701317	G	A	0.017661219	9.10E-10	-0.00199366	0.49	G	A	0.016321078	1.80E-05
rs794001	4	1701317	A	G	-0.012029938	3.00E-05	-0.010150535	0.00043	NA	NA	NA	NA
rs6831256	4	3473139	A	G	-0.013875818	1.50E-06	-0.013428902	3.20E-06	A	G	-0.013008187	-0.014265414
rs11722554	4	5016883	G	A	-0.015101522	1.60E-07	0.001174796	0.68	G	A	-0.008609129	0.003101998
rs6446315	4	5035587	G	A	-0.010475056	0.00028	-0.001121337	0.7	G	A	-0.016748294	-0.001282028
rs1949733	4	8503359	A	G	0.010129086	0.00044	0.008159943	0.0047	A	G	0.007361642	0.0073 1204
rs763318	4	12963574	G	A	-0.022150612	1.60E-14	0.002470081	0.39	G	A	-0.013052423	-0.001232048
rs2320299	4	17972372	G	A	-0.040991233	7.20E-46	-0.002282227	0.43	G	A	-0.027123289	0.00304318
rs6449353	4	18033488	T	C	-0.046754005	3.90E-59	-0.003322675	0.25	T	C	-0.034041174	-0.000862478
rs34811474	4	25408838	G	A	0.008338708	0.0038	0.009542903	0.00093	G	A	0.007571102	0.011391478
rs10031777	4	48498290	T	C	0.010767279	0.00019	0.008969703	0.0019	T	C	0.012265617	0.002941453
rs17081935	4	57823476	C	T	0.023190126	8.80E-16	0.000295722	0.92	C	T	0.01593679	0.000737845
rs141374503	4	73179445	C	T	-0.006124664	0.034	-0.006275262	0.03	C	T	-0.003042776	-0.008232108
rs788908	4	73414286	C	T	-0.013591953	2.40E-06	0.00884178	0.0022	C	T	-0.003167504	0.007723213
rs7697556	4	73515313	T	C	-0.03137413	1.40E-27	-0.000958236	0.74	T	C	-0.018229578	-0.000480778
rs710841	4	82149831	C	T	0.028942859	1.00E-23	0.002441687	0.4	C	T	0.024775861	-0.003278803
rs61730641	4	87730980	C	T	-0.017344552	1.80E-09	-0.016323512	1.50E-08	C	T	-0.008564857	-0.014182337
rs13107325	4	103188709	C	T	-0.010527725	0.00026	-0.010524341	0.00026	C	T	-0.004920199	-0.011392218
rs10010325	4	106106353	C	A	0.026496298	3.90E-20	0.010256185	0.00038	C	A/T	0.016939446	0.00804446
rs1562975	4	109408608	G	A	0.01736374	1.70E-09	-0.001715328	0.55	G	A	0.015198345	-0.001110337
rs149385790	4	120422407	T	G	0.009555858	0.00092	0.010643071	0.00022	T	G	0.001725568	0.0141141
rs7699214	4	120716967	A	G	0.005026019	0.081	-0.00298049	0.3	A	G	0.008442182	0.009719704
rs28532673	4	122664323	G	A	0.011973967	3.30E-05	-0.00023764	0.93	G	A	0.010285739	-0.001073831
rs12648093	4	123838758	A	G	-0.014291612	7.20E-07	0.000627978	0.83	A	G	-0.011744535	-0.000383678
rs116807401	4	135121721	T	C	0.006904515	0.017	0.006738709	0.019	T	C	0.003874081	0.012787038
rs11941589	4	140115744	G	A	-0.009296015	0.0013	-0.009990956	0.00053	G	A	-0.00912764	-0.007687639
rs28925904	4	144359490	C	T	-0.012033718	3.00E-05	-0.012665929	1.10E-05	C	T	-0.001776477	-0.011355357
rs1812175	4	145574844	A	G	0.051583047	1.40E-71	-0.00026787	0.93	A	G	0.037753898	-0.001292803
rs6854783	4	145643079	G	A	0.029425837	1.90E-24	-0.007266727	0.012	G	A	0.026430047	-0.001858563
rs1492820	4	145650021	G	A	0.03464989	2.90E-33	-0.006961867	0.016	G	A	0.031067889	-0.002516416
rs2709828	4	152355268	C	T	-0.011266789	9.30E-05	-0.004640564	0.11	C	T	-0.008396834	-0.002994912
rs34343821	4	154557616	C	T	0.009494706	0.00099	0.010234359	0.00039	C	T	0.003934205	0.008734723
rs4862155	4	184236868	G	A	-0.016405376	1.30E-08	-0.010635338	0.00023	G	A	-0.010934016	-0.006978512
rs55656741	5	31515657	G	A	0.006775608	0.019	0.003847659	0.18	G	A	0.011090532	0.003220866
rs31198	5	31515657	C	T	0.025009428	4.20E-18	0.004884937	0.09	NA	NA	NA	NA
rs146301345	5	32784907	G	A	0.011540651	6.30E-05	0.011049928	0.00013	G	A	-0.000244362	0.009707652
rs1173727	5	32830521	T	C	-0.027520717	1.40E-21	-0.000665364	0.82	T	C	-0.022372368	0.000770265
rs11745439	5	33230034	A	G	0.018044935	3.90E-10	-0.000595229	0.84	A	G	0.013933525	-0.003103396
rs292182	5	36954812	G	A	-0.018246453	2.50E-10	0.003266588	0.26	G	A	-0.015774919	-2.86E-05
rs11959928	5	39397132	T	A	0.015606051	6.20E-08	0.008480165	0.0033	T	A	0.003905746	-0.004069219
rs13188386	5	42473555	G	A	-0.017723288	7.90E-10	-0.010973889	0.00014	G	A	-0.009201997	-0.005477766
rs2973011	5	42782492	T	C	-0.025533716	8.30E-19	-0.019687385	8.60E-12	T	C	-0.012737907	-0.008564517
rs4865615	5	54960673	C	G	-0.023309604	6.30E-16	0.000276806	0.92	C	G	-0.018347121	-0.000612434
rs889312	5	56031884	C	A	0.014617651	4.00E-07	0.009302803	0.0013	C	A	0.009276441	0.006906476
rs61736454	5	64766798	G	A	-0.013902951	1.40E-06	-0.014751431	3.10E-07	G	A	-0.000255793	-0.011977817
rs3756668	5	67596088	G	A	-0.015052665	1.80E-07	0.000804242	0.78	G	A	-0.011959291	-0.001258958
rs10037512	5	88354675	T	C	-0.025413096	1.20E-18	0.000432381	0.88	T	C	-0.021519462	-0.001816862
rs2247870	5	90151589	G	A	0.009552747	0.00092	-0.000749869	0.79	G	A	0.010198105	-0.000362183
rs41276257	5	95115959	C	T	0.009452098	0.001	0.010670443	0.00021	C	T	0.006021464	0.00985292
rs6235	5	95728898	C	G	0.008846534	0.0022	-0.000630438	0.83	C	G	0.009718761	0.003527654
rs35658696	5	102338811	A	G	-0.012057767	2.90E-05	-0.013224552	4.50E-06	A	G	-0.007859923	-0.007913554
rs13177718	5	108113344	C	T	-0.010282004	0.00036	0.001710059	0.55	C	T	-0.014161038	-0.000568043
rs459552	5	112176756	T	A	-0.00919854	0.0014	-0.011922488	3.50E-05	T	A	-0.00864381	-0.006825265
rs6595440	5	122718736	G	C	-0.018088388	3.50E-10	-0.000704562	0.81	G	C	-0.016532691	-0.001691938
rs34821177	5	126250812	C	T	0.007654554	0.0079	0.008923592	0.002	C	T	0.001408616	0.007901557
rs78727187	5	127668685	G	T	0.020172176	2.60E-12	0.017320449	1.90E-09	G	T	0.010095911	0.017723012
rs154001	5	127685135	C	T	0.017467391	1.40E-09	0.010515684	0.00027	C	T	0.011816316	0.002431285
rs272893	5	131663062	T	C	0.024479465	2.10E-17	0.000804324	0.78	T	C	0.022684943	0.001529444
rs62623707	5	135288632	A	G	-0.005616165	0.051	-0.006435509	0.026	A	G	-0.005697509	-0.008651836
rs61743469	5	140562739	G	A	0.006662375	0.021	0.00723559	0.012	G	A	0.004387776	0.009207686
rs3910203	5	141573265	G	A	0.012919716	7.40E-06	0.012017241	3.10E-05	G	A	0.007030754	0.006664345
rs4282339	5	168256240	G	A	-0.020860948	4.70E-13	0.00163334	0.57	G	A	-0.017988079	9.09E-05
rs11745536	5	170838791	G	A	-0.01746677	1.40E-09	-0.012851053	8.30E-06	G	A	-0.012439277	-0.008582826
rs4868125	5	171281875	C	G	0.030257417	9.20E-26	0.003696172	0.2	C	G	0.021504344	-0.001309067
rs34471628	5	172196752	A	G	0.012136735	2.60E-05	0.012778806	9.30E-06	A	G	0.006906399	0.005276402
rs148833559	5	172755066	C	A	0.010160053	0.00043	0.009545579	0.00093	C	A	-0.001782986	0.016788138
rs889014	5	172984114	C	T	-0.016882348	4.80E-09	-0.000422199	0.88	C	T	-0.018078012	0.000847418
rs1966265	5	176516631	G	A	0.035395314	1.20E-34	0.025460785	1.00E-18	G	A	0.018253594	0.02046274
rs422421	5	176517326	T	C	0.029384311	2.20E-24	-0.000388265	0.89	T	C	0.017826268	0.000643069
rs28932177	5	176637471	G	A	0.01851935	1.30E-10	0.004621582	0.11	G	A	0.012479703	-0.001189237
rs78247455	5	176722005	G	A	-0.022916373	1.90E-15	-9.13E-05	0.97	G	A	-0.013718377	-0.001801744
rs1445845	5	178507090	G	A	-0.010759908	0.00019	0.00042441	0.88	G	A	-0.012601118	-0.000707053
rs6879260	5	179731014	T	C	0.017653282	9.20E-10	-0.003192745	0.27	T	C	0.016730973	-0.000750979
rs1570534	6	1901495	C	T	0.013871672	1.50E-06	0.011402012	7.70E-05	C	T	0.008863699	0.005054645
rs148543891	6	1901495	G	A	-0.001697365	0.56	-0.001682949	0.56	NA	NA	NA	NA
rs2323150	6	1901495	A	G	0.026835146	1.30E-20	0.005233235	0.07	NA	NA	NA	NA
rs9379084	6	7231843	G	A	-0.022166705	1.50E-14	-0.02038553	1.50E-12	G	A	-0.014926652	-0.021144749
rs12198986	6	7720059	G	A	0.034875403	1.10E-33	-0.000934569	0.75	G	A	0.026621425	0.002341353
rs2228375	6	17675246	T	C	0.001445825	0.62	-0.001103631	0.7	T	C	0.008800347	-0.002443932
rs1047014	6	19841493	T	C	0.020308662	1.90E-12	-0.000490961	0.86	T	C	0.014519225	0.000128493
rs16891235	6	26017542	T	C	-0.003383738	0.24	-0.01404833	1.10E-06	T	C	-0.000859868	-0.01277499
rs198845	6	26107790	G	T	0.026132644	1.30E-19	0.010400939	0.00031	G	T	0.021805353	0.010095788
rs10946808	6	26233387	A	G	-0.044544785	7.60E-54	-0.003264657	0.26	A	G	-0.031890296	0.004293245
rs4947339	6	28916252	C	T	-0.02249533	6.10E-15	-0.000660126	0.82	C	T	-0.017568949	0.001096301
rs7757648	6	30851933	G	A	-0.011540243	6.30E-05	-0.000928087	0.75	G	A/T	-0.011346744	-0.002255687
rs2256183	6	31380529	A	G	-0.030168581	1.30E-25	-0.006959548	0.016	A	G	-0.019550918	-0.000591946
rs6457617	6	32663851	C	T	-0.024963536	4.80E-18	-0.009938109	0.00057	C	T	-0.015352153	-0.00782966
rs4713668	6	33690796	C	T	0.017404585	1.60E-09	0.00904975	0.0017	C	T	0.011637221	0.004387722
rs7742369	6	34165721	A	G	0.039463443	1.20E-42	0.007436857	0.0099	A	G	0.028760921	0.00450617
rs2780226	6	34199092	C	T	-0.041814209	1.20E-47	-0.002086882	0.47	C	T	-0.03225905	-0.00475913
rs2814993	6	34618893	G	A	0.034481329	5.80E-33	0.000655801	0.82	G	A	0.02576188	0.003158142
rs34427075	6	34730395	C	T	-0.029284389	3.10E-24	-0.001232413	0.67	C	T	-0.016180865	-0.002039944
rs4713858	6	35402785	A	G	0.020761745	6.00E-13	0.004275121	0.14	A	G	0.016779693	0.001821443
rs6922865	6	36094188	T	G	-0.009376729	0.0011	-0.006928601	0.016	T	G	-0.005146099	-0.007017877
rs2842643	6	41650736	C	T	-0.002918398	0.31	0.001238644	0.67	C	T	-0.005540002	-0.002294668
rs33966734	6	41903798	C	A	-0.016516575	1.00E-08	-0.016044158	2.60E-08	C	A	-0.00730451	-0.022794673
rs2242416	6	43273604	A	G	0.010520516	0.00026	0.011007389	0.00013	A	G	0.008194746	0.008078326
rs9472414	6	44946506	T	A	-0.012216488	2.30E-05	-0.008119625	0.0049	T	A	-0.016898421	-0.00864364
rs9395066	6	45095163	A	C	0.012606207	1.20E-05	0.000407095	0.89	A	C	0.01719001	-0.003064142
rs10807372	6	47649574	A	G	0.012900045	7.70E-06	0.000418591	0.88	A	G	0.008162809	-0.000770561
rs61740375	6	56919443	A	G	0.003512214	0.22	0.00336574	0.24	A	G	0.007880378	0.005797225
rs6903448	6	76173832	C	T	-0.01732719	1.90E-09	0.000838083	0.77	C	T	-0.016358324	0.001005002
rs9360921	6	76265642	T	G	0.025000384	4.30E-18	0.004374927	0.13	T	G	0.018919572	0.00598612
rs1875845	6	80196848	C	T	0.007274401	0.012	0.002900214	0.31	C	T	0.005332111	0.003026672
rs648831	6	80956208	C	T	0.025540683	8.10E-19	0.00064612	0.82	C	T	0.021659984	0.00147074
rs9443804	6	81315597	A	G	0.013243967	4.40E-06	0.003536286	0.22	A	G	0.015573839	-0.000798014
rs4706980	6	83838673	G	A	0.014784962	2.90E-07	0.015479511	7.90E-08	G	A	0.006887725	0.00599182
rs7759938	6	105378954	C	T	-0.036963467	1.30E-37	-0.000956119	0.74	C	T	-0.027515164	0.00093059
rs3800229	6	108996963	G	T	0.020172932	2.60E-12	0.006251065	0.03	G	T	0.012856652	0.003323815
rs1476387	6	109764535	G	T	-0.018555556	1.20E-10	0.00068077	0.81	G	T	-0.016898508	-0.000505003
rs1999930	6	116387134	C	T	0.013121281	4.60E-06	0.002749812	0.34	C	T	0.01019262	-0.002403939
rs961764	6	117522156	C	G	0.019439089	1.60E-11	0.000258492	0.93	C	G	0.015591095	0.001349995
rs1490388	6	126835655	C	T	0.036077896	6.40E-36	0.00171967	0.55	C	T	0.024918787	0.000966167
rs2876066	6	130322179	C	A	-0.015074698	1.70E-07	-0.000313097	0.91	C	A	-0.013025547	-0.003355426
rs6569648	6	130349119	C	T	-0.038129593	6.40E-40	0.000751545	0.79	C	T	-0.027186352	-0.001290584
rs7752169	6	136227558	T	C	0.007267997	0.012	0.008587016	0.0029	T	C	0.005458993	0.003672237
rs642858	6	140273647	G	A	-0.012530179	1.40E-05	-0.011305589	8.80E-05	G	A	-0.009446738	-0.008982076
rs2931796	6	141443540	C	T	-0.011067198	0.00012	-0.007399065	0.01	C	T	-0.008808011	-0.009087723

rs225717	6	142548099	C	T	0.017700741	8.30E-10	0.007196273	0.013	C	T	0.013974142	0.006049945
rs6570507	6	142679572	G	A	-0.043014525	2.50E-50	-0.001997417	0.49	G	A	-0.032762584	-3.02E-05
rs3811102	6	146125793	A	T	-0.011928251	3.50E-05	-0.000513628	0.86	A	T	-0.009259531	0.002344077
rs543650	6	152110943	T	G	0.023836036	1.40E-16	0.006670383	0.021	T	G	0.019887423	0.006027927
rs1539312	6	158743188	G	A	-0.012683534	1.10E-05	0.002040432	0.48	G	A	-0.012630657	0.000242625
rs12206717	6	158910698	G	A	-0.012245049	2.20E-05	-0.001131718	0.69	G	A	-0.018434896	-0.003159253
rs2147457	6	168810725	A	G	-0.018565359	1.20E-10	-0.004050347	0.16	A	G	-0.011917415	-0.002665896
rs6948971	7	1854263	A	G	0.004107847	0.15	0.002095889	0.47	A	G	0.007176892	0.009668715
rs798497	7	2795957	A	G	-0.044410138	1.60E-53	0.002289293	0.43	A	G	-0.031569981	0.006770665
rs4470914	7	19616522	C	T	0.020466636	1.30E-12	0.002282801	0.43	C	T	0.015622681	-0.000603398
rs12534093	7	23502974	T	A	-0.026667674	2.30E-20	0.000549981	0.85	T	A	-0.02000883	0.001203595
rs1055144	7	25871109	C	T	0.017201775	2.40E-09	-0.001060133	0.71	C	T	0.010504345	0.0006494
rs849141	7	28185091	A	G	-0.0343937	8.40E-33	0.000851555	0.77	A	G	-0.027445935	0.002714324
rs1802074	7	37947103	C	T	0.012387619	1.70E-05	0.01503895	1.80E-07	C	T	0.003648881	0.004324845
rs6959212	7	38128326	T	C	0.017499418	1.30E-09	-0.002890982	0.32	T	C	0.015712263	0.000376813
rs1079866	7	41470093	C	G	0.004258149	0.14	0.005140944	0.075	C	G	0.006198914	0.006468415
rs1007358	7	46201355	A	G	0.020119698	3.00E-12	0.001028339	0.72	A	G	0.011526465	0.002301915
rs17172694	7	46437154	G	T	-0.015940828	3.20E-08	0.000632988	0.83	G	T	-0.01391634	0.001234943
rs10248619	7	50751090	T	C	-0.00812642	0.0048	0.000512353	0.86	T	C	-0.008519566	-0.002391101
rs11982736	7	55855180	G	A	-0.009595415	0.00088	-0.001460338	0.61	G	A	-0.009072044	-0.002329807
rs17145713	7	72904810	C	T	0.009849106	0.00064	0.009508155	0.00097	C	T	0.008070116	0.009607567
rs41511151	7	73482987	G	A	-0.008360691	0.0037	-0.006123524	0.034	G	A	0.000627795	-0.008776069
rs42235	7	92248076	C	T	0.041731987	1.80E-47	0.003363546	0.24	C	T	0.036863396	-0.005882537
rs17277546	7	99489571	G	A	0.009010238	0.0018	-0.001411972	0.62	G	A	0.012700551	-0.000654916
rs7636	7	100490077	G	A	-0.00552314	0.055	-0.003170394	0.27	G	A	-0.011548338	-0.009971696
rs4728142	7	128573967	G	A	-0.003948278	0.17	-0.003991441	0.17	G	A	-0.00537701	-0.00909642
rs11556924	7	129663496	C	T	0.011751483	4.60E-05	0.012951761	7.10E-06	C	T	0.006137518	0.007117652
rs4731907	7	132526350	T	C	-0.008585705	0.0029	-0.008339458	0.0038	T	C	-0.008547661	-0.010141895
rs77841106	7	135082953	G	C	0.011142195	0.00011	0.007919878	0.006	G	C	0.006489864	0.007113241
rs17480616	7	135123060	G	C	0.017668481	8.90E-10	0.016715669	6.70E-09	G	C	0.005358089	0.012353761
rs273957	7	137600690	C	T	0.014606671	4.10E-07	0.001385641	0.63	C	T	0.011417657	0.000662137
rs2293177	7	140244560	C	T	0.012334906	1.90E-05	0.012615167	1.20E-05	C	T	0.003486819	0.004350435
rs822552	7	148650634	C	G	0.028740195	2.10E-23	0.020609297	8.80E-13	C	G	0.016296776	0.011053433
rs3807375	7	150667210	C	T	0.016166276	2.10E-08	0.010139514	0.00044	C	T	0.009462175	0.004557185
rs7834383	8	13273477	G	T	0.006401123	0.026	-0.001166751	0.69	G	T	0.011363794	-0.002435846
rs1063582	8	23167353	T	G	-0.020620953	8.60E-13	-0.000604937	0.83	T	G	-0.014885833	0.002918809
rs2942202	8	23418444	A	C	-0.017229027	2.30E-09	-0.013500207	2.80E-06	A	C	-0.009393791	-0.005779948
rs1013209	8	24116304	C	T	-0.018695207	8.90E-11	-0.001996484	0.49	C	T	-0.015336218	0.000582159
rs2979531	8	30383013	A	G	-0.01381783	1.60E-06	-0.012948195	7.10E-06	A	G	-0.011202308	-0.011949485
rs3136797	8	42226805	C	G	0.007528937	0.009	0.006771932	0.019	C	G	0.004277361	0.007247578
rs10958476	8	57095808	T	C	0.031923863	1.70E-28	-0.000626138	0.83	T	C	0.023500856	-0.000853236
rs9650315	8	57155598	G	T	-0.035705462	3.20E-35	0.000365056	0.9	G	T	-0.023761573	-0.00179499
rs7846385	8	78160179	T	C	0.030418084	5.10E-26	-0.001392692	0.63	T	C	0.02069692	-0.00372512
rs2304787	8	87568644	T	G	0.010815803	0.00018	0.011993545	3.20E-05	T	G	0.007818747	0.004128369
rs2293889	8	116599199	T	G	-0.012451234	1.60E-05	-0.000192531	0.95	T	G/C	-0.010128635	-0.001795249
rs2469997	8	120353267	G	C	0.010906494	0.00016	-0.002304408	0.42	G	C	0.010319225	-0.002279374
rs956749	8	120744399	C	T	0.01404006	1.10E-06	0.012395912	1.70E-05	C	T	0.007829844	0.007387912
rs2954029	8	126490972	A	T	0.011344182	8.30E-05	0.006716764	0.02	A	T	0.009881344	0.006262566
rs2019960	8	129192271	T	C	-0.015393248	9.40E-08	-0.01566867	5.50E-08	T	C	-0.005664171	-0.004575531
rs4144738	8	130760850	A	G	-0.030145639	1.40E-25	-0.012593153	1.30E-05	A	G	-0.017909386	-0.004615689
rs112892337	8	135614553	G	C	0.016483559	1.10E-08	0.015216613	1.30E-07	G	C	0.000339751	0.014841184
rs75596750	8	135622851	G	A	0.013976546	1.30E-06	0.012470467	1.50E-05	G	A	0.00097094	0.009253268
rs12680655	8	135637337	C	G	-0.028186899	1.40E-22	-0.000636667	0.83	C	G	-0.021786629	0.001331924
rs12541381	8	135649848	G	A	-0.030255069	9.30E-26	-0.017365991	1.70E-09	G	A	-0.012935095	-0.0053052
rs11136344	8	145059425	T	C	-0.02299458	1.50E-15	-0.001304322	0.65	T	C	-0.01299323	-0.002211527
rs11575580	9	34660864	C	T	-0.010040687	5.00E-04	-0.010458292	0.00029	C	T	0.001845848	-0.011913025
rs11144688	9	78542286	G	A	-0.024902709	5.80E-18	0.001251056	0.66	G	A	-0.019381784	0.001684551
rs7866939	9	85126163	T	C	0.011458727	7.10E-05	0.012311133	2.00E-05	T	C	0.005514409	0.006452576
rs1982151	9	86617265	A	G	-0.022639968	4.10E-15	-0.005048816	0.08	A	G	-0.014621386	-0.014846296
rs353785	9	89099362	T	C	0.023940248	1.00E-16	-0.002876409	0.32	T	C	0.017317664	-0.001108291
rs10746839	9	90883630	A	G	-0.02179712	4.00E-14	-0.000615509	0.83	A	G	-0.01644455	-0.000828063
rs10761129	9	94486321	C	T	-0.014411545	5.80E-07	-0.010786621	0.00018	C	T	-0.00973601	-0.005129292
rs921122	9	95063947	C	T	0.00264144	0.36	0.005512246	0.056	C	T	0.005426496	0.006990058
rs9969804	9	95429120	A	C	-0.014552224	4.50E-07	-0.002195062	0.45	A	C	-0.018789648	0.000484694
rs1257763	9	96893945	A	G	-0.023429856	4.40E-16	0.00018939	0.95	A	G	-0.015987892	0.001031391
rs357564	9	98209594	G	A	-0.027481156	1.60E-21	-0.010710694	2.00E-04	G	A	-0.021058735	-0.010087115
rs10990303	9	98410405	C	T	0.025663491	5.60E-19	0.000130654	0.96	C	T	0.020843077	0.002971928
rs2075663	9	101748356	A	G	-0.012232169	2.20E-05	0.001058685	0.71	A	G	-0.011912274	4.78E-05
rs2090409	9	108967088	C	A	-0.01875615	7.80E-11	-0.005539323	0.055	C	A	-0.014124394	-0.00352169
rs7027110	9	109599046	G	A	0.019198012	2.80E-11	-0.001828513	0.53	G	A	0.016702347	-0.006578819
rs2230792	9	111660851	C	T	0.009036723	0.0017	0.009484351	0.001	C	T	0.004709732	0.005585076
rs1468758	9	113807082	C	T	-0.020203796	2.40E-12	0.000418263	0.88	C	T	-0.010799178	-0.000966315
rs10982134	9	117050998	G	A	-0.008193887	0.0045	-0.006494375	0.024	G	A	-0.005920264	-0.004458084
rs7869550	9	119134796	A	G	-0.023449535	4.20E-16	0.000545103	0.85	A	G	-0.018715937	-0.000375817
rs10817896	9	119232655	C	T	-0.004961482	0.085	-0.00335332	0.24	C	T	-0.008785643	-0.008303142
rs7025486	9	124422403	G	A	0.012532168	1.40E-05	0.011873435	3.80E-05	G	A	0.008068986	0.009862844
rs7466269	9	133464084	A	G	-0.02586493	3.00E-19	-0.0004537	0.87	A	G	-0.017576798	0.000979537
rs28473627	9	136996067	A	G	-0.009326267	0.0012	-0.009977576	0.00054	A	G	-0.008733035	-0.007022125
rs12684650	9	139110654	C	T	-0.023531781	3.30E-16	-0.012716653	1.00E-05	C	T	-0.016903947	-0.004683098
rs12338076	9	139121740	A	C	0.022998859	1.50E-15	0.000665128	0.82	A	C/T	0.019546537	-0.004066647
rs3812594	9	139368953	G	A	0.019310684	2.10E-11	-0.00297605	0.3	G	A	0.013602745	-0.002255912
rs12774134	10	4963227	C	T	-0.023203353	8.50E-16	0.001543468	0.59	C	T	-0.014326717	-1.98E-05
rs2631681	10	4963227	T	C	-0.023064339	1.30E-15	-0.005483505	0.057	NA	NA	NA	NA
rs7909670	10	12918764	C	T	-0.020658537	7.80E-13	-0.003364556	0.24	C	T	-0.014523356	-0.001519102
rs2230469	10	22839628	T	C	0.007924603	0.006	0.007953377	0.0058	T	C	0.009294937	0.009569574
rs274312	10	25244392	C	T	0.007528627	0.009	0.008906408	0.002	C	T	0.005780205	0.006896372
rs10821936	10	63723577	C	T	-0.01106501	0.00012	-0.012121077	2.60E-05	C	T	-0.005906923	-0.00777995
rs10997975	10	69933921	G	A	0.02325056	7.40E-16	0.000686589	0.81	G	A	0.014524217	0.000814899
rs12221107	10	70332862	C	T	-0.019266639	2.40E-11	-0.017600521	1.00E-09	C	T	-0.012409364	-0.00864928
rs41274586	10	79580976	G	A	-0.019643048	9.60E-12	-0.012945656	7.10E-06	G	A	-0.005261281	-0.010538226
rs1248696	10	79616605	T	C	-0.009862651	0.00062	-0.009486518	0.001	T	C	0.000430535	-0.007679648
rs41291604	10	97919011	A	G	0.007523305	0.0091	0.006418526	0.026	A	G	0.005246272	0.002920211
rs1983864	10	100017453	T	G	0.013956184	1.30E-06	0.014835097	2.70E-07	T	G	0.008776503	0.008270184
rs11599750	10	101805442	C	T	-0.011274497	9.20E-05	-6.52E-05	0.98	C	T	-0.012596598	0.002825265
rs11591349	10	102744331	A	T	0.013317066	3.90E-06	-0.001388774	0.63	A	T	0.010908351	0.003254781
rs2281880	10	104269217	G	A	0.028241433	1.20E-22	0.004944818	0.086	G	A	0.015944542	0.002719752
rs2487999	10	105659826	T	C	-0.01490304	2.40E-07	-0.004070991	0.16	T	C	-0.008845936	0.000148058
rs3736946	10	114169276	A	G	-0.00297844	0.3	-0.004520806	0.12	A	G	-0.007632515	-0.00866244
rs2234962	10	121429633	T	C	-0.018239491	2.50E-10	-0.018176469	2.90E-10	T	C	-0.006826394	-0.005033639
rs6585827	10	124165615	G	A	0.019943314	4.60E-12	-0.000616824	0.83	G	A	0.011451406	0.001559866
rs12812	11	1977552	G	A	0.020896314	4.30E-13	0.006518654	0.024	G	A	0.014189021	0.005698917
rs10770125	11	2169014	A	G	0.019427223	1.60E-11	0.011300125	8.90E-05	A	G	0.00994197	0.00490909
rs1004446	11	2170143	G	A	0.005657645	0.05	-0.006408601	0.026	G	A	0.007765049	0.000222215
rs2237886	11	2810731	C	T	0.028238749	1.20E-22	-0.001405076	0.63	C	T	0.01809831	0.0001576
rs110419	11	8252853	A	G	-0.010483864	0.00028	-0.007929221	0.006	A	G	-0.011423466	-0.012175928
rs3206824	11	11986061	T	C	0.011646866	5.40E-05	0.01267986	1.10E-05	T	C	0.009663234	0.011760747
rs7926971	11	12698040	A	G	0.017700226	8.30E-10	-0.000588259	0.84	A	G	0.015337346	0.000744308
rs757081	11	17351683	C	G	0.014537233	4.60E-07	-0.000337717	0.91	C	G	0.015307814	-0.002091621
rs11024739	11	18645843	C	A	-0.018360777	1.90E-10	-0.019491129	1.40E-11	C	A	-0.009948628	-0.012364581
rs138273386	11	27016360	G	A	-0.008235521	0.0043	-0.009432181	0.0011	G	A	-0.000359093	-0.013488074
rs2183848	11	30394734	G	A	-0.010053263	0.00049	-0.002301601	0.42	G	A	-0.013174222	0.003275982
rs16938437	11	46052575	C	T	-0.010792809	0.00018	-0.007817049	0.0067	C	T	-0.009835917	-0.000864477
rs10838738	11	47663049	A	G	-0.019783776	6.80E-12	-0.0089435	0.0019	A	G	-0.014875886	-0.004921745
rs102275	11	61557803	T	C	-0.016143231	2.20E-08	-0.016926961	4.30E-09	T	C	-0.010439849	-0.009787878
rs514076	11	64990041	G	C	0.015010387	1.90E-07	0.00890295	0.002	G	C	0.01136539	0.006589655
rs71455793	11	65715204	G	A	-0.025562571	7.60E-19	-0.015292578	1.10E-07	G	A	-0.017613489	-0.007665164
rs7112925	11	66826160	C	T	-0.025041898	3.80E-18	0.000858406	0.77	C	T	-0.015560722	0.000145988
rs3736228	11	68201295	C	T	-0.022496523	6.10E-15	-0.003575866	0.21	C	T	-0.011722442	2.95E-05
rs3829241	11	68855363	G	A	-0.015940711	3.20E-08	-0.008870056	0.0021	G	A	-0.011336505	-0.001833195
rs634552	11	75282052	T	G	-0.028476355	5.30E-23	0.000588099	0.84	T	G	-0.019582536	0.001822844
rs2510044	11	77909014	G	A	0.002955328	0.31	0.004605944	0.11	G	A	0.003146123	0.004145227
rs641393	11	85436352	G	A	0.012971534	6.80E-06	0.011399354	7.70E-05	G	A	0.007658809	0.005927799
rs138059525	11	94533444	G	A	-0.009174886	0.0015	-0.009731603	0.00074	G	A	-0.002008207	-0.017468746
rs12269901	11	116973929	G	C	-0.011574844	6.00E-05	-0.010171681	0.00042	G	C	-0.008048901	-0.009673343
rs494459	11	118574675	C	T	0.009399763	0.0011	-0.000675673	0.81	C	T	0.01408422	-0.000148796
rs654723	11	128586155	C	A	0.008437261	0.0034	0.007683938	0.0077	C	A	0.010400512	0.004762482
rs527118	12	371410	T	C	-0.014465153	5.30E-07	-0.007977567	0.0057	T	C	-0.005515983	-0.00366111
rs11063069	12	4374373	A	G	-0.008018001	0.0054	-0.009329902	0.0012	A	G	-0.008744436	-0.007780286
rs4072796	12	7548996	C	G	0.001927813	0.5	0.001004348	0.73	C	G	0.003767773	0.008241353
rs2856321	12	11855773	G	A	-0.020146324	2.80E-12	0.001662979	0.56	G	A	-0.018230854	0.002061816
rs3213764	12	14587301	A	G	0.016290425	1.60E-08	-0.002108371	0.46	A	G	0.010491852	0.001105197

rs10770705	12	20857467	A	C	-0.018268056	2.40E-10	-0.001287018	0.66	A	C	-0.01808474	0.001794865
rs11049488	12	28412372	G	A	-0.030289441	8.20E-26	-0.000681087	0.81	G	A	-0.02300027	0.001927663
rs10876041	12	50901882	T	C	-0.01751902	1.20E-09	-0.018002405	4.30E-10	T	C	-0.007427942	-0.007905392
rs59626664	12	56636975	C	G	0.01954026	1.20E-11	0.002039545	0.48	C	G	0.011987728	-4.66E-05
rs2277339	12	57146069	T	G	-0.011896694	3.70E-05	-0.014011149	1.20E-06	T	G	-0.00757132	-0.013037922
rs147996581	12	58138971	G	A	-0.004022665	0.16	-0.004963628	0.085	G	A	-0.003432262	-0.004718534
rs4760332	12	58222672	C	A	-0.022591256	4.70E-15	-0.001775096	0.54	C	A	-0.013024799	0.000368856
rs8756	12	66359752	C	A	-0.045029483	5.60E-55	-0.000986255	0.73	C	A	-0.038375204	9.57E-05
rs12424086	12	66364509	T	C	-0.035092079	4.50E-34	-0.009195725	0.0014	T	C	-0.028179961	-0.003582268
rs4026608	12	66394664	C	T	0.022316178	1.00E-14	0.014072058	1.10E-06	C	T	0.012188076	0.005673151
rs8793	12	66546100	A	G	0.011883355	3.80E-05	0.011697267	5.00E-05	A	G	0.010087152	0.009053278
rs61743810	12	69140339	G	C	-0.011999559	3.20E-05	-0.011185906	1.00E-04	G	C	-0.0040575	-0.009735058
rs10748128	12	69827658	G	T	0.02311264	1.10E-15	-0.002836388	0.33	G	T	0.021312011	-0.002587192
rs17783015	12	90231386	C	T	-0.009608006	0.00086	-0.001567125	0.59	C	T	-0.008945786	0.003128001
rs3825199	12	93976954	A	G	0.037963091	1.40E-39	-0.000516391	0.86	A	G	0.025947076	-0.00026615
rs3812813	12	95927762	T	C	-0.003039948	0.29	-0.003426963	0.23	T	C	-0.005566472	-0.003409711
rs7978999	12	102368065	T	C	-0.01656086	9.30E-09	0.003835278	0.18	T	C	-0.01532948	0.003090769
rs7296248	12	103077198	C	T	0.017847279	6.00E-10	0.011167337	0.00011	C	T	0.009706929	0.004098058
rs11612024	12	104354173	C	T	0.014856053	2.60E-07	0.007019777	0.015	C	T	0.011817281	0.005711284
rs117801489	12	104408832	T	C	0.012108352	2.70E-05	0.012671693	1.10E-05	T	C	0.004136219	0.011527103
rs1196761	12	105606172	G	A	0.005501196	0.056	0.005044252	0.08	G	A	0.006032152	0.006526096
rs10861661	12	107174646	A	C	-0.01059282	0.00024	-0.006745765	0.019	A	C	-0.009214586	-0.004391967
rs4076700	12	117383320	G	A	0.016742065	6.40E-09	0.003753448	0.19	G	A	0.010372581	-0.000226873
rs13141	12	121756084	G	A	-0.016805987	5.60E-09	-0.01593253	3.30E-08	G	A	-0.005006968	-0.011596884
rs11835818	12	122494809	T	C	0.00937244	0.0012	-0.002139334	0.46	T	C	0.014315864	-0.000385949
rs1060105	12	123806219	C	T	0.027248954	3.40E-21	-0.001267359	0.66	C	T	0.021121174	0.0017328
rs1809889	12	124801226	T	C	-0.02262445	4.30E-15	-0.000637792	0.82	T	C	-0.017285695	0.004696495
rs2442455	13	21189941	G	A	0.006689208	0.02	0.006596774	0.022	G	A	0.00688939	0.009911351
rs2770928	13	21562832	C	T	0.019057594	3.90E-11	0.005849577	0.042	C	T	0.009912246	0.000978517
rs7332115	13	33147548	T	G	0.011065677	0.00012	-0.002011815	0.49	T	G	0.011089776	0.000458144
rs9315204	13	33693837	C	T	-0.010694621	0.00021	-0.002110188	0.46	C	T	-0.008579237	-0.003412626
rs2755237	13	41109429	A	C	-0.013385405	3.40E-06	-0.013906132	1.40E-06	A	C	-0.005853813	-0.00770975
rs2066674	13	50842259	G	A	0.030167676	1.30E-25	0.016235344	1.80E-08	G	A	0.017871515	0.00767789
rs3118914	13	51116901	G	T	-0.035439668	1.00E-34	-4.19E-05	0.99	G	T	-0.031281049	0.001670365
rs279070	13	51133655	A	G	0.008766075	0.0024	-0.003236068	0.26	A	G	0.004462176	-0.005953262
rs1359790	13	80717156	G	A	0.007619823	0.0082	0.000284853	0.92	G	A	0.009792455	-0.002909331
rs7319045	13	92024574	A	G	-0.022648682	4.00E-15	0.000651754	0.82	A	G	-0.015710207	0.000465574
rs2044117	13	101708310	G	A	-0.005766182	0.046	-0.006746989	0.019	G	A	-0.002132742	-0.001670962
rs17880989	14	23313633	G	A	0.014225148	8.10E-07	0.013989216	1.20E-06	G	A	0.002988804	0.008671387
rs12050260	14	23761094	T	C	0.015236392	1.30E-07	0.00397062	0.17	T	C	0.007357595	-0.006050721
rs34354104	14	24707479	G	A	0.016599809	8.60E-09	0.011984858	3.20E-05	G	A	0.010348944	0.004097569
rs1950500	14	24830850	T	C	-0.020298454	1.90E-12	-0.000192448	0.95	T	C	-0.020364348	0.001358857
rs117295933	14	45403699	C	A	-0.005753479	0.046	-0.006011856	0.037	C	A	-0.004525041	-0.008847125
rs8022503	14	55265828	T	C	0.015985888	3.00E-08	0.004983165	0.084	T	C	0.012229636	-0.00011128
rs10483727	14	61072875	T	C	-0.028453383	5.70E-23	0.000462944	0.87	T	C	-0.025312077	0.000250911
rs6573513	14	63855760	C	T	-0.012068717	2.80E-05	-0.010829949	0.00017	C	T	-0.003375611	-0.003879145
rs4466998	14	65475540	C	A	-0.013259758	4.20E-06	-0.003571076	0.22	C	A	-0.005475317	0.00126066
rs8017304	14	68785077	G	A	0.005566348	0.054	0.002846204	0.32	G	A	0.01221308	0.010238553
rs41286548	14	70633411	C	T	-0.009465576	0.001	-0.00848372	0.0033	C	T	-0.004030341	-0.010778452
rs862034	14	74990746	A	G	0.020591846	9.20E-13	-0.000545568	0.85	A	G	0.01705963	-0.000551124
rs10083386	14	75347585	C	A	0.012144336	2.50E-05	0.006916541	0.016	C	A	0.006665603	0.004748137
rs2303345	14	76156609	C	T	-0.012567884	1.30E-05	-0.013333219	3.80E-06	C	T	-0.005801273	-0.00567111
rs10146997	14	79945162	A	G	0.009687561	0.00078	0.011099694	0.00012	A	G	0.00860356	0.007982622
rs7153027	14	92427222	A	C	-0.020794499	5.50E-13	-0.000214839	0.94	A	C	-0.016805042	-0.000433789
rs28929474	14	94844947	C	T	0.030013594	2.20E-25	0.01517069	1.40E-07	C	T	0.015870962	0.024039578
rs41286560	14	101349454	G	T	-0.007508438	0.0092	-0.008082056	0.0051	G	T	0.001569167	-0.009972388
rs7158139	14	102792631	G	A	-0.009091585	0.0016	-0.002086554	0.47	G	A	-0.010097764	-0.002762331
rs116858574	15	34520687	T	C	0.003611116	0.21	0.004348107	0.13	T	C	0.002804747	0.007870282
rs141308595	15	34520687	T	G	0.003991749	0.17	0.003462252	0.23	NA	NA	NA	NA
rs1899	15	41689232	C	T	-0.011368241	8.10E-05	-0.003893121	0.18	C	T	-0.011997173	-0.002317924
rs150494621	15	44153571	C	T	0.006974037	0.016	0.007726801	0.0074	C	T	-0.003032045	0.00769023
rs56170748	15	50932357	C	T	0.013002543	6.50E-06	0.006581092	0.022	C	T	0.010356604	0.003769678
rs16964211	15	51530495	G	A	-0.016147786	2.10E-08	-0.000424574	0.88	G	A	-0.01514891	0.000833507
rs3743266	15	60781513	T	C	-0.012845441	8.40E-06	-0.013303884	3.90E-06	T	C	-0.009872569	-0.011626459
rs7178424	15	62380259	C	T	-0.016289155	1.60E-08	0.001122798	0.7	C	T	-0.011375596	0.002504086
rs3743171	15	65916527	A	T	0.012053992	2.90E-05	0.011999011	3.20E-05	A	T	0.007722954	0.009105377
rs7173826	15	67528374	T	G	-0.009531731	0.00095	-0.007034383	0.015	T	G	-0.007582901	-0.004328814
rs10152591	15	70048157	A	C	-0.023021585	1.40E-15	0.001331659	0.64	A	C	-0.015254016	0.001517185
rs975210	15	70364352	G	A	0.021241883	1.70E-13	-0.000145224	0.96	G	A	0.015807595	0.001039813
rs34815962	15	72462255	C	T	0.017154517	2.70E-09	0.008491952	0.0032	C	T	0.012722065	0.003563967
rs893817	15	74229065	G	A	-0.015878084	3.70E-08	0.000915121	0.75	G	A	-0.016323561	-0.003378883
rs5742915	15	74336633	T	C	0.029421298	1.90E-24	0.000156214	0.96	T	C	0.016822147	-0.003380779
rs4886707	15	75755467	C	T	0.018626064	1.00E-10	0.015788853	4.40E-08	C	T	0.009123485	0.007702803
rs11636648	15	77335891	C	T	-0.011971984	3.30E-05	-0.008325454	0.0039	C	T	-0.011098907	-0.00674766
rs7183263	15	84573041	T	G	0.042956735	3.40E-50	0.010433905	3.00E-04	T	G	0.028769245	0.003856377
rs8032301	15	85635890	T	C	0.010234419	0.00039	0.010050337	0.00049	T	C	0.005442568	0.007267742
rs16943741	15	86278479	A	G	-0.016946467	4.20E-09	-0.014247796	7.80E-07	A	G	-0.008284253	-0.004996138
rs8028537	15	89345947	A	G	0.029845523	4.10E-25	0.000612446	0.83	A	G	0.021203331	0.002838031
rs34949187	15	89386652	G	A	-0.021219861	1.80E-13	-0.021931828	2.80E-14	G	A	-0.009815789	-0.010125228
rs16942341	15	89388905	C	T	-0.040577486	5.60E-45	0.002085911	0.47	C	T	-0.020021296	0.002176423
rs938608	15	89398605	G	T	-0.016961841	4.00E-09	0.001161641	0.69	G	T	-0.016449984	-0.000142925
rs3817428	15	89415247	C	G	-0.031326233	1.70E-27	0.000207338	0.94	C	G	-0.019452315	0.004803588
rs2589957	15	90903311	A	G	0.012184143	2.40E-05	0.013080524	5.70E-06	A	G	0.006600265	0.006802823
rs899609	15	94570578	T	C	0.007903018	0.0061	0.000369711	0.9	T	C	0.009403713	0.001634146
rs2871865	15	99194896	C	G	-0.030900176	8.50E-27	0.000794877	0.78	C	G	-0.023243231	0.002277874
rs11634977	15	100516472	G	A	0.016541653	9.60E-09	-0.000561067	0.85	G	A	0.015416759	-0.00358261
rs72755233	15	100692953	G	A	-0.045838758	6.60E-57	-0.043863377	2.90E-52	G	A	-0.010059829	-0.037209964
rs4533267	15	100786271	A	G	-0.027864985	4.30E-22	-0.009796839	0.00068	A	G	-0.018196677	-0.005352748
rs62621399	15	101717888	C	T	0.014850575	2.60E-07	0.010250352	0.00038	C	T	0.009270536	0.005398256
rs62621400	15	101718239	C	G	-0.029223818	3.80E-24	-0.020235246	2.20E-12	C	G	-0.008565334	-0.015626784
rs2071979	16	624114	A	G	0.011907772	3.60E-05	-9.69E-05	0.97	A	G	0.012509983	0.003367905
rs2303262	16	624114	T	C	0.019569354	1.10E-11	0.00420824	0.14	NA	NA	NA	NA
rs837763	16	624114	T	C	0.011047319	0.00013	0.011305364	8.80E-05	NA	NA	NA	NA
rs2071950	16	774692	A	G	0.021700913	5.20E-14	0.008377248	0.0037	A	G	0.016467567	0.007125864
rs10960	16	2140680	T	C	-0.019969922	4.30E-12	-0.012845418	8.40E-06	T	C	-0.014414077	-0.007279567
rs26857	16	2260567	C	T	0.013289155	4.00E-06	-0.001564424	0.59	C	T	0.013092056	-0.000623894
rs61733564	16	4812705	A	G	0.013578204	2.50E-06	0.009978211	0.00054	A	G	0.014705894	0.010766032
rs1659127	16	14388305	G	A	0.018008521	4.20E-10	0.001211871	0.67	G	A/C	0.013840987	-0.004439671
rs1136001	16	15131974	G	T	-0.014081424	1.00E-06	-0.014684398	3.50E-07	G	T	-0.007908026	-0.008138811
rs11074471	16	20748331	C	A	-0.009610872	0.00086	-0.006852283	0.017	C	A	-0.007366029	-0.006198382
rs113388806	16	24804954	A	T	0.014022429	1.20E-06	0.01101784	0.00013	A	T	0.007824438	0.011111429
rs9928448	16	30072530	T	C	0.013081351	5.70E-06	0.000606805	0.83	T	C	0.009752047	0.002026417
rs141923065	16	31474091	A	G	0.004620492	0.11	0.00533937	0.064	A	G	0.003023744	0.012037834
rs34667348	16	47684830	C	A	0.005716098	0.047	0.006857905	0.017	C	A/T	0.001927078	0.010284805
rs8052655	16	67409180	G	A	-0.01569636	5.20E-08	0.002823688	0.33	G	A	-0.011124111	-0.000914883
rs140385822	16	67470505	G	A	-0.009001862	0.0018	-0.010570411	0.00025	G	A	0.000395584	-0.009587259
rs4783718	16	69547741	T	C	0.022123795	1.70E-14	0.001158846	0.69	T	C	0.015554698	0.00232975
rs3931036	16	70548297	G	A	-0.013758625	1.80E-06	-0.00642146	0.026	G	A	-0.008293842	-0.002378725
rs9921412	16	71988106	C	T	-0.010267322	0.00037	-0.002805274	0.33	C	T	-0.009406406	-0.002281989
rs2063506	16	73793552	A	G	-0.011356419	8.20E-05	-0.011447923	7.20E-05	A	G	-0.008766316	-0.00925007
rs9927661	16	78343690	G	A	-0.011816019	4.20E-05	-0.011395815	7.70E-05	G	A	-0.007350492	-0.006620583
rs149615348	16	84900645	G	A	-0.013230478	4.50E-06	-0.012412232	1.70E-05	G	A	-0.005569129	-0.00392106
rs148934412	16	84902472	G	A	-0.001969186	0.49	-0.002584244	0.37	G	A	0.003165199	-0.013226697
rs2326458	16	84987679	C	A	-0.02129457	1.50E-13	-0.000529865	0.85	C	A	-0.01096063	-0.000422041
rs201226914	16	88798919	G	T	-0.014022447	1.20E-06	-0.012897071	7.70E-06	G	T	-0.000557832	-0.009642719
rs7184427	16	88804734	A	G	0.01896067	4.80E-11	0.009923946	0.00058	A	G	0.012394202	0.00442947
rs1126464	16	89704365	G	C	0.018925932	5.20E-11	0.015994672	2.90E-08	G	C	0.005091142	0.006627376
rs1136287	17	1673276	C	T	-0.017135324	2.80E-09	-0.016898126	4.60E-09	C	T	-0.009112957	-0.008943737
rs9217	17	7363088	T	C	0.028645331	2.90E-23	-0.002768882	0.34	T	C	0.016278027	-0.001628734
rs7946	17	17409560	C	T	0.003743271	0.19	0.001560479	0.59	C	T	0.007744251	0.006391598
rs4640244	17	21284223	A	G	-0.018845728	6.30E-11	0.002780807	0.33	A	G	-0.012962843	0.004667661
rs542939	17	27889986	T	C	0.02302587	1.40E-15	0.017270022	2.10E-09	T	C	0.006654345	0.013077282
rs3816780	17	29161358	C	T	0.002665237	0.36	0.000836548	0.77	C	T	0.001331158	0.000131137
rs3760318	17	29247715	G	A	-0.037951157	1.40E-39	0.00291961	0.31	G	A	-0.025894196	0.00043845
rs1043515	17	36922196	A	G	0.019188983	2.80E-11	0.000492976	0.86	A	G	0.013962058	-0.000774183
rs13695	17	38545193	C	T	0.017653332	9.20E-10	0.008381878	0.0036	C	T	0.011964376	0.005561484
rs2290207	17	38640744	C	T	0.007694978	0.0076	0.00017395	0.95	C	T	0.005034916	-0.003257552
rs2292751	17	40725799	C	T	0.00857541	0.0029	-0.001610174	0.58	C	T	0.011450441	0.002001525
rs4986172	17	43216281	C	T	-0.021853985	3.50E-14	0.001861638	0.52	C	T	-0.018231487	0.003071228
rs8070723	17	44081064	A	G	-0.011649012	5.30E-05	-0.002002506	0.49	A	G	-0.007083007	0.000126213
rs80267077	17	45786621	G	A	-0.013977597	1.20E-06	-0.005994176	0.038	G	A	-0.01028959	-0.006609865

rs15563	17	47005193	A	G	-0.023148924	9.90E-16	0.000905272	0.75	A	G	-0.015520008	0.000369454
rs2072153	17	47390014	G	C	0.016194232	1.90E-08	-0.001610472	0.58	G	C/A	0.01661174	-0.00100741
rs227724	17	54778817	A	T	0.018386942	1.80E-10	0.000245931	0.93	A	T	0.018336594	-0.001523288
rs4794665	17	54850329	A	G	-0.027751869	6.30E-22	-0.000438341	0.88	A	G	-0.018393518	0.000707709
rs757608	17	59497277	A	G	-0.035505281	7.60E-35	0.000162545	0.96	A	G	-0.028178727	0.001324594
rs2378871	17	59638769	A	C	-0.020718133	6.70E-13	0.001020436	0.72	A	C	-0.010830392	0.002413423
rs7209435	17	61712964	T	C	0.036673339	4.60E-37	-0.001005883	0.73	T	C	0.024450129	-0.004577089
rs13030	17	61908556	C	T	-0.025845155	3.10E-19	0.004850345	0.093	C	T	-0.022648095	0.003247784
rs3760238	17	62050528	T	C	-0.01647471	1.10E-08	-0.012545599	1.40E-05	T	C	-0.007876505	-0.004522042
rs2240308	17	63554591	G	A	0.017628004	9.70E-10	0.005172424	0.073	G	A	0.009314883	0.000961351
rs9912468	17	64318357	G	C	0.01096968	0.00014	0.010132159	0.00044	G	C	0.008650684	0.005798827
rs12602912	17	65870073	C	T	0.012872984	8.00E-06	0.013565667	2.50E-06	C	T	0.009051698	0.008488916
rs77542162	17	67081278	A	G	0.017593185	1.00E-09	0.016404477	1.30E-08	A	G	0.003612535	0.008464884
rs11867479	17	68090207	C	T	0.02257153	4.90E-15	0.000384738	0.89	C	T	0.014612752	-0.003212961
rs2158917	17	69926109	C	T	0.015482407	7.90E-08	-0.00121598	0.67	C	T	0.012280078	-0.000252007
rs1057040	17	76799795	G	A	-0.011448834	7.20E-05	-0.002417828	0.4	G	A	-0.012386482	-0.002908928
rs4239020	17	80176641	C	T	-0.013598547	2.40E-06	-0.001037124	0.72	C	T	-0.01238723	4.43E-05
rs563155	18	166819	T	C	0.007765202	0.0071	0.007998241	0.0055	T	C	0.006950651	0.008249494
rs6505780	18	13069782	C	T	-0.0113147	8.70E-05	0.000174008	0.95	C	T	-0.011469968	-0.000173563
rs11082304	18	20720973	G	T	0.038655237	5.50E-41	0.013179665	4.90E-06	G	T	0.02325907	0.008088373
rs4369779	18	20735408	T	C	0.049179496	3.10E-65	-0.001309492	0.65	T	C	0.031272171	0.003989847
rs9967417	18	46959500	G	C	-0.028765666	1.90E-23	0.001080557	0.71	G	C	-0.022757977	0.00368028
rs8099594	18	46991160	A	G	-0.024567238	1.60E-17	-0.001563425	0.59	A	G	-0.021190234	0.001437513
rs17782313	18	57851097	T	C	0.022448136	6.90E-15	-0.002189628	0.45	T	C	0.014512555	0.000715377
rs77169818	18	74980601	A	T	-0.010824339	0.00017	-0.000826571	0.77	A	T	-0.010408989	0.00127512
rs12982744	19	2177193	C	G	0.028642944	3.00E-23	-0.000151857	0.96	C	G	0.020422451	-0.000867289
rs147110934	19	2177193	T	G	0.024135048	5.70E-17	0.024301382	3.50E-17	NA	NA	NA	NA
rs2261988	19	4910889	G	T	0.02031051	1.90E-12	0.017788459	6.90E-10	G	T	0.010873424	0.008188329
rs891088	19	7184762	A	G	0.019378752	1.80E-11	-0.000169552	0.95	A	G	0.018443759	-0.002424677
rs7248104	19	7224431	G	A	0.005512195	0.056	-0.003679789	0.2	G	A	0.012228088	0.001420531
rs4072910	19	8644031	G	C	-0.025782226	3.80E-19	0.000923003	0.75	G	C	-0.017107899	0.000460263
rs7255721	19	8669931	G	C	-0.013285964	4.10E-06	-0.017251044	2.20E-09	G	C	-0.012418461	-0.015613559
rs7249094	19	8672000	G	A	-0.016125836	2.20E-08	-0.0156251	6.00E-08	G	A	-0.000177796	-0.013038847
rs2228612	19	10273372	T	C	0.010838047	0.00017	0.008990788	0.0018	T	C	0.009477335	0.005622452
rs8102380	19	10801185	G	A	-0.01742612	1.50E-09	-0.000399763	0.89	G	A	-0.012614942	-0.00069027
rs7188	19	11275139	A	C	-0.015509289	7.50E-08	-0.011664333	5.20E-05	A	C	-0.012226107	-0.010861368
rs67102109	19	12154799	G	C	0.020660298	7.80E-13	0.001216941	0.67	G	C	0.012400672	-2.34E-05
rs11085824	19	13001547	A	G	0.007773758	0.007	0.007187713	0.013	A	G	0.002620221	0.001974545
rs2279008	19	17283303	T	C	-0.018332524	2.00E-10	-0.01760938	1.00E-09	T	C	-0.01312621	-0.010880609
rs7259041	19	18123738	T	C	-0.011444466	7.20E-05	-0.011325937	8.60E-05	T	C	-0.008578974	-0.008277172
rs1064395	19	19361735	G	A	0.013571882	2.50E-06	-0.002497723	0.39	G	A	0.012595475	0.001196236
rs547483	19	37441365	T	C	-0.009582714	0.00089	-0.006954365	0.016	T	C	-0.008177065	-0.003331902
rs2231940	19	41944237	T	C	0.026785428	1.50E-20	0.002784202	0.33	T	C	0.017445707	-0.002174869
rs1206038	19	42863035	A	G	-0.013679804	2.10E-06	-0.008897915	0.002	A	G	-0.010852923	-0.001633638
rs3208856	19	45296806	C	T	0.009136887	0.0015	0.008847782	0.0022	C	T	-0.005531961	-0.005868288
rs75175362	19	46914927	C	T	0.009432922	0.0011	0.011301808	8.90E-05	C	T	0.005918791	0.006074172
rs13346368	19	48198675	A	G	0.006036084	0.036	-0.001080742	0.71	A	G	0.010716773	-0.001797468
rs447802	19	49116359	T	C	0.010520755	0.00026	0.011709428	4.90E-05	T	C	0.003550031	0.009221919
rs4252548	19	55879672	C	T	-0.024685096	1.10E-17	0.001439828	0.62	C	T	-0.004410394	-0.024936332
rs1741344	20	4101800	C	T	-0.022590529	4.70E-15	0.000699232	0.81	C	T	-0.013596947	0.000647609
rs967417	20	6620893	G	A	-0.033107813	1.60E-30	-0.002607016	0.37	G	A	-0.027046	-0.003643194
rs2145270	20	6621685	C	T	-0.038207344	4.40E-40	-0.002210821	0.44	C	T	-0.027504675	-0.005122376
rs4815025	20	21142523	C	G	-0.01249476	1.50E-05	-0.002711739	0.35	C	G	-0.010722177	0.00159032
rs7274811	20	32333181	G	T	-0.027587148	1.10E-21	0.002748713	0.34	G	T	-0.024319146	-0.000957387
rs6088619	20	33411871	A	G	0.026470893	4.30E-20	0.002706433	0.35	A	G	0.021492487	-9.09E-05
rs143384	20	34025756	A	G	0.068649128	2.70E-125	-0.004642016	0.11	A	G	0.044911123	-0.003894506
rs6060750	20	34596371	C	T	0.036333738	2.10E-36	0.003725903	0.2	C	T	0.025009999	0.000124551
rs4608	20	35865054	C	T	0.014044342	1.10E-06	0.00378889	0.19	C	T	0.010063345	0.001748318
rs2664521	20	47253150	T	C	0.013719072	2.00E-06	0.011139472	0.00011	T	C	0.008180498	0.008963701
rs6512577	20	47865784	C	T	0.024993076	4.40E-18	-4.37E-05	0.99	C	T	0.020807663	-0.000175467
rs4647958	20	48600631	T	C	-0.018339448	2.00E-10	-0.009176257	0.0015	T	C	-0.008919213	-0.00243588
rs13831	20	57475191	A	G	-0.010902598	0.00016	1.83E-05	0.99	A	G	-0.010489761	0.001733728
rs16982520	20	57758720	A	G	0.009944597	0.00056	0.011743253	4.60E-05	A	G	0.008109518	0.006851364
rs2236200	20	60986019	A	C	-0.00954344	0.00093	-0.00142186	0.62	A	C	-0.004951361	0.002858963
rs2830585	21	28305212	C	T	-0.010070549	0.00048	-0.009289543	0.0013	C	T	-0.009013292	-0.011182298
rs2834442	21	35690786	T	A	0.013154681	5.10E-06	-0.001850437	0.52	T	A	0.015318158	-0.000382453
rs1003719	21	38491095	A	G	-0.011565318	6.00E-05	-0.012187155	2.40E-05	A	G	-0.007805499	-0.008925595
rs2230033	21	39671476	G	A	-0.027146364	4.70E-21	-0.001538828	0.59	G	A	-0.011782173	0.001237066
rs147348682	22	17625915	G	T	-0.008385917	0.0036	-0.005942323	0.039	NA	NA	NA	NA
rs35665085	22	17625915	A	G	0.010362212	0.00033	0.009287983	0.0013	NA	NA	NA	NA
rs1005640	22	20789074	T	C	0.01198624	3.20E-05	0.012577121	1.30E-05	T	C	0.010402982	0.011004944
rs4822455	22	24255296	C	T	0.005671748	0.049	0.00807731	0.0051	C	T	0.006806441	0.007803078
rs77885044	22	28501414	C	T	-0.016286721	1.60E-08	-0.014588396	4.20E-07	C	T	-0.006641116	-0.005742523
rs2413338	22	35663523	C	T	0.006139521	0.033	0.006517629	0.024	C	T	0.0061359	0.004836464
rs9610841	22	38121152	C	A	0.011767944	4.50E-05	0.000236892	0.93	C	A	0.011361321	-0.000548632
rs2284063	22	38544298	A	G	0.005659059	0.05	0.009372808	0.0012	A	G	0.006424428	0.00901482
rs5764698	22	45749983	G	T	-0.01162526	5.50E-05	-0.003178634	0.27	G	T	-0.007609635	-0.002480498

Supplementary Table 13. Gene-based results in the all-ancestries analysis (P<1e-4). Only non-synonymous and splice site variants with MAF <5% were included in the tests, as detailed in the Online Methods (including a definition of the "broad" and "strict" masks. The MAF cutoff changes with the VT approach.

Test	Gene	N	Gene-based P-value	Number of variants	MAF cutoff	Top single variant P-value	Top single variant MAF
Skat_broad	*SERPINA1*	458927	2.79E-54	12	0.05	1.73E-44	0.0156
Skat_broad	*IL11*	458927	1.77E-50	3	0.05	2.26E-50	0.0249
Skat_broad	*SCMH1*	458927	3.27E-35	12	0.05	2.16E-24	0.0036
Skat_broad	*FBN2*	458253	1.66E-29	44	0.05	1.40E-33	0.0052
Skat_broad	*ACAN*	458927	1.72E-28	29	0.05	2.39E-22	0.0104
Skat_broad	*PTPN13*	458927	9.11E-27	47	0.05	1.18E-20	0.0129
Skat_broad	*MATN3*	458253	1.13E-22	11	0.05	4.37E-23	0.0253
Skat_broad	*ZFAT*	458253	1.89E-21	18	0.05	6.92E-27	0.0033
Skat_broad	*ZNF628*	458927	7.77E-20	6	0.05	2.55E-19	0.0180
Skat_broad	*IHH*	456994	8.95E-19	3	0.05	4.35E-14	0.0007
Skat_broad	*STC2*	458253	8.58E-18	7	0.05	9.31E-15	0.0008
Skat_broad	*PDE11A*	458253	9.48E-18	33	0.05	2.06E-08	0.0234
Skat_broad	*CCND3*	458927	1.25E-17	4	0.05	2.84E-15	0.0120
Skat_broad	*CYTL1*	458927	2.63E-17	2	0.05	2.64E-17	0.0373
Skat_broad	*AMOTL1*	458927	2.78E-17	14	0.05	7.49E-17	0.0081
Skat_broad	*PDE5A*	458253	1.71E-16	16	0.05	1.80E-16	0.0012
Skat_broad	*LAMB2*	455040	3.55E-16	46	0.05	8.17E-14	0.0375
Skat_broad	*GMPR2*	458927	5.94E-16	8	0.05	2.72E-15	0.0417
Skat_broad	*TSNAXIP1*	458927	7.82E-16	21	0.05	2.00E-14	0.0362
Skat_broad	*ANKS3*	458927	2.89E-15	20	0.05	4.15E-14	0.0223
Skat_broad	*ABCB6*	458253	4.95E-15	32	0.05	5.78E-13	0.0083
Skat_broad	*DUSP1*	458253	9.10E-15	4	0.05	3.69E-14	0.0315
Skat_broad	*SSC5D*	458927	2.80E-14	5	0.05	6.79E-15	0.0219
Skat_broad	*PARD6A*	458927	5.31E-14	3	0.05	5.54E-14	0.0361
Skat_broad	*DLG5*	458927	5.79E-14	28	0.05	1.05E-12	0.0151
Skat_broad	*PTH1R*	458927	1.01E-13	5	0.05	9.82E-13	0.0023
Skat_broad	*TMEM150B*	458927	1.25E-13	5	0.05	2.68E-13	0.0071
Skat_broad	*NPR3*	458927	1.66E-13	4	0.05	7.38E-10	0.0022
Skat_broad	*CRISPLD2*	458927	4.45E-13	13	0.05	2.26E-13	0.0007
Skat_broad	*IL11RA*	458927	5.92E-13	6	0.05	7.57E-13	0.0145
Skat_broad	*SMG7*	458253	7.41E-13	14	0.05	6.53E-12	0.0055
Skat_broad	*GRAMD2*	458927	1.50E-12	8	0.05	1.80E-12	0.0056
Skat_broad	*SLC8A3*	458927	2.75E-12	23	0.05	6.21E-12	0.0182
Skat_broad	*FIBIN*	458927	3.84E-12	5	0.05	5.45E-12	0.0037
Skat_broad	*LRP5*	458927	4.39E-12	27	0.05	3.88E-11	0.0437
Skat_broad	*ANAPC5*	458253	6.06E-12	8	0.05	1.90E-11	0.0080
Skat_broad	*TTC28*	458927	1.09E-11	14	0.05	2.63E-10	0.0109
Skat_broad	*NPAS4*	458927	1.47E-11	7	0.05	3.12E-11	0.0070
Skat_broad	*MYH7B*	455040	1.62E-11	53	0.05	4.22E-11	0.0159
Skat_broad	*GLT8D2*	458253	3.53E-11	11	0.05	7.72E-10	0.0148
Skat_broad	*ADAMTS3*	458927	4.47E-11	22	0.05	3.94E-10	0.0024
Skat_broad	*CLIP1*	458253	1.36E-10	13	0.05	8.46E-11	0.0237
Skat_broad	*ZNF646*	458927	1.53E-10	18	0.05	4.98E-10	0.0068
Skat_broad	*C6orf1*	458927	1.86E-10	7	0.05	9.87E-10	0.0011
Skat_broad	*OSGIN1*	458927	1.86E-10	15	0.05	2.06E-05	0.0052
Skat_broad	*PHKB*	458927	2.70E-10	26	0.05	8.28E-14	0.0042
Skat_broad	*DISP1*	458253	5.57E-10	16	0.05	1.32E-09	0.0072
Skat_broad	*LCAT*	458927	1.65E-09	2	0.05	1.65E-09	0.0254
Skat_broad	*ARMC5*	458927	3.22E-09	5	0.05	2.09E-12	0.0048
Skat_broad	*GAB1*	458253	9.06E-09	3	0.05	9.09E-09	0.0163
Skat_broad	*EPS15*	455040	1.14E-08	13	0.05	2.33E-08	0.0170
Skat_broad	*MCL1*	458253	1.37E-08	5	0.05	1.37E-08	0.0117
Skat_broad	*TIA1*	458927	1.81E-08	9	0.05	1.33E-06	0.0093
Skat_broad	*MMP14*	458927	1.91E-08	10	0.05	2.76E-08	0.0226
Skat_broad	*CYP11A1*	458927	1.95E-08	5	0.05	6.78E-08	0.0034
Skat_broad	*CD248*	458927	1.99E-08	10	0.05	7.08E-08	0.0076
Skat_broad	*DCBLD2*	458927	2.21E-08	13	0.05	7.37E-08	0.0442
Skat_broad	*ANGPTL4*	458927	2.48E-08	8	0.05	4.77E-07	0.0198
Skat_broad	*NOX4*	455040	3.27E-08	7	0.05	1.99E-05	0.0026
Skat_broad	*ZNF19*	458927	3.36E-08	6	0.05	5.87E-08	0.0274
Skat_broad	*QARS*	455040	3.72E-08	15	0.05	4.01E-07	0.0022
Skat_broad	*CSAD*	458927	4.12E-08	14	0.05	1.12E-06	0.0037
Skat_broad	*BMP3*	458927	4.52E-08	9	0.05	1.10E-07	0.0215
Skat_broad	*KIAA1614*	458253	4.60E-08	14	0.05	2.57E-07	0.0251
Skat_broad	*MGA*	458927	5.37E-08	27	0.05	3.06E-05	0.0164

Skat_broad	*TTN*	458253	5.56E-08	718	0.05	1.73E-05	0.0033
Skat_broad	*ANO1*	458927	5.79E-08	12	0.05	1.07E-07	0.0061
Skat_broad	*LECT2*	458253	6.63E-08	6	0.05	3.36E-07	0.0382
Skat_broad	*MXD3*	458253	7.43E-08	4	0.05	1.26E-07	0.0124
Skat_broad	*ADAMTS6*	458927	8.25E-08	14	0.05	3.23E-08	0.0018
Skat_broad	*HSD11B2*	457668	8.64E-08	5	0.05	1.29E-07	0.0015
Skat_broad	*FBXL19*	457097	9.64E-08	2	0.05	9.67E-08	0.0079
Skat_broad	*ST3GAL6*	458927	1.17E-07	6	0.05	1.23E-07	0.0440
Skat_broad	*SLC35E3*	458927	1.28E-07	6	0.05	1.30E-07	0.0206
Skat_broad	*COL5A2*	454366	1.47E-07	26	0.05	3.15E-06	0.0195
Skat_broad	*CRISPLD1*	456833	1.52E-07	12	0.05	4.74E-07	0.0019
Skat_broad	*KLHL28*	458927	1.56E-07	11	0.05	6.20E-07	0.0148
Skat_broad	*MARCH3*	458253	1.61E-07	5	0.05	1.67E-07	0.0310
Skat_broad	*TSPAN31*	447299	2.20E-07	2	0.05	2.18E-07	0.0025
Skat_broad	*ENGASE*	458927	2.38E-07	18	0.05	4.64E-07	0.0258
Skat_broad	*ADAMTSL3*	458927	2.40E-07	27	0.05	1.67E-06	0.0191
Skat_broad	*PEX1*	458927	3.35E-07	23	0.05	2.22E-06	0.0332
Skat_broad	*CCDC47*	458356	4.37E-07	6	0.05	4.30E-07	0.0024
Skat_broad	*COMP*	458253	4.62E-07	11	0.05	5.32E-07	0.0412
Skat_broad	*CNPY2*	454646	5.03E-07	1	0.05	5.03E-07	0.0002
Skat_broad	*TXLNA*	456145	6.89E-07	4	0.05	1.39E-06	0.0032
Skat_broad	*SRSF9*	458253	8.53E-07	2	0.05	8.54E-07	0.0292
Skat_broad	*SETD2*	458927	1.00E-06	15	0.05	1.62E-05	0.0017
Skat_broad	*PHC3*	458253	1.15E-06	12	0.05	1.32E-05	0.0072
Skat_broad	*BNC2*	458253	1.27E-06	23	0.05	9.78E-06	0.0281
Skat_broad	*AR*	348677	1.57E-06	6	0.05	3.78E-06	0.0022
Skat_broad	*MC3R*	458927	2.42E-06	6	0.05	2.60E-06	0.0012
Skat_broad	*ELN*	458927	2.75E-06	13	0.05	1.70E-06	0.0037
Skat_broad	*CHD1*	455040	3.04E-06	14	0.05	2.10E-06	0.0116
Skat_broad	*APOH*	458927	3.41E-06	5	0.05	4.28E-06	0.0265
Skat_broad	*CDC23*	454366	3.67E-06	4	0.05	5.74E-06	0.0069
Skat_broad	*LTBP1*	458927	3.68E-06	26	0.05	1.83E-07	0.0093
Skat_broad	*POR*	458927	3.77E-06	15	0.05	1.38E-05	0.0034
Skat_broad	*SREK1IP1*	254128	4.17E-06	1	0.05	4.17E-06	0.0334
Skat_broad	*EFEMP1*	457668	4.31E-06	4	0.05	2.55E-06	0.0015
Skat_broad	*MTMR11*	458253	4.36E-06	13	0.05	4.50E-06	0.0057
Skat_broad	*ABCC1*	458253	4.43E-06	31	0.05	4.62E-06	0.0114
Skat_broad	*FNDC3B*	458253	4.65E-06	25	0.05	2.72E-06	0.0115
Skat_broad	*CIRH1A*	458927	5.29E-06	10	0.05	6.89E-06	0.0388
Skat_broad	*WDR76*	457668	5.33E-06	9	0.05	1.16E-06	0.0067
Skat_broad	*FOXM1*	458927	5.47E-06	16	0.05	3.35E-06	0.0198
Skat_broad	*GHSR*	458253	5.73E-06	8	0.05	1.60E-05	0.0008
Skat_broad	*UPF2*	458253	6.01E-06	6	0.05	1.93E-06	0.0063
Skat_broad	*APOLD1*	454900	6.83E-06	5	0.05	1.10E-06	0.0020
Skat_broad	*SLC38A2*	458927	6.94E-06	12	0.05	1.72E-05	0.0136
Skat_broad	*PRKAG1*	458927	6.94E-06	4	0.05	8.82E-06	0.0294
Skat_broad	*UBP1*	458356	6.98E-06	5	0.05	1.17E-06	0.0100
Skat_broad	*GRM4*	458356	7.22E-06	9	0.05	3.46E-06	0.0010
Skat_broad	*POLB*	458927	7.24E-06	8	0.05	6.94E-06	0.0153
Skat_broad	*RAPGEF3*	458927	7.37E-06	19	0.05	4.50E-06	0.0105
Skat_broad	*GPR162*	457668	7.51E-06	12	0.05	8.49E-07	0.0006
Skat_broad	*ABCA6*	458927	8.10E-06	38	0.05	1.11E-05	0.0149
Skat_broad	*PPP1R9A*	458927	8.15E-06	17	0.05	3.88E-07	0.0075
Skat_broad	*MPP2*	458927	8.28E-06	7	0.05	9.28E-06	0.0134
Skat_broad	*UFC1*	456994	8.39E-06	4	0.05	8.88E-06	0.0019
Skat_broad	*EIF6*	454469	8.58E-06	5	0.05	7.41E-06	0.0103
Skat_broad	*UBTD2*	458253	9.82E-06	3	0.05	3.99E-06	0.0185
Skat_broad	*ZNF335*	458927	1.01E-05	19	0.05	4.98E-06	0.0217
Skat_broad	*FBXL12*	458927	1.02E-05	8	0.05	7.86E-06	0.0019
Skat_broad	*FLNB*	458927	1.04E-05	64	0.05	1.25E-06	0.0009
Skat_broad	*E2F7*	458927	1.06E-05	15	0.05	1.04E-05	0.0187
Skat_broad	*WDR6*	453781	1.20E-05	13	0.05	1.01E-05	0.0053
Skat_broad	*MYOG*	458253	1.23E-05	5	0.05	7.46E-06	0.0280
Skat_broad	*FAM166A*	458253	1.24E-05	12	0.05	1.32E-05	0.0240
Skat_broad	*ARRDC4*	458927	1.36E-05	10	0.05	4.07E-06	0.0360
Skat_broad	*ADAMTS17*	458253	1.38E-05	29	0.05	1.84E-04	0.0001
Skat_broad	*G6PC*	458356	1.44E-05	9	0.05	3.70E-04	0.0003
Skat_broad	*SHARPIN*	458253	1.44E-05	4	0.05	4.15E-06	0.0392
Skat_broad	*KLC1*	458253	1.47E-05	4	0.05	1.19E-05	0.0223
Skat_broad	*LTBP4*	458927	1.47E-05	16	0.05	1.23E-05	0.0116

Skat_broad	*DKK1*	458927	1.47E-05	3	0.05	1.24E-05	0.0035
Skat_broad	*THBS3*	458253	1.50E-05	14	0.05	1.40E-05	0.0149
Skat_broad	*KLHL25*	458927	1.52E-05	14	0.05	1.04E-05	0.0054
Skat_broad	*ITIH4*	458927	1.56E-05	15	0.05	1.02E-04	0.0021
Skat_broad	*B4GALNT3*	458927	1.59E-05	30	0.05	1.37E-05	0.0003
Skat_broad	*CACNA2D2*	458927	1.63E-05	9	0.05	1.15E-05	0.0282
Skat_broad	*SLC43A1*	458927	1.76E-05	7	0.05	1.64E-05	0.0301
Skat_broad	*PRAM1*	458927	1.86E-05	9	0.05	2.42E-05	0.0040
Skat_broad	*C16orf70*	458927	1.91E-05	6	0.05	1.64E-04	0.0268
Skat_broad	*SAMD4A*	458927	2.00E-05	13	0.05	4.35E-04	0.0042
Skat_broad	*LRRC8A*	457682	2.08E-05	5	0.05	1.36E-05	0.0049
Skat_broad	*TXNDC5*	458927	2.15E-05	12	0.05	1.56E-05	0.0093
Skat_broad	*KIF7*	458927	2.18E-05	34	0.05	2.34E-05	0.0042
Skat_broad	*ZCCHC6*	458927	2.20E-05	9	0.05	1.98E-05	0.0057
Skat_broad	*RIC8B*	458253	2.23E-05	6	0.05	1.74E-05	0.0067
Skat_broad	*OR9G4*	455040	2.33E-05	7	0.05	1.83E-05	0.0088
Skat_broad	*KIAA0922*	458253	2.46E-05	22	0.05	2.03E-07	0.0101
Skat_broad	*GLI3*	458927	2.50E-05	21	0.05	3.32E-05	0.0066
Skat_broad	*ZNF304*	458927	2.63E-05	6	0.05	1.20E-05	0.0255
Skat_broad	*UGGT2*	458927	2.69E-05	32	0.05	1.34E-04	0.0260
Skat_broad	*LLGL1*	458253	2.73E-05	15	0.05	8.20E-05	0.0047
Skat_broad	*SNED1*	458927	2.92E-05	10	0.05	3.24E-07	0.0054
Skat_broad	*N4BP1*	453556	2.95E-05	3	0.05	3.15E-05	0.0074
Skat_broad	*SPEG*	458253	2.99E-05	37	0.05	1.23E-05	0.0105
Skat_broad	*RNF135*	458356	3.00E-05	4	0.05	3.52E-05	0.0082
Skat_broad	*ZBTB20*	458253	3.02E-05	5	0.05	4.12E-05	0.0062
Skat_broad	*TET1*	458927	3.02E-05	12	0.05	2.93E-05	0.0179
Skat_broad	*C15orf39*	458927	3.15E-05	16	0.05	2.21E-04	0.0080
Skat_broad	*LMF1*	458927	3.50E-05	15	0.05	3.09E-05	0.0288
Skat_broad	*NFIC*	458927	3.61E-05	9	0.05	7.39E-05	0.0014
Skat_broad	*SLC38A4*	458356	3.63E-05	4	0.05	4.42E-05	0.0015
Skat_broad	*TNRC6A*	458927	3.68E-05	42	0.05	1.08E-09	0.0358
Skat_broad	*ITGB7*	458927	3.75E-05	10	0.05	2.00E-05	0.0123
Skat_broad	*DDX19B*	458927	3.77E-05	2	0.05	4.11E-05	0.0110
Skat_broad	*CCNF*	458927	3.79E-05	12	0.05	2.11E-05	0.0036
Skat_broad	*CSGALNACT1*	458253	3.85E-05	22	0.05	2.45E-05	0.0114
Skat_broad	*ZDHHC1*	458927	3.94E-05	4	0.05	3.24E-05	0.0245
Skat_broad	*MAPKAPK2*	458253	4.10E-05	5	0.05	4.13E-05	0.0014
Skat_broad	*ERGIC3*	452946	4.15E-05	4	0.05	4.90E-05	0.0006
Skat_broad	*ENPP2*	458253	4.17E-05	15	0.05	8.00E-05	0.0048
Skat_broad	*FAM46A*	458927	4.19E-05	2	0.05	4.71E-05	0.0068
Skat_broad	*WNK4*	458927	4.38E-05	16	0.05	4.08E-05	0.0130
Skat_broad	*TNXB*	455040	4.72E-05	36	0.05	2.23E-04	0.0105
Skat_broad	*CORO6*	458927	4.81E-05	7	0.05	5.37E-05	0.0159
Skat_broad	*SENP6*	458927	4.83E-05	19	0.05	1.69E-04	0.0035
Skat_broad	*CERS2*	458253	5.06E-05	4	0.05	4.84E-05	0.0061
Skat_broad	*PDE8A*	458927	5.29E-05	13	0.05	5.13E-05	0.0310
Skat_broad	*FLII*	458253	5.30E-05	26	0.05	4.92E-05	0.0222
Skat_broad	*PMPCA*	458253	5.35E-05	13	0.05	4.16E-05	0.0149
Skat_broad	*BCAM*	458927	5.49E-05	19	0.05	4.54E-05	0.0294
Skat_broad	*TARS2*	458253	5.50E-05	11	0.05	1.37E-06	0.0072
Skat_broad	*ASB3*	458927	5.69E-05	9	0.05	5.07E-05	0.0168
Skat_broad	*SLC12A7*	458253	5.76E-05	22	0.05	1.86E-04	0.0026
Skat_broad	*CCDC113*	458356	5.88E-05	8	0.05	7.80E-05	0.0028
Skat_broad	*GPI*	458927	5.96E-05	11	0.05	5.84E-05	0.0208
Skat_broad	*PRKG2*	458356	6.30E-05	9	0.05	6.37E-05	0.0024
Skat_broad	*WRN*	458927	6.42E-05	21	0.05	2.67E-05	0.0043
Skat_broad	*TMEM43*	458253	6.90E-05	13	0.05	1.40E-04	0.0131
Skat_broad	*MYBL1*	458927	6.91E-05	9	0.05	1.33E-04	0.0137
Skat_broad	*KCNK6*	458927	7.48E-05	4	0.05	7.61E-05	0.0098
Skat_broad	*PEX16*	458927	7.93E-05	6	0.05	7.63E-05	0.0265
Skat_broad	*HIGD1B*	458927	8.40E-05	3	0.05	7.30E-05	0.0237
Skat_broad	*C10orf76*	458253	8.58E-05	4	0.05	8.08E-05	0.0059
Skat_broad	*RNF144B*	456730	8.62E-05	5	0.05	2.71E-05	0.0006
Skat_broad	*HERC1*	458927	8.88E-05	42	0.05	7.44E-07	0.0309
Skat_broad	*EXOC3L1*	458927	9.26E-05	14	0.05	2.39E-05	0.0129
Skat_broad	*NUDT12*	456994	9.88E-05	8	0.05	6.89E-05	0.0016
SKAT_strict	*PTPN13*	458927	1.32E-23	13	0.05	1.18E-20	0.0129
SKAT_strict	*GMPR2*	458927	2.43E-15	5	0.05	2.72E-15	0.0417
SKAT_strict	*STC2*	443140	9.31E-15	1	0.05	9.31E-15	0.0008

SKAT_strict	*ZFAT*	456423	7.41E-14	4	0.05	8.77E-13	0.0008
SKAT_strict	*CRISPLD2*	457097	1.10E-13	3	0.05	2.26E-13	0.0007
SKAT_strict	*GRAMD2*	457668	1.71E-12	4	0.05	1.80E-12	0.0056
SKAT_strict	*FIBIN*	458927	3.95E-12	4	0.05	5.45E-12	0.0037
SKAT_strict	*PDE11A*	458253	1.14E-11	10	0.05	3.25E-08	0.0334
SKAT_strict	*ADAMTS3*	458356	3.17E-10	7	0.05	3.94E-10	0.0024
SKAT_strict	*GLT8D2*	458253	7.67E-10	2	0.05	7.72E-10	0.0148
SKAT_strict	*FLNB*	458927	1.63E-09	23	0.05	1.25E-06	0.0009
SKAT_strict	*CCDC3*	454900	1.67E-08	4	0.05	3.32E-05	0.0001
SKAT_strict	*ELL*	447196	8.14E-08	1	0.05	8.14E-08	0.0004
SKAT_strict	*BMP3*	436912	1.10E-07	1	0.05	1.10E-07	0.0215
SKAT_strict	*HERC1*	458927	6.69E-07	4	0.05	7.44E-07	0.0309
SKAT_strict	*RANBP9*	448995	9.24E-07	1	0.05	9.24E-07	0.0010
SKAT_strict	*APOH*	458927	2.92E-06	2	0.05	4.28E-06	0.0265
SKAT_strict	*AR*	322097	3.88E-06	2	0.05	3.78E-06	0.0022
SKAT_strict	*RAPGEF3*	458927	6.16E-06	7	0.05	4.50E-06	0.0105
SKAT_strict	*PAM*	458253	6.22E-06	4	0.05	3.07E-06	0.0424
SKAT_strict	*ASH1L*	457682	6.30E-06	3	0.05	6.26E-06	0.0013
SKAT_strict	*ABCC1*	458253	6.79E-06	11	0.05	4.62E-06	0.0114
SKAT_strict	*FOXM1*	458927	8.93E-06	2	0.05	3.35E-06	0.0198
SKAT_strict	*G6PC*	458356	9.41E-06	3	0.05	3.70E-04	0.0003
SKAT_strict	*CRISPLD1*	450774	1.19E-05	3	0.05	1.64E-05	0.0001
SKAT_strict	*ABCA6*	458927	1.27E-05	4	0.05	1.11E-05	0.0149
SKAT_strict	*FAM166A*	458253	1.50E-05	5	0.05	1.32E-05	0.0240
SKAT_strict	*B4GALNT3*	458356	1.53E-05	9	0.05	1.37E-05	0.0003
SKAT_strict	*NOSTRIN*	457682	1.69E-05	1	0.05	1.69E-05	0.0011
SKAT_strict	*C18orf25*	457668	1.78E-05	2	0.05	1.93E-05	0.0033
SKAT_strict	*ZCCHC6*	457668	2.00E-05	3	0.05	1.98E-05	0.0057
SKAT_strict	*POR*	458356	2.29E-05	5	0.05	1.38E-05	0.0034
SKAT_strict	*COL7A1*	454469	3.68E-05	8	0.05	3.69E-05	0.0037
SKAT_strict	*SLC22A5*	448995	4.47E-05	4	0.05	2.89E-05	0.0007
SKAT_strict	*ANKS6*	456423	4.59E-05	6	0.05	2.97E-05	0.0015
SKAT_strict	*NFIC*	457097	4.69E-05	2	0.05	7.39E-05	0.0014
SKAT_strict	*GPI*	458927	5.91E-05	3	0.05	5.84E-05	0.0208
SKAT_strict	*WRN*	458927	6.22E-05	7	0.05	2.67E-05	0.0043
SKAT_strict	*UGGT2*	458927	7.32E-05	9	0.05	1.34E-04	0.0260
SKAT_strict	*PTCH1*	450188	7.67E-05	1	0.05	7.67E-05	2.88E-05
SKAT_strict	*DOT1L*	454900	9.85E-05	1	0.05	9.85E-05	0.0006
VT_broad	*IL11*	458927	3.69E-48	3	0.0249	2.26E-50	0.0249
VT_broad	*ZFAT*	458253	1.18E-34	14	0.0031	6.92E-27	0.0033
VT_broad	*SERPINA1*	458927	4.56E-34	11	0.0147	1.73E-44	0.0156
VT_broad	*SCMH1*	458927	3.10E-19	8	0.0034	2.16E-24	0.0036
VT_broad	*PDE11A*	458253	9.70E-19	33	0.0331	2.06E-08	0.0234
VT_broad	*IHH*	456994	3.31E-18	3	0.0041	4.35E-14	0.0007
VT_broad	*ZNF628*	458927	4.41E-18	6	0.0130	2.55E-19	0.0180
VT_broad	*ACAN*	458927	4.71E-18	29	0.0252	2.39E-22	0.0104
VT_broad	*CYTL1*	458927	4.19E-17	2	0.0371	2.64E-17	0.0373
VT_broad	*STC2*	458253	3.33E-15	5	0.0011	9.31E-15	0.0008
VT_broad	*GMPR2*	458927	3.39E-14	8	0.0415	2.72E-15	0.0417
VT_broad	*DUSP1*	458253	3.67E-14	4	0.0296	3.69E-14	0.0315
VT_broad	*PARD6A*	458927	1.90E-13	3	0.0344	5.54E-14	0.0361
VT_broad	*FIBIN*	458927	2.11E-13	4	0.0210	5.45E-12	0.0037
VT_broad	*IL11RA*	458927	4.80E-13	6	0.0147	7.57E-13	0.0145
VT_broad	*NPR3*	458927	9.21E-13	4	0.0025	7.38E-10	0.0022
VT_broad	*TMEM150B*	458927	1.13E-12	3	0.0072	2.68E-13	0.0071
VT_broad	*ADAMTS3*	458927	1.63E-12	21	0.0114	3.94E-10	0.0024
VT_broad	*ARMC5*	458927	3.53E-12	4	0.0048	2.09E-12	0.0048
VT_broad	*PDE5A*	458253	2.28E-11	10	0.0011	1.80E-16	0.0012
VT_broad	*MATN3*	458253	2.37E-11	11	0.0253	4.37E-23	0.0253
VT_broad	*TSNAXIP1*	458927	3.91E-11	21	0.0363	2.00E-14	0.0362
VT_broad	*GLT8D2*	458253	8.43E-11	10	0.0152	7.72E-10	0.0148
VT_broad	*FBN2*	458253	1.19E-10	38	0.0079	1.40E-33	0.0052
VT_broad	*AMOTL1*	458927	3.25E-10	14	0.0211	7.49E-17	0.0081
VT_broad	*ANAPC5*	458253	4.55E-10	5	0.0076	1.90E-11	0.0080
VT_broad	*CRISPLD1*	456833	4.81E-10	11	0.0211	4.74E-07	0.0019
VT_broad	*CSAD*	458927	1.01E-09	13	0.0047	1.12E-06	0.0037
VT_broad	*LAMB2*	455040	1.89E-09	46	0.0354	8.17E-14	0.0375
VT_broad	*CRISPLD2*	458927	2.54E-09	7	0.0007	2.26E-13	0.0007
VT_broad	*LRP5*	458927	3.29E-09	27	0.0437	3.88E-11	0.0437
VT_broad	*GRAMD2*	458927	4.43E-09	8	0.0055	1.80E-12	0.0056

VT_broad	*LCAT*	458927	5.09E-09	2	0.0248	1.65E-09	0.0254
VT_broad	*LECT2*	458253	8.12E-09	6	0.0381	3.36E-07	0.0382
VT_broad	*SNED1*	458927	2.86E-08	8	0.0058	3.24E-07	0.0054
VT_broad	*SSC5D*	458927	4.94E-08	5	0.0191	6.79E-15	0.0219
VT_broad	*GAB1*	458253	5.22E-08	3	0.0164	9.09E-09	0.0163
VT_broad	*WDR76*	457668	5.90E-08	8	0.0064	1.16E-06	0.0067
VT_broad	*MCL1*	458253	5.95E-08	5	0.0287	1.37E-08	0.0117
VT_broad	*ANKS3*	458927	6.42E-08	19	0.0225	4.15E-14	0.0223
VT_broad	*HSD11B2*	457668	8.76E-08	5	0.0035	1.29E-07	0.0015
VT_broad	*FBXL19*	457097	1.23E-07	2	0.0078	9.67E-08	0.0079
VT_broad	*NPAS4*	458927	1.26E-07	7	0.0070	3.12E-11	0.0070
VT_broad	*MARCH3*	458253	1.43E-07	5	0.0301	1.67E-07	0.0310
VT_broad	*PHKB*	458927	1.68E-07	22	0.0043	8.28E-14	0.0042
VT_broad	*MC3R*	458927	1.81E-07	3	0.0013	2.60E-06	0.0012
VT_broad	*SMG7*	458253	1.82E-07	14	0.0055	6.53E-12	0.0055
VT_broad	*ADAMTS6*	458927	1.92E-07	12	0.0022	3.23E-08	0.0018
VT_broad	*CCDC3*	456423	2.74E-07	3	0.0001	3.32E-05	0.0001
VT_broad	*SLC8A3*	458927	3.05E-07	21	0.0177	6.21E-12	0.0182
VT_broad	*KLHL28*	458927	3.50E-07	11	0.0138	6.20E-07	0.0148
VT_broad	*SLC35E3*	458927	3.52E-07	6	0.0252	1.30E-07	0.0206
VT_broad	*CNPY2*	454646	5.03E-07	1	0.0002	5.03E-07	0.0002
VT_broad	*G6PC*	458356	5.19E-07	6	0.0012	3.70E-04	0.0003
VT_broad	*TSPAN31*	447299	6.10E-07	2	0.0025	2.18E-07	0.0025
VT_broad	*PHC3*	458253	6.16E-07	9	0.0071	1.32E-05	0.0072
VT_broad	*GH1*	458927	1.05E-06	3	0.0020	7.15E-09	0.0021
VT_broad	*ST3GAL6*	458927	1.24E-06	6	0.0426	1.23E-07	0.0440
VT_broad	*EIF6*	454469	1.25E-06	5	0.0105	7.41E-06	0.0103
VT_broad	*SRSF9*	458253	1.47E-06	2	0.0242	8.54E-07	0.0292
VT_broad	*MXD3*	458253	1.52E-06	4	0.0117	1.26E-07	0.0124
VT_broad	*UFC1*	456994	1.90E-06	4	0.0034	8.88E-06	0.0019
VT_broad	*NOX4*	455040	2.26E-06	6	0.0025	1.99E-05	0.0026
VT_broad	*AR*	348677	2.84E-06	4	0.0012	3.78E-06	0.0022
VT_broad	*CIRH1A*	458927	3.05E-06	10	0.0391	6.89E-06	0.0388
VT_broad	*CCND3*	458927	3.86E-06	4	0.0043	2.84E-15	0.0120
VT_broad	*SREK1IP1*	254128	4.17E-06	1	0.0334	4.17E-06	0.0334
VT_broad	*SLC38A4*	458356	4.37E-06	4	0.0209	4.42E-05	0.0015
VT_broad	*CYP11A1*	458927	6.21E-06	5	0.0033	6.78E-08	0.0034
VT_broad	*DCBLD2*	458927	7.20E-06	13	0.0448	7.37E-08	0.0442
VT_broad	*RIC8B*	458253	7.45E-06	6	0.0210	1.74E-05	0.0067
VT_broad	*COMP*	458253	7.81E-06	11	0.0407	5.32E-07	0.0412
VT_broad	*UGGT2*	458927	8.29E-06	32	0.0264	1.34E-04	0.0260
VT_broad	*ACTN4*	458927	8.40E-06	5	0.0050	9.66E-05	0.0054
VT_broad	*FLNB*	458927	8.73E-06	49	0.0009	1.25E-06	0.0009
VT_broad	*POLB*	458927	9.43E-06	8	0.0135	6.94E-06	0.0153
VT_broad	*PEX1*	458927	1.15E-05	23	0.0329	2.22E-06	0.0332
VT_broad	*ZNF19*	458927	1.25E-05	6	0.0275	5.87E-08	0.0274
VT_broad	*CCDC47*	458356	1.26E-05	4	0.0024	4.30E-07	0.0024
VT_broad	*SHARPIN*	458253	1.45E-05	4	0.0342	4.15E-06	0.0392
VT_broad	*PRKAG1*	458927	1.50E-05	4	0.0292	8.82E-06	0.0294
VT_broad	*PTH1R*	458927	1.51E-05	4	0.0023	9.82E-13	0.0023
VT_broad	*TET2*	458253	1.60E-05	16	0.0342	2.14E-04	0.0338
VT_broad	*CACNA2D2*	458927	2.12E-05	9	0.0280	1.15E-05	0.0282
VT_broad	*MPP2*	458927	2.21E-05	7	0.0133	9.28E-06	0.0134
VT_broad	*GALNT5*	457682	2.22E-05	7	0.0039	1.83E-05	0.0005
VT_broad	*ADAMTSL3*	458927	2.27E-05	26	0.0224	1.67E-06	0.0191
VT_broad	*APOH*	458927	2.50E-05	5	0.0265	4.28E-06	0.0265
VT_broad	*MYH7B*	455040	2.59E-05	53	0.0216	4.22E-11	0.0159
VT_broad	*FAM46A*	458927	2.75E-05	2	0.0064	4.71E-05	0.0068
VT_broad	*OSGIN1*	458927	3.02E-05	13	0.0048	2.06E-05	0.0052
VT_broad	*N4BP1*	453556	3.16E-05	2	0.0051	3.15E-05	0.0074
VT_broad	*RANBP9*	458253	3.20E-05	3	0.0025	9.24E-07	0.0010
VT_broad	*C18orf25*	458927	3.25E-05	1	0.0032	1.93E-05	0.0033
VT_broad	*DISP1*	458253	3.43E-05	15	0.0210	1.32E-09	0.0072
VT_broad	*SLC22A5*	454366	3.83E-05	11	0.0035	2.89E-05	0.0007
VT_broad	*CCDC113*	458356	4.20E-05	8	0.0245	7.80E-05	0.0028
VT_broad	*MMP14*	458927	4.72E-05	10	0.0220	2.76E-08	0.0226
VT_broad	*ZBTB20*	458253	5.37E-05	4	0.0060	4.12E-05	0.0062
VT_broad	*TET1*	458927	5.41E-05	12	0.0285	2.93E-05	0.0179
VT_broad	*ZNF646*	458927	5.49E-05	17	0.0066	4.98E-10	0.0068
VT_broad	*TXLNA*	456145	5.62E-05	4	0.0031	1.39E-06	0.0032

VT_broad	*KIAA1614*	458253	5.75E-05	14	0.0246	2.57E-07	0.0251
VT_broad	*DKK1*	458927	5.83E-05	3	0.0036	1.24E-05	0.0035
VT_broad	*CDC23*	454366	6.76E-05	4	0.0066	5.74E-06	0.0069
VT_broad	*FAM187B*	458927	7.56E-05	10	0.0005	0.002	0.0002
VT_broad	*TMEM43*	458253	7.81E-05	13	0.0126	1.40E-04	0.0131
VT_broad	*KLC1*	458253	8.11E-05	4	0.0211	1.19E-05	0.0223
VT_broad	*HOXD12*	458253	9.45E-05	4	0.0004	0.003	0.0004
VT_broad	*THBS3*	458253	9.49E-05	14	0.0209	1.40E-05	0.0149
VT_broad	*FBXL12*	458927	9.95E-05	8	0.0019	7.86E-06	0.0019
VT_strict	*ZFAT*	456423	1.22E-15	4	0.0017	8.77E-13	0.0008
VT_strict	*STC2*	443140	9.31E-15	1	0.0008	9.31E-15	0.0008
VT_strict	*GMPR2*	458927	1.60E-14	5	0.0415	2.72E-15	0.0417
VT_strict	*CRISPLD2*	457097	1.92E-13	3	0.0007	2.26E-13	0.0007
VT_strict	*FIBIN*	458927	2.41E-13	3	0.0036	5.45E-12	0.0037
VT_strict	*GRAMD2*	457668	3.36E-11	4	0.0055	1.80E-12	0.0056
VT_strict	*PDE11A*	458253	1.93E-10	10	0.0331	3.25E-08	0.0334
VT_strict	*GLT8D2*	458253	9.16E-10	2	0.0152	7.72E-10	0.0148
VT_strict	*CCDC3*	454900	1.24E-09	4	0.0017	3.32E-05	0.0001
VT_strict	*ADAMTS3*	458356	5.52E-09	7	0.0025	3.94E-10	0.0024
VT_strict	*PTPN13*	458927	5.89E-09	12	0.0209	1.18E-20	0.0129
VT_strict	*B4GALNT3*	458356	3.18E-08	6	0.0004	1.37E-05	0.0003
VT_strict	*ELL*	447196	8.14E-08	1	0.0004	8.14E-08	0.0004
VT_strict	*BMP3*	436912	1.10E-07	1	0.0215	1.10E-07	0.0215
VT_strict	*FLNB*	458927	1.16E-07	20	0.0009	1.25E-06	0.0009
VT_strict	*UGGT2*	458927	4.45E-07	8	0.0158	1.34E-04	0.0260
VT_strict	*RANBP9*	448995	9.24E-07	1	0.0010	9.24E-07	0.0010
VT_strict	*CRISPLD1*	450774	1.81E-06	3	0.0213	1.64E-05	0.0001
VT_strict	*G6PC*	458356	1.97E-06	2	0.0004	3.70E-04	0.0003
VT_strict	*SCUBE3*	456833	4.84E-06	1	7.11E-05	1.02E-06	0.0001
VT_strict	*ABCA6*	458927	5.83E-06	4	0.0106	1.11E-05	0.0149
VT_strict	*HERC1*	458927	6.10E-06	3	0.0239	7.44E-07	0.0309
VT_strict	*AR*	322097	6.65E-06	1	0.0013	3.78E-06	0.0022
VT_strict	*RAPGEF3*	458927	7.60E-06	7	0.0100	4.50E-06	0.0105
VT_strict	*FAM166A*	458253	8.59E-06	5	0.0235	1.32E-05	0.0240
VT_strict	*APOH*	458927	1.35E-05	2	0.0265	4.28E-06	0.0265
VT_strict	*NOSTRIN*	457682	1.69E-05	1	0.0011	1.69E-05	0.0011
VT_strict	*PAM*	458253	2.13E-05	4	0.0425	3.07E-06	0.0424
VT_strict	*FOXM1*	458927	2.63E-05	2	0.0199	3.35E-06	0.0198
VT_strict	*C18orf25*	457668	2.72E-05	1	0.0032	1.93E-05	0.0033
VT_strict	*ASH1L*	457682	3.59E-05	3	0.0012	6.26E-06	0.0013
VT_strict	*ZCCHC6*	457668	3.61E-05	3	0.0224	1.98E-05	0.0057
VT_strict	*OGDHL*	458927	4.11E-05	7	0.0054	0.002	0.0055
VT_strict	*TMEM43*	458253	4.50E-05	2	0.0126	1.40E-04	0.0131
VT_strict	*ABCC1*	458253	6.60E-05	11	0.0110	4.62E-06	0.0114
VT_strict	*COL7A1*	454469	7.17E-05	8	0.0290	3.69E-05	0.0037
VT_strict	*PTCH1*	450188	7.67E-05	1	2.88E-05	7.67E-05	2.88E-05
VT_strict	*GPI*	458927	8.83E-05	3	0.0207	5.84E-05	0.0208
VT_strict	*DOT1L*	454900	9.85E-05	1	0.0006	9.85E-05	0.0006

Supplementary Table 14. Gene-based results in the European-ancestry analysis (P<1e-4). Only non-synonymous and splice site variants with MAF <5% were included in the tests, as detailed in the Online Methods (including a definition of the "broad" and "strict" masks). The MAF cutoff changes with the VT approach.

Test	Gene	N	Gene-based P-value	Number of variants	MAF cutoff	Top single variant P-value	Top single variant MAF
SKAT_broad	*IL11*	381625	7.80E-56	3	0.05	1.14E-55	0.0261
SKAT_broad	*SERPINA1*	381625	5.91E-55	12	0.05	8.37E-45	0.0184
SKAT_broad	*SCMH1*	381625	6.74E-36	12	0.05	1.76E-25	0.0042
SKAT_broad	*FANCE*	381625	1.58E-31	7	0.05	7.94E-29	0.0148
SKAT_broad	*FBN2*	381625	8.97E-29	44	0.05	2.46E-33	0.0060
SKAT_broad	*ACAN*	381625	4.47E-26	35	0.05	1.00E-21	0.0092
SKAT_broad	*NSD1*	381625	7.98E-26	16	0.05	1.33E-25	0.0229
SKAT_broad	*PTPN13*	381625	1.46E-24	47	0.05	1.38E-19	0.0145
SKAT_broad	*TBX15*	381625	4.20E-24	9	0.05	1.07E-23	0.0424
SKAT_broad	*MATN3*	381625	1.10E-22	11	0.05	3.57E-23	0.0262
SKAT_broad	*ZFAT*	381625	1.36E-20	18	0.05	4.45E-26	0.0039
SKAT_broad	*CLPS*	381625	1.47E-20	6	0.05	3.29E-21	0.0151
SKAT_broad	*GALR1*	381625	1.13E-18	8	0.05	5.57E-18	0.0470
SKAT_broad	*ZNF628*	381625	1.56E-18	6	0.05	5.22E-18	0.0206
SKAT_broad	*IHH*	381625	4.23E-18	3	0.05	4.31E-15	0.0008
SKAT_broad	*CYTL1*	381625	2.46E-17	2	0.05	2.47E-17	0.0402
SKAT_broad	*CCND3*	381625	4.95E-17	4	0.05	6.58E-17	0.0133
SKAT_broad	*GMPR2*	381625	9.74E-17	8	0.05	9.90E-16	0.0480
SKAT_broad	*PDE11A*	381625	1.65E-16	34	0.05	1.45E-08	0.0362
SKAT_broad	*STC2*	381625	4.83E-16	7	0.05	1.41E-14	0.0010
SKAT_broad	*AMOTL1*	381625	5.46E-16	14	0.05	1.03E-15	0.0092
SKAT_broad	*ABCB6*	381625	5.42E-15	32	0.05	3.56E-13	0.0095
SKAT_broad	*TSNAXIP1*	381625	5.44E-15	21	0.05	5.69E-14	0.0408
SKAT_broad	*CRISPLD2*	381625	7.05E-15	13	0.05	6.04E-13	0.0008
SKAT_broad	*DUSP1*	381625	7.29E-15	4	0.05	5.33E-14	0.0362
SKAT_broad	*ANKS3*	381625	1.17E-14	20	0.05	2.27E-13	0.0252
SKAT_broad	*LRRC36*	381625	1.61E-14	13	0.05	3.70E-17	0.0428
SKAT_broad	*TMEM150B*	381625	3.75E-14	5	0.05	9.91E-14	0.0080
SKAT_broad	*SSC5D*	381625	1.27E-13	5	0.05	1.34E-14	0.0233
SKAT_broad	*PARD6A*	381625	2.93E-13	2	0.05	3.17E-13	0.0408
SKAT_broad	*IL11RA*	381625	6.50E-13	6	0.05	6.85E-13	0.0163
SKAT_broad	*GRAMD2*	381625	6.93E-13	7	0.05	7.64E-13	0.0063
SKAT_broad	*LAMB2*	377738	7.26E-13	45	0.05	8.99E-12	0.0394
SKAT_broad	*LRP5*	381625	1.44E-12	27	0.05	8.65E-12	0.0481
SKAT_broad	*NPR3*	381625	1.87E-12	4	0.05	1.03E-08	0.0025
SKAT_broad	*KCTD19*	381625	1.90E-12	13	0.05	1.27E-14	0.0418
SKAT_broad	*PTH1R*	381625	3.34E-12	5	0.05	1.44E-11	0.0025
SKAT_broad	*FIBIN*	381625	3.41E-12	5	0.05	5.00E-12	0.0044
SKAT_broad	*ANAPC5*	381625	5.16E-12	8	0.05	1.70E-11	0.0089
SKAT_broad	*DLG5*	381625	7.17E-12	28	0.05	3.57E-11	0.0174
SKAT_broad	*TTC28*	381625	7.84E-12	14	0.05	1.98E-10	0.0121
SKAT_broad	*SMG7*	381625	2.09E-11	14	0.05	7.71E-11	0.0061
SKAT_broad	*SLC8A3*	381625	2.63E-11	23	0.05	2.28E-11	0.0205
SKAT_broad	*NPAS4*	381625	2.77E-11	7	0.05	4.53E-11	0.0082
SKAT_broad	*OSGIN1*	381625	4.29E-11	15	0.05	7.90E-06	0.0000
SKAT_broad	*MYH7B*	377738	4.36E-11	54	0.05	7.77E-11	0.0186
SKAT_broad	*GLT8D2*	381625	5.91E-11	10	0.05	1.04E-09	0.0173
SKAT_broad	*C6orf1*	381625	7.47E-11	7	0.05	6.59E-10	0.0012
SKAT_broad	*CLIP1*	381625	9.09E-11	13	0.05	2.24E-11	0.0276
SKAT_broad	*PHKB*	381625	1.01E-10	26	0.05	6.11E-14	0.0049
SKAT_broad	*ADAMTS6*	381625	1.43E-10	14	0.05	9.50E-09	0.0019
SKAT_broad	*DCAF16*	381625	1.71E-10	4	0.05	1.80E-10	0.0280
SKAT_broad	*ADAMTS3*	381625	4.27E-10	22	0.05	1.77E-08	0.0027
SKAT_broad	*ARMC5*	381625	5.52E-10	5	0.05	6.03E-12	0.0056
SKAT_broad	*ZNF646*	381625	6.06E-10	19	0.05	9.66E-10	0.0080
SKAT_broad	*DISP1*	381625	1.12E-09	16	0.05	1.57E-09	0.0079
SKAT_broad	*PDE5A*	381625	1.32E-09	17	0.05	6.23E-17	0.0014
SKAT_broad	*SLC35E3*	381625	1.90E-09	6	0.05	2.02E-09	0.0224
SKAT_broad	*ACHE*	381625	2.36E-09	6	0.05	4.88E-09	0.0432
SKAT_broad	*LCAT*	381625	2.73E-09	2	0.05	2.72E-09	0.0296
SKAT_broad	*MCL1*	381625	3.08E-09	5	0.05	3.10E-09	0.0137
SKAT_broad	*TIA1*	381625	9.56E-09	9	0.05	4.66E-07	0.0104
SKAT_broad	*GAB1*	381625	9.81E-09	2	0.05	9.88E-09	0.0186
SKAT_broad	*ADAMTSL3*	381625	1.56E-08	27	0.05	5.62E-08	0.0211
SKAT_broad	*MMP14*	381625	1.90E-08	10	0.05	2.22E-08	0.0266

SKAT_broad	*CSAD*	381625	2.29E-08	14	0.05	6.92E-07	0.0040
SKAT_broad	*MXD3*	381625	2.87E-08	4	0.05	4.21E-08	0.0142
SKAT_broad	*ANGPTL4*	381625	3.43E-08	8	0.05	7.73E-07	0.0219
SKAT_broad	*QARS*	377738	3.67E-08	15	0.05	1.93E-07	0.0024
SKAT_broad	*ZNF19*	381625	3.72E-08	6	0.05	3.80E-08	0.0318
SKAT_broad	*EPS15*	377738	4.21E-08	13	0.05	6.47E-08	0.0196
SKAT_broad	*GPR162*	381625	5.94E-08	12	0.05	4.00E-07	0.0007
SKAT_broad	*CD248*	381625	6.57E-08	10	0.05	1.22E-07	0.0085
SKAT_broad	*PEX1*	381625	8.19E-08	23	0.05	6.59E-07	0.0366
SKAT_broad	*HSD11B2*	381625	8.53E-08	5	0.05	1.31E-07	0.0017
SKAT_broad	*MARCH3*	381625	8.84E-08	5	0.05	9.18E-08	0.0359
SKAT_broad	*LECT2*	381625	9.30E-08	6	0.05	1.13E-07	0.0435
SKAT_broad	*DCBLD2*	381625	9.75E-08	14	0.05	1.65E-07	0.0470
SKAT_broad	*BMP3*	381625	1.10E-07	10	0.05	1.80E-07	0.0246
SKAT_broad	*ZNF304*	381625	1.13E-07	5	0.05	1.98E-06	0.0284
SKAT_broad	*ANO1*	381625	1.15E-07	12	0.05	2.17E-07	0.0072
SKAT_broad	*FBXL19*	381625	1.20E-07	2	0.05	1.20E-07	0.0092
SKAT_broad	*TSPAN31*	372028	1.45E-07	2	0.05	1.44E-07	0.0029
SKAT_broad	*MGA*	381625	1.70E-07	27	0.05	5.76E-05	0.0188
SKAT_broad	*COL5A2*	377738	1.76E-07	26	0.05	2.53E-06	0.0217
SKAT_broad	*CRISPLD1*	380102	2.21E-07	12	0.05	6.79E-07	0.0023
SKAT_broad	*ST3GAL6*	381625	2.27E-07	6	0.05	1.95E-07	0.0471
SKAT_broad	*ABCC1*	381625	2.88E-07	31	0.05	1.19E-06	0.0134
SKAT_broad	*LTBP1*	381625	4.18E-07	26	0.05	9.52E-07	0.0109
SKAT_broad	*FOXM1*	381625	5.21E-07	16	0.05	7.07E-07	0.0225
SKAT_broad	*KLHL28*	381625	5.55E-07	11	0.05	1.58E-06	0.0161
SKAT_broad	*TXLNA*	380102	5.79E-07	4	0.05	1.76E-06	0.0037
SKAT_broad	*CCDC47*	381625	7.25E-07	5	0.05	7.16E-07	0.0028
SKAT_broad	*WDR76*	381625	1.56E-06	9	0.05	1.91E-06	0.0075
SKAT_broad	*IMPG1*	381625	1.57E-06	11	0.05	1.80E-07	0.0118
SKAT_broad	*KLHL25*	381625	1.64E-06	14	0.05	1.50E-06	0.0050
SKAT_broad	*UBTD2*	381625	1.72E-06	3	0.05	1.88E-06	0.0213
SKAT_broad	*BNC2*	381625	1.78E-06	24	0.05	5.80E-06	0.0322
SKAT_broad	*TNXB*	377738	1.90E-06	38	0.05	3.14E-05	0.0107
SKAT_broad	*PHC3*	381625	2.09E-06	12	0.05	1.18E-05	0.0081
SKAT_broad	*FLNB*	381625	2.21E-06	65	0.05	1.22E-06	0.0011
SKAT_broad	*BCAM*	381625	2.24E-06	19	0.05	3.13E-06	0.0324
SKAT_broad	*KIAA1614*	381625	2.42E-06	14	0.05	1.72E-06	0.0263
SKAT_broad	*DLK1*	381625	2.47E-06	11	0.05	1.20E-06	0.0021
SKAT_broad	*AR*	302229	2.51E-06	6	0.05	7.04E-06	0.0026
SKAT_broad	*SPEG*	381625	2.57E-06	38	0.05	8.64E-07	0.0112
SKAT_broad	*CYP1A1*	381625	2.93E-06	19	0.05	3.24E-06	0.0364
SKAT_broad	*SRSF9*	381625	3.48E-06	2	0.05	4.14E-06	0.0345
SKAT_broad	*GRM4*	381625	3.86E-06	9	0.05	3.05E-06	0.0012
SKAT_broad	*CYP11A1*	381625	3.86E-06	5	0.05	2.26E-07	0.0038
SKAT_broad	*FNDC3B*	381625	4.13E-06	24	0.05	3.75E-06	0.0131
SKAT_broad	*UBP1*	381625	4.77E-06	5	0.05	3.34E-06	0.0113
SKAT_broad	*PPP1R9A*	381625	4.80E-06	17	0.05	2.10E-07	0.0087
SKAT_broad	*CIRH1A*	381625	4.86E-06	10	0.05	3.89E-06	0.0439
SKAT_broad	*ERGIC3*	376215	4.92E-06	4	0.05	6.74E-06	0.0006
SKAT_broad	*ENGASE*	381625	4.98E-06	19	0.05	1.21E-06	0.0299
SKAT_broad	*NOX4*	377738	5.12E-06	7	0.05	1.63E-04	0.0026
SKAT_broad	*VARS2*	377738	5.26E-06	19	0.05	2.07E-06	0.0292
SKAT_broad	*SHARPIN*	381625	5.59E-06	4	0.05	6.05E-06	0.0455
SKAT_broad	*UFC1*	381625	5.95E-06	4	0.05	8.49E-06	0.0023
SKAT_broad	*CHD1*	377738	5.97E-06	14	0.05	7.40E-06	0.0129
SKAT_broad	*MTMR11*	381625	5.98E-06	15	0.05	5.62E-06	0.0067
SKAT_broad	*ELN*	381625	6.07E-06	13	0.05	3.31E-06	0.0042
SKAT_broad	*APOLD1*	380102	6.17E-06	6	0.05	3.41E-06	0.0024
SKAT_broad	*MPP2*	381625	6.69E-06	7	0.05	3.84E-06	0.0157
SKAT_broad	*RAPGEF3*	381625	6.76E-06	19	0.05	7.49E-06	0.0122
SKAT_broad	*QPCT*	381625	6.92E-06	11	0.05	3.12E-05	0.0314
SKAT_broad	*ZFPL1*	381625	7.80E-06	8	0.05	3.25E-06	0.0179
SKAT_broad	*COMP*	381625	8.09E-06	12	0.05	3.70E-06	0.0450
SKAT_broad	*POLB*	381625	8.96E-06	8	0.05	7.67E-06	0.0178
SKAT_broad	*POR*	381625	9.58E-06	15	0.05	2.59E-05	0.0040
SKAT_broad	*KIAA0922*	381625	9.72E-06	22	0.05	8.05E-08	0.0113
SKAT_broad	*NOSTRIN*	381625	1.01E-05	10	0.05	1.09E-05	0.0012
SKAT_broad	*CBLC*	381625	1.03E-05	6	0.05	1.61E-07	0.0345
SKAT_broad	*UPF2*	381625	1.08E-05	6	0.05	4.21E-06	0.0069

SKAT_broad	*CACNA2D2*	381625	1.17E-05	8	0.05	4.11E-06	0.0329
SKAT_broad	*ABCA6*	381625	1.18E-05	37	0.05	1.74E-05	0.0169
SKAT_broad	*KIF7*	381625	1.22E-05	33	0.05	1.85E-05	0.0046
SKAT_broad	*SLC38A2*	381625	1.24E-05	11	0.05	5.15E-05	0.0157
SKAT_broad	*LTBP4*	381625	1.24E-05	16	0.05	1.37E-05	0.0135
SKAT_broad	*G6PC*	381625	1.28E-05	9	0.05	9.53E-05	0.0003
SKAT_broad	*SETD2*	381625	1.29E-05	16	0.05	3.56E-05	0.0020
SKAT_broad	*TTN*	381625	1.34E-05	761	0.05	1.78E-07	0.0134
SKAT_broad	*WDR6*	377738	1.42E-05	13	0.05	8.98E-06	0.0063
SKAT_broad	*C10orf76*	381625	1.43E-05	4	0.05	1.25E-05	0.0068
SKAT_broad	*NKAPL*	377738	1.47E-05	8	0.05	5.37E-04	0.0081
SKAT_broad	*TET1*	381625	1.49E-05	14	0.05	1.49E-05	0.0220
SKAT_broad	*MAPKAPK2*	381625	1.58E-05	3	0.05	1.42E-05	0.0014
SKAT_broad	*EFEMP1*	381625	1.59E-05	4	0.05	1.27E-05	0.0016
SKAT_broad	*KLC1*	381625	1.61E-05	4	0.05	1.41E-05	0.0254
SKAT_broad	*PEX16*	381625	1.62E-05	6	0.05	1.74E-05	0.0292
SKAT_broad	*DKK1*	381625	1.63E-05	3	0.05	1.83E-05	0.0040
SKAT_broad	*ITGB7*	381625	1.68E-05	10	0.05	1.79E-05	0.0141
SKAT_broad	*RNF144B*	380102	1.68E-05	5	0.05	1.12E-05	0.0007
SKAT_broad	*APOH*	381625	1.69E-05	5	0.05	1.58E-05	0.0291
SKAT_broad	*PRKAG1*	381625	1.75E-05	4	0.05	1.94E-05	0.0340
SKAT_broad	*PRAM1*	381625	1.77E-05	9	0.05	1.73E-05	0.0046
SKAT_broad	*FAM134A*	381625	1.78E-05	6	0.05	2.89E-05	0.0044
SKAT_broad	*ZDHHC1*	381625	1.79E-05	4	0.05	1.50E-05	0.0272
SKAT_broad	*GLI3*	381625	1.82E-05	20	0.05	2.62E-05	0.0073
SKAT_broad	*SLC38A4*	381625	1.90E-05	4	0.05	1.90E-05	0.0018
SKAT_broad	*SNED1*	381625	1.90E-05	10	0.05	5.49E-07	0.0064
SKAT_broad	*SNX15*	381625	1.98E-05	10	0.05	1.55E-05	0.0178
SKAT_broad	*RIC8B*	381625	2.01E-05	6	0.05	2.32E-05	0.0075
SKAT_broad	*LRRC8A*	381625	2.05E-05	5	0.05	2.12E-05	0.0057
SKAT_broad	*SAMD4A*	381625	2.14E-05	12	0.05	7.33E-04	0.0047
SKAT_broad	*EIF6*	377738	2.16E-05	5	0.05	2.49E-05	0.0120
SKAT_broad	*C16orf70*	381625	2.24E-05	6	0.05	2.75E-04	0.0308
SKAT_broad	*B4GALNT3*	381625	2.39E-05	30	0.05	4.08E-05	0.0180
SKAT_broad	*SREK1IP1*	192725	2.43E-05	1	0.05	2.43E-05	0.0407
SKAT_broad	*TIAM2*	381625	2.48E-05	35	0.05	2.06E-08	0.0029
SKAT_broad	*ZNF335*	381625	2.52E-05	19	0.05	2.92E-05	0.0246
SKAT_broad	*MYOG*	381625	2.62E-05	5	0.05	1.05E-05	0.0322
SKAT_broad	*THBS3*	381625	2.68E-05	14	0.05	1.95E-05	0.0170
SKAT_broad	*ZCCHC6*	381625	2.68E-05	8	0.05	2.96E-05	0.0064
SKAT_broad	*USP31*	381625	2.80E-05	19	0.05	2.99E-05	0.0198
SKAT_broad	*CDC23*	377738	2.84E-05	4	0.05	3.16E-05	0.0079
SKAT_broad	*ITIH4*	381625	2.95E-05	14	0.05	2.48E-04	0.0025
SKAT_broad	*UGGT2*	381625	3.03E-05	33	0.05	8.78E-05	0.0300
SKAT_broad	*OR9G4*	377738	3.36E-05	7	0.05	3.36E-05	0.0104
SKAT_broad	*DDX19B*	381625	3.36E-05	2	0.05	3.69E-05	0.0123
SKAT_broad	*NUDT12*	381625	3.38E-05	8	0.05	3.48E-05	0.0019
SKAT_broad	*SLC43A1*	381625	3.39E-05	7	0.05	3.56E-05	0.0367
SKAT_broad	*ARRDC4*	381625	3.42E-05	10	0.05	5.63E-06	0.0406
SKAT_broad	*ZNF324*	372028	3.61E-05	5	0.05	7.04E-06	0.0006
SKAT_broad	*N4BP1*	381625	3.66E-05	3	0.05	4.03E-05	0.0086
SKAT_broad	*PDIA2*	381625	4.01E-05	15	0.05	2.04E-05	0.0145
SKAT_broad	*FLII*	381625	4.18E-05	26	0.05	4.80E-05	0.0258
SKAT_broad	*CORO6*	381625	4.42E-05	7	0.05	5.03E-05	0.0176
SKAT_broad	*PDE8A*	381625	4.43E-05	12	0.05	4.59E-05	0.0353
SKAT_broad	*SLC12A7*	381625	4.56E-05	23	0.05	9.12E-05	0.0029
SKAT_broad	*HIGD1B*	381625	4.58E-05	3	0.05	4.63E-05	0.0271
SKAT_broad	*TXNDC5*	381625	4.59E-05	11	0.05	4.55E-05	0.0104
SKAT_broad	*PRKG2*	381625	4.83E-05	9	0.05	5.12E-05	0.0028
SKAT_broad	*ZNF423*	381625	4.87E-05	18	0.05	5.38E-05	0.0316
SKAT_broad	*WNK4*	381625	4.91E-05	17	0.05	2.67E-05	0.0150
SKAT_broad	*CYP19A1*	381625	4.97E-05	6	0.05	5.37E-05	0.0348
SKAT_broad	*PMPCA*	381625	5.04E-05	10	0.05	4.01E-05	0.0172
SKAT_broad	*C5orf42*	381625	5.26E-05	21	0.05	7.35E-04	0.0370
SKAT_broad	*MC3R*	381625	5.26E-05	5	0.05	7.49E-05	0.0013
SKAT_broad	*TARS2*	381625	5.30E-05	11	0.05	2.71E-06	0.0081
SKAT_broad	*C15orf39*	381625	5.31E-05	16	0.05	2.44E-04	0.0089
SKAT_broad	*NFIC*	381625	6.05E-05	9	0.05	9.22E-05	0.0017
SKAT_broad	*FAM46A*	381625	6.12E-05	2	0.05	6.10E-05	0.0080
SKAT_broad	*PRSS38*	381625	6.47E-05	11	0.05	7.67E-04	0.0374

SKAT_broad	*GPI*	381625	6.63E-05	11	0.05	6.36E-05	0.0230
SKAT_broad	*SENP6*	381625	6.72E-05	19	0.05	3.74E-04	0.0041
SKAT_broad	*FBXL12*	381625	6.91E-05	10	0.05	7.14E-05	0.0020
SKAT_broad	*CSGALNACT1*	381625	6.99E-05	22	0.05	4.84E-05	0.0131
SKAT_broad	*CERS2*	381625	7.14E-05	4	0.05	6.51E-05	0.0068
SKAT_broad	*ENPP2*	381625	7.16E-05	15	0.05	1.08E-04	0.0054
SKAT_broad	*PCK2*	381625	7.18E-05	33	0.05	1.45E-04	0.0155
SKAT_broad	*ATP6V0A2*	381625	7.18E-05	15	0.05	3.86E-05	0.0364
SKAT_broad	*RNF135*	381625	7.35E-05	4	0.05	7.34E-05	0.0096
SKAT_broad	*TNRC6A*	381625	7.47E-05	42	0.05	1.96E-09	0.0401
SKAT_broad	*TGFB3*	380102	8.12E-05	4	0.05	4.02E-05	0.0011
SKAT_broad	*TBX2*	381625	8.16E-05	4	0.05	8.01E-05	0.0132
SKAT_broad	*SPTLC1*	381625	8.44E-05	6	0.05	7.91E-05	0.0278
SKAT_broad	*SPSB3*	381625	8.56E-05	6	0.05	3.02E-05	0.0059
SKAT_broad	*ASB3*	381625	8.72E-05	9	0.05	6.36E-05	0.0188
SKAT_broad	*GYS1*	381625	8.79E-05	6	0.05	8.21E-05	0.0083
SKAT_broad	*E2F7*	381625	8.97E-05	15	0.05	1.07E-04	0.0210
SKAT_broad	*RRS1*	381625	9.66E-05	11	0.05	5.05E-05	0.0402
SKAT_strict	*PTPN13*	381625	1.95E-22	12	0.05	1.38E-19	0.0145
SKAT_strict	*GMPR2*	381625	8.65E-16	5	0.05	9.90E-16	0.0480
SKAT_strict	*STC2*	369802	1.41E-14	1	0.05	1.41E-14	0.0010
SKAT_strict	*CRISPLD2*	381625	3.47E-13	3	0.05	6.04E-13	0.0008
SKAT_strict	*ZFAT*	381625	3.88E-13	4	0.05	1.92E-12	0.0009
SKAT_strict	*GRAMD2*	381625	7.27E-13	4	0.05	7.64E-13	0.0063
SKAT_strict	*PDE11A*	381625	1.61E-12	10	0.05	1.45E-08	0.0362
SKAT_strict	*FIBIN*	381625	3.52E-12	4	0.05	5.00E-12	0.0044
SKAT_strict	*GLT8D2*	381625	1.03E-09	2	0.05	1.04E-09	0.0173
SKAT_strict	*FLNB*	381625	2.42E-09	23	0.05	1.22E-06	0.0011
SKAT_strict	*ADAMTS3*	381625	1.49E-08	7	0.05	1.77E-08	0.0027
SKAT_strict	*BMP3*	359610	1.80E-07	1	0.05	1.80E-07	0.0246
SKAT_strict	*FOXM1*	381625	2.40E-07	2	0.05	7.07E-07	0.0225
SKAT_strict	*CCDC3*	380102	3.04E-07	4	0.05	2.32E-05	0.0001
SKAT_strict	*HERC1*	381625	3.25E-07	4	0.05	3.34E-07	0.0368
SKAT_strict	*RANBP9*	377738	8.77E-07	1	0.05	8.77E-07	0.0011
SKAT_strict	*G6PC*	381625	5.51E-06	3	0.05	9.53E-05	0.0003
SKAT_strict	*ABCC1*	381625	6.07E-06	11	0.05	1.19E-06	0.0134
SKAT_strict	*PAM*	381625	7.85E-06	4	0.05	6.87E-06	0.0484
SKAT_strict	*CRISPLD1*	380102	8.50E-06	3	0.05	6.27E-06	0.0001
SKAT_strict	*AR*	275649	9.75E-06	2	0.05	7.04E-06	0.0026
SKAT_strict	*RAPGEF3*	381625	1.07E-05	7	0.05	7.49E-06	0.0122
SKAT_strict	*NOSTRIN*	381625	1.09E-05	1	0.05	1.09E-05	0.0012
SKAT_strict	*ABCA6*	381625	1.65E-05	4	0.05	1.74E-05	0.0169
SKAT_strict	*APOH*	381625	1.72E-05	2	0.05	1.58E-05	0.0291
SKAT_strict	*B4GALNT3*	381625	1.84E-05	9	0.05	4.08E-05	0.0180
SKAT_strict	*COL7A1*	377738	2.15E-05	8	0.05	1.83E-05	0.0041
SKAT_strict	*CARD9*	378603	2.20E-05	2	0.05	2.89E-05	0.0000
SKAT_strict	*UGGT2*	381625	2.29E-05	10	0.05	8.78E-05	0.0300
SKAT_strict	*C18orf25*	381625	2.52E-05	2	0.05	2.53E-05	0.0038
SKAT_strict	*ZCCHC6*	381625	2.84E-05	2	0.05	2.96E-05	0.0064
SKAT_strict	*POR*	381625	3.09E-05	5	0.05	2.59E-05	0.0040
SKAT_strict	*ATP6V0A2*	380102	4.02E-05	5	0.05	3.86E-05	0.0364
SKAT_strict	*ASH1L*	381625	4.04E-05	3	0.05	3.93E-05	0.0015
SKAT_strict	*GPI*	381625	6.47E-05	3	0.05	6.36E-05	0.0230
SKAT_strict	*SLC22A5*	377738	7.07E-05	4	0.05	5.79E-05	0.0008
SKAT_strict	*NFIC*	381625	8.02E-05	2	0.05	9.22E-05	0.0017
VT_broad	*IL11*	381625	2.19E-53	3	0.0261	1.14E-55	0.0261
VT_broad	*SERPINA1*	381625	4.76E-35	12	0.0251	8.37E-45	0.0184
VT_broad	*ZFAT*	381625	5.09E-35	14	0.0037	4.45E-26	0.0039
VT_broad	*NSD1*	381625	7.09E-24	16	0.0271	1.33E-25	0.0229
VT_broad	*SCMH1*	381625	2.46E-23	8	0.0039	1.76E-25	0.0042
VT_broad	*TBX15*	381625	1.87E-20	9	0.0415	1.07E-23	0.0424
VT_broad	*ZNF628*	381625	5.05E-18	6	0.0143	5.22E-18	0.0206
VT_broad	*IHH*	381625	6.36E-18	3	0.0048	4.31E-15	0.0008
VT_broad	*FANCE*	381625	7.04E-18	7	0.0151	7.94E-29	0.0148
VT_broad	*ACAN*	381625	3.58E-17	35	0.0285	1.00E-21	0.0092
VT_broad	*CYTL1*	381625	3.90E-17	2	0.0400	2.47E-17	0.0402
VT_broad	*LRRC36*	381625	5.17E-17	13	0.0410	3.70E-17	0.0428
VT_broad	*GALR1*	381625	2.22E-16	8	0.0457	5.57E-18	0.0470
VT_broad	*STC2*	381625	8.88E-16	5	0.0013	1.41E-14	0.0010
VT_broad	*CCND3*	381625	3.00E-15	4	0.0047	6.58E-17	0.0133

VT_broad	*PDE5A*	381625	4.44E-15	11	0.0014	6.23E-17	0.0014
VT_broad	*GMPR2*	381625	6.22E-15	8	0.0478	9.90E-16	0.0480
VT_broad	*PDE11A*	381625	2.07E-14	34	0.0360	1.45E-08	0.0362
VT_broad	*DUSP1*	381625	2.16E-14	4	0.0337	5.33E-14	0.0362
VT_broad	*TMEM150B*	381625	1.88E-13	3	0.0082	9.91E-14	0.0080
VT_broad	*FIBIN*	381625	2.42E-13	4	0.0252	5.00E-12	0.0044
VT_broad	*IL11RA*	381625	3.75E-13	6	0.0165	6.85E-13	0.0163
VT_broad	*NPR3*	381625	4.11E-13	4	0.0029	1.03E-08	0.0025
VT_broad	*MATN3*	381625	4.22E-13	11	0.0262	3.57E-23	0.0262
VT_broad	*PARD6A*	381625	1.08E-12	2	0.0384	3.17E-13	0.0408
VT_broad	*TSNAXIP1*	381625	1.11E-11	21	0.0408	5.69E-14	0.0408
VT_broad	*ARMC5*	381625	2.50E-11	4	0.0057	6.03E-12	0.0056
VT_broad	*ADAMTS3*	381625	2.64E-11	21	0.0129	1.77E-08	0.0027
VT_broad	*GLT8D2*	381625	4.23E-11	10	0.0251	1.04E-09	0.0173
VT_broad	*GRAMD2*	381625	4.83E-11	7	0.0065	7.64E-13	0.0063
VT_broad	*CLPS*	381625	6.65E-11	6	0.0251	3.29E-21	0.0151
VT_broad	*CRISPLD1*	380102	6.73E-11	12	0.0253	6.79E-07	0.0023
VT_broad	*CRISPLD2*	381625	1.31E-10	7	0.0008	6.04E-13	0.0008
VT_broad	*AMOTL1*	381625	1.57E-10	14	0.0251	1.03E-15	0.0092
VT_broad	*ANAPC5*	381625	2.06E-10	5	0.0089	1.70E-11	0.0089
VT_broad	*DCAF16*	381625	2.11E-10	4	0.0280	1.80E-10	0.0280
VT_broad	*LRP5*	381625	3.84E-10	27	0.0481	8.65E-12	0.0481
VT_broad	*CSAD*	381625	2.41E-09	13	0.0044	6.92E-07	0.0040
VT_broad	*LECT2*	381625	2.43E-09	6	0.0434	1.13E-07	0.0435
VT_broad	*SNED1*	381625	4.28E-09	8	0.0062	5.49E-07	0.0064
VT_broad	*NPAS4*	381625	5.74E-09	7	0.0082	4.53E-11	0.0082
VT_broad	*ANKS3*	381625	7.71E-09	19	0.0254	2.27E-13	0.0252
VT_broad	*LCAT*	381625	7.81E-09	2	0.0288	2.72E-09	0.0296
VT_broad	*SLC35E3*	381625	8.45E-09	6	0.0286	2.02E-09	0.0224
VT_broad	*MCL1*	381625	1.74E-08	5	0.0344	3.10E-09	0.0137
VT_broad	*ADAMTS6*	381625	2.03E-08	13	0.0026	9.50E-09	0.0019
VT_broad	*ACHE*	381625	2.49E-08	6	0.0416	4.88E-09	0.0432
VT_broad	*GAB1*	381625	3.30E-08	2	0.0187	9.88E-09	0.0186
VT_broad	*G6PC*	381625	3.61E-08	6	0.0014	9.53E-05	0.0003
VT_broad	*HSD11B2*	381625	6.15E-08	5	0.0042	1.31E-07	0.0017
VT_broad	*MARCH3*	381625	9.76E-08	5	0.0337	9.18E-08	0.0359
VT_broad	*SMG7*	381625	1.11E-07	14	0.0063	7.71E-11	0.0061
VT_broad	*PHKB*	381625	1.40E-07	22	0.0050	6.11E-14	0.0049
VT_broad	*NOX4*	377738	1.40E-07	6	0.0027	1.63E-04	0.0026
VT_broad	*LAMB2*	377738	1.51E-07	45	0.0371	8.99E-12	0.0394
VT_broad	*PHC3*	381625	1.82E-07	9	0.0080	1.18E-05	0.0081
VT_broad	*SSC5D*	381625	2.26E-07	5	0.0201	1.34E-14	0.0233
VT_broad	*FBXL19*	381625	2.41E-07	2	0.0092	1.20E-07	0.0092
VT_broad	*PEX1*	381625	2.49E-07	23	0.0363	6.59E-07	0.0366
VT_broad	*UGGT2*	381625	2.60E-07	33	0.0298	8.78E-05	0.0300
VT_broad	*ZNF19*	381625	3.29E-07	6	0.0319	3.80E-08	0.0318
VT_broad	*DISP1*	381625	3.53E-07	14	0.0079	1.57E-09	0.0079
VT_broad	*TSPAN31*	372028	5.32E-07	2	0.0029	1.44E-07	0.0029
VT_broad	*BMP3*	381625	5.64E-07	10	0.0233	1.80E-07	0.0246
VT_broad	*SLC8A3*	381625	5.85E-07	23	0.0251	2.28E-11	0.0205
VT_broad	*KLHL28*	381625	8.22E-07	11	0.0149	1.58E-06	0.0161
VT_broad	*WDR76*	381625	9.69E-07	8	0.0076	1.91E-06	0.0075
VT_broad	*MXD3*	381625	1.09E-06	4	0.0134	4.21E-08	0.0142
VT_broad	*UFC1*	381625	1.66E-06	4	0.0040	8.49E-06	0.0023
VT_broad	*ST3GAL6*	381625	1.97E-06	6	0.0478	1.95E-07	0.0471
VT_broad	*FBN2*	381625	2.03E-06	33	0.0062	2.46E-33	0.0060
VT_broad	*MMP14*	381625	3.35E-06	10	0.0260	2.22E-08	0.0266
VT_broad	*CIRH1A*	381625	3.38E-06	10	0.0444	3.89E-06	0.0439
VT_broad	*KCTD19*	381625	3.88E-06	13	0.0385	1.27E-14	0.0418
VT_broad	*AR*	302229	4.27E-06	4	0.0014	7.04E-06	0.0026
VT_broad	*EIF6*	377738	5.54E-06	5	0.0122	2.49E-05	0.0120
VT_broad	*CCDC3*	381625	6.34E-06	4	0.0002	2.32E-05	0.0001
VT_broad	*SRSF9*	381625	7.17E-06	2	0.0276	4.14E-06	0.0345
VT_broad	*VARS2*	377738	7.31E-06	19	0.0292	2.07E-06	0.0292
VT_broad	*NKAPL*	377738	8.13E-06	8	0.0253	5.37E-04	0.0081
VT_broad	*PRKAG1*	381625	1.00E-05	4	0.0337	1.94E-05	0.0340
VT_broad	*MPP2*	381625	1.13E-05	7	0.0156	3.84E-06	0.0157
VT_broad	*ENGASE*	381625	1.13E-05	19	0.0303	1.21E-06	0.0299
VT_broad	*PTH1R*	381625	1.15E-05	4	0.0025	1.44E-11	0.0025
VT_broad	*TET1*	381625	1.31E-05	14	0.0343	1.49E-05	0.0220

VT_broad	*RANBP9*	381625	1.46E-05	3	0.0030	8.77E-07	0.0011
VT_broad	*CCDC47*	381625	1.46E-05	4	0.0027	7.16E-07	0.0028
VT_broad	*EPS15*	377738	1.47E-05	13	0.0191	6.47E-08	0.0196
VT_broad	*TNRC6A*	381625	1.57E-05	42	0.0387	1.96E-09	0.0401
VT_broad	*ABCC1*	381625	1.64E-05	31	0.0292	1.19E-06	0.0134
VT_broad	*RIC8B*	381625	1.69E-05	6	0.0252	2.32E-05	0.0075
VT_broad	*B4GALNT3*	381625	1.85E-05	17	0.0004	4.08E-05	0.0180
VT_broad	*POLB*	381625	1.90E-05	8	0.0155	7.67E-06	0.0178
VT_broad	*SLC38A4*	381625	2.11E-05	4	0.0251	1.90E-05	0.0018
VT_broad	*COMP*	381625	2.31E-05	12	0.0445	3.70E-06	0.0450
VT_broad	*SREK1IP1*	192725	2.43E-05	1	0.0407	2.43E-05	0.0407
VT_broad	*ADAMTSL3*	381625	2.67E-05	27	0.0251	5.62E-08	0.0211
VT_broad	*C10orf76*	381625	2.69E-05	4	0.0065	1.25E-05	0.0068
VT_broad	*ADAMTS10*	381625	2.73E-05	11	0.0010	1.24E-03	0.0010
VT_broad	*SHARPIN*	381625	2.89E-05	4	0.0399	6.05E-06	0.0455
VT_broad	*TXLNA*	380102	3.70E-05	4	0.0036	1.76E-06	0.0037
VT_broad	*PCDHB14*	381625	4.30E-05	4	0.0002	6.72E-04	0.0001
VT_broad	*C18orf25*	381625	4.35E-05	1	0.0037	2.53E-05	0.0038
VT_broad	*OSGIN1*	381625	4.53E-05	13	0.0057	7.90E-06	0.0000
VT_broad	*CYP11A1*	381625	4.55E-05	5	0.0038	2.26E-07	0.0038
VT_broad	*C19orf44*	381625	4.72E-05	1	2.62E-06	5.86E-06	0.0000
VT_broad	*FAM187B*	381625	4.85E-05	11	0.0005	1.21E-03	0.0002
VT_broad	*N4BP1*	381625	4.88E-05	2	0.0058	4.03E-05	0.0086
VT_broad	*CACNA2D2*	381625	5.07E-05	8	0.0327	4.11E-06	0.0329
VT_broad	*ACTN4*	381625	5.39E-05	5	0.0059	5.16E-05	0.0063
VT_broad	*DCBLD2*	381625	5.70E-05	14	0.0476	1.65E-07	0.0470
VT_broad	*UBTD2*	381625	6.07E-05	2	0.0210	1.88E-06	0.0213
VT_broad	*LTBP4*	381625	6.24E-05	16	0.0136	1.37E-05	0.0135
VT_broad	*DKK1*	381625	6.25E-05	3	0.0042	1.83E-05	0.0040
VT_broad	*MAPKAPK2*	381625	6.63E-05	3	0.0013	1.42E-05	0.0014
VT_broad	*KLC1*	381625	7.82E-05	4	0.0237	1.41E-05	0.0254
VT_broad	*CCDC113*	381625	8.17E-05	8	0.0294	1.32E-04	0.0031
VT_broad	*SNX15*	381625	8.46E-05	10	0.0251	1.55E-05	0.0178
VT_broad	*KLHL25*	381625	8.71E-05	12	0.0251	1.50E-06	0.0050
VT_broad	*ZNF646*	381625	8.82E-05	19	0.0251	9.66E-10	0.0080
VT_broad	*ELN*	381625	8.92E-05	13	0.0038	3.31E-06	0.0042
VT_broad	*DDX19B*	381625	9.04E-05	2	0.0120	3.69E-05	0.0123
VT_broad	*TTC28*	381625	9.42E-05	13	0.0123	1.98E-10	0.0121
VT_broad	*SLC25A40*	381625	9.59E-05	6	0.0094	1.57E-04	0.0094
VT_strict	*GMPR2*	381625	4.33E-15	5	0.0478	9.90E-16	0.0480
VT_strict	*STC2*	369802	1.41E-14	1	0.0010	1.41E-14	0.0010
VT_strict	*ZFAT*	381625	6.57E-14	4	0.0019	1.92E-12	0.0009
VT_strict	*FIBIN*	381625	2.35E-13	3	0.0042	5.00E-12	0.0044
VT_strict	*CRISPLD2*	381625	3.04E-13	3	0.0008	6.04E-13	0.0008
VT_strict	*GRAMD2*	381625	1.40E-11	4	0.0065	7.64E-13	0.0063
VT_strict	*PDE11A*	381625	2.36E-11	10	0.0360	1.45E-08	0.0362
VT_strict	*GLT8D2*	381625	1.23E-09	2	0.0177	1.04E-09	0.0173
VT_strict	*CCDC3*	380102	5.36E-09	3	0.0002	2.32E-05	0.0001
VT_strict	*PTPN13*	381625	8.79E-09	11	0.0144	1.38E-19	0.0145
VT_strict	*BMP3*	359610	1.80E-07	1	0.0246	1.80E-07	0.0246
VT_strict	*B4GALNT3*	381625	3.10E-07	9	0.0180	4.08E-05	0.0180
VT_strict	*ADAMTS3*	381625	3.49E-07	7	0.0028	1.77E-08	0.0027
VT_strict	*UGGT2*	381625	4.78E-07	9	0.0182	8.78E-05	0.0300
VT_strict	*RANBP9*	377738	8.77E-07	1	0.0011	8.77E-07	0.0011
VT_strict	*CRISPLD1*	380102	8.92E-07	3	0.0253	6.27E-06	0.0001
VT_strict	*G6PC*	381625	1.31E-06	2	0.0004	9.53E-05	0.0003
VT_strict	*HERC1*	381625	1.99E-06	3	0.0274	3.34E-07	0.0368
VT_strict	*FOXM1*	381625	2.27E-06	2	0.0226	7.07E-07	0.0225
VT_strict	*CARD9*	378603	2.37E-06	2	1.72E-05	2.89E-05	9.50E-06
VT_strict	*SCUBE3*	380102	3.08E-06	1	0.0001	8.91E-07	0.0001
VT_strict	*FLNB*	381625	3.20E-06	20	0.0011	1.22E-06	0.0011
VT_strict	*ABCC1*	381625	3.68E-06	11	0.0127	1.19E-06	0.0134
VT_strict	*NOSTRIN*	381625	1.09E-05	1	0.0012	1.09E-05	0.0012
VT_strict	*AR*	275649	1.23E-05	1	0.0015	7.04E-06	0.0026
VT_strict	*C19orf44*	381625	1.94E-05	1	2.62E-06	5.86E-06	2.64E-06
VT_strict	*C18orf25*	381625	2.12E-05	2	0.0092	2.53E-05	0.0038
VT_strict	*ABCA6*	381625	2.48E-05	4	0.0124	1.74E-05	0.0169
VT_strict	*RAPGEF3*	381625	2.74E-05	7	0.0116	7.49E-06	0.0122
VT_strict	*PAM*	381625	3.62E-05	4	0.0486	6.87E-06	0.0484
VT_strict	*APOH*	381625	4.95E-05	2	0.0290	1.58E-05	0.0291

VT_strict	*ZCCHC6*	381625	6.20E-05	2	0.0064	2.96E-05	0.0064
VT_strict	*COL7A1*	377738	8.31E-05	8	0.0349	1.83E-05	0.0041

Supplementary Table 15. Gene-based results in the African-, East Asian-, Hispanics-, and South Asian-ancestry analysis (P<1e-4). Only non-synonymous and splice site variants with MAF <5% were included in the tests, as detailed in the Online Methods (including a definition of the "broad" and "strict" masks. The MAF cutoff changes with the VT approach.

Population	Test	Gene	N	Gene-based P-value	Number of variants	MAF cutoff	Top single variant P-value	Top single variant MAF
African American	SKAT_broad	*GH1*	27494	1.58E-07	4	0.05	2.22E-07	0.0302
African American	SKAT_broad	*CNPY2*	27494	1.95E-07	1	0.05	1.95E-07	0.0036
African American	SKAT_broad	*ELL*	27494	2.23E-05	6	0.05	2.40E-05	0.0060
African American	SKAT_broad	*E2F7*	27494	2.85E-05	10	0.05	4.96E-05	0.0028
African American	SKAT_broad	*GNGT2*	27494	3.18E-05	2	0.05	9.12E-06	0.0103
African American	SKAT_broad	*MUC4*	27494	6.26E-05	18	0.05	4.55E-06	0.0274
African American	SKAT_strict	*GNGT2*	27494	9.12E-06	1	0.05	9.12E-06	0.0103
African American	SKAT_strict	*ELL*	27295	2.40E-05	1	0.05	2.40E-05	0.0060
African American	VT_broad	*CNPY2*	27494	1.95E-07	1	0.0036	1.95E-07	0.0036
African American	VT_broad	*GNGT2*	27494	1.82E-05	1	0.0103	9.12E-06	0.0103
African American	VT_broad	*GH1*	27494	2.74E-05	4	0.0299	2.22E-07	0.0302
African American	VT_strict	*GNGT2*	27494	9.12E-06	1	0.0103	9.12E-06	0.0103
African American	VT_strict	*LIPE*	27494	2.05E-05	4	0.0016	2.57E-05	0.0016
African American	VT_strict	*ELL*	27295	2.40E-05	1	0.0060	2.40E-05	0.0060
East Asian	SKAT_broad	*ADAMTSL3*	8767	2.86E-05	10	0.05	9.79E-04	0.0172
East Asian	SKAT_broad	*PRSS55*	8767	6.31E-05	4	0.05	5.95E-05	0.0057
East Asian	SKAT_broad	*OR52L1*	7790	6.95E-05	1	0.05	6.95E-05	0.0009
East Asian	SKAT_strict	*OR52L1*	7790	6.95E-05	1	0.05	6.95E-05	0.0009
East Asian	VT_broad	*DHX16*	8767	2.98E-06	5	0.0010	3.93E-05	0.0013
East Asian	VT_broad	*ADAMTSL3*	8767	6.34E-05	10	0.0172	9.79E-04	0.0172
East Asian	VT_broad	*OR52L1*	7790	6.95E-05	1	0.0009	6.95E-05	0.0009
East Asian	VT_broad	*XYLT1*	8767	8.35E-05	5	0.0001	7.91E-04	0.0001
East Asian	VT_strict	*OR52L1*	7790	6.95E-05	1	0.0009	6.95E-05	0.0009
Hispanics	SKAT_broad	*ADAMTS17*	10776	8.69E-06	20	0.05	1.68E-05	0.0420
Hispanics	SKAT_strict	*NFS1*	8627	4.66E-05	1	0.05	4.66E-05	0.0001
Hispanics	SKAT_strict	*PNPLA3*	8627	9.22E-05	1	0.05	9.22E-05	0.0002
Hispanics	VT_broad	*TFRC*	9517	8.14E-05	3	0.0004	1.52E-04	0.0005
Hispanics	VT_broad	*FAM114A2*	10776	9.57E-05	3	9.28E-05	9.20E-05	0.0001
Hispanics	VT_strict	*NFS1*	8627	4.66E-05	1	0.0001	4.66E-05	0.0001
Hispanics	VT_strict	*PNPLA3*	8627	9.22E-05	1	0.0002	9.22E-05	0.0002
South Asian	SKAT_broad	*METTL3*	29591	3.40E-09	4	0.05	3.43E-09	0.0096
South Asian	SKAT_broad	*ADH4*	29591	2.34E-06	5	0.05	2.32E-05	0.0005
South Asian	SKAT_broad	*C14orf28*	29591	9.81E-06	3	0.05	8.74E-06	0.0017
South Asian	SKAT_broad	*RECQL5*	29591	1.28E-05	14	0.05	2.80E-06	0.0008
South Asian	SKAT_broad	*BFAR*	29591	1.37E-05	7	0.05	2.39E-05	0.0009
South Asian	SKAT_broad	*EMILIN1*	29591	3.43E-05	5	0.05	1.45E-04	0.0003
South Asian	SKAT_broad	*PARP8*	29591	4.33E-05	5	0.05	5.40E-05	0.006
South Asian	SKAT_broad	*IL33*	29591	5.51E-05	6	0.05	5.64E-05	0.001
South Asian	SKAT_broad	*TMEM39B*	29591	9.55E-05	1	0.05	9.55E-05	1.69E-05
South Asian	SKAT_strict	*C14orf28*	29591	9.92E-06	2	0.05	8.74E-06	0.002
South Asian	SKAT_strict	*CEACAM7*	29474	9.55E-05	1	0.05	9.55E-05	1.70E-05
South Asian	VT_broad	*METTL3*	29591	3.75E-08	4	0.0096	3.43E-09	0.010
South Asian	VT_broad	*TRIO*	29591	1.48E-05	16	0.0012	1.29E-03	0.001
South Asian	VT_broad	*EML4*	29591	1.74E-05	5	5.07E-05	8.71E-04	5.07E-05
South Asian	VT_broad	*C14orf28*	29591	2.51E-05	3	0.0017	8.74E-06	0.002
South Asian	VT_broad	*SPACA1*	29591	6.07E-05	2	0.0003	1.40E-04	2.88E-04
South Asian	VT_broad	*TMEM39B*	29591	9.55E-05	1	1.69E-05	9.55E-05	1.69E-05
South Asian	VT_strict	*C14orf28*	29591	1.54E-05	2	0.0017	8.74E-06	0.002
South Asian	VT_strict	*CEACAM7*	29474	9.55E-05	1	1.70E-05	9.55E-05	1.70E-05

Supplementary Table 16. Stepwise conditional results for the gene-based findings.

Gene	Discovery gene-based P-value	Conditional test	P-value					Condition variants				# of variants conditioned on to have gene-based P>0.05
			No condition	Round1	Round2	Round3	Round4	Round1	Round2	Round3	Round4	
OSGIN1	4.30E-11	SKAT	4.30E-11	6.17E-11	4.87E-08	7.51E-06	0.370878	16:83999434	16:83999565	16:83999548	16:83998995	4
CRISPLD1	6.70E-11	GRANVIL	1.93E-11	2.49E-07	0.00058762	0.00497027	0.0949753	8:75929615	8:75926254	8:75941664	8:75929305	4
CSAD	2.40E-09	GRANVIL	2.43E-10	0.00020515	0.0110453	0.251158	NA	12:53566174	12:53566324	12:53566222	NA	3
SNED1	4.30E-09	GRANVIL	1.98E-06	0.0135217	0.143642	NA	NA	2:241974013	2:241976210	NA	NA	2
G6PC	3.60E-08	GRANVIL	3.91E-08	8.29E-06	0.00423934	0.188989	NA	17:41063408	17:41062979	17:41055964	NA	3
NOX4	1.40E-07	GRANVIL	4.64E-08	0.00010659	0.155708	NA	NA	11:89182666	11:89182686	NA	NA	2
UGGT2	2.60E-07	GRANVIL	2.72E-08	2.35E-05	0.0142021	NA	NA	13:96511868	13:96546850	NA	NA	3
FLNB	2.40E-09	SKAT	2.40E-09	0.00020376	0.565395	NA	NA	3:58104626	3:58116478	NA	NA	2
B4GALNT3	3.10E-07	GRANVIL	5.95E-08	2.00E-07	0.00012596	0.00161352	0.0252624	12:670520	12:667217	12:661265	12:670531	4
CCDC3	5.40E-09	GRANVIL	2.38E-08	6.88E-05	0.409502	NA	NA	10:13040481	10:13040400	NA	NA	2

Notes: The Discovery gene-based P-values are the results reported in Table 3 of the manuscript.
For genes discovered with the VT method, we used the burden GRANVIL test in the conditional analyses in order to keep constant the variants included in the test.
The No condition P-values are the P-values from the SKAT test for OSGIN1 and FLNB, and GRANVIL for the other 8 genes (initially discovered with VT).

Supplementary Table 17. Biological information about the 10 height genes identified by gene-based association testing.

Gene	Function	Expression pattern (BioGPS)	OMIM
OSGIN1	This gene encodes an oxidative stress response protein that regulates cell death. Expression of the gene is regulated by p53 and is induced by DNA damage. The protein regulates apoptosis by inducing cytochrome c release from mitochondria. It also appears to be a key regulator of both inflammatory and anti-inflammatory molecules. The loss of this protein correlates with uncontrolled cell growth and tumor formation. Naturally occurring read-through transcription exists between this gene and the neighboring upstream malonyl-CoA decarboxylase (MLYCD) gene, but the read-through transcripts are unlikely to produce a protein product.	Ubiquitous expression. Stronger expression in liver, adrenal gland, and cerebellum peduncles.	Nothing.
CRISPLD1	Chiquet et al (2011) reported that variation in CRISPLD2 is associated with nonsyndromic cleft lip and palate. Both *CRISPLD1* and *CRISPLD2* are expressed in murine craniofacies. They could play a role in the folic acid pathway and cartilage formation.	Ubiquitous. Expression slightly higher in prostate.	Nothing.
CSAD	This gene encodes a member of the group 2 decarboxylase family. A similar protein in rodents plays a role in multiple biological processes as the rate-limiting enzyme in taurine biosynthesis, catalyzing the decarboxylation of cysteinesulfinate to hypotaurine. Alternatively spliced transcript variants encoding multiple isoforms have been observed for this gene.	Very high expression in fetal brain. Also high in amygdala, and to a lesser extent in thyroid and adipocyte.	Nothing
SNED1	Gene with no assigned functions. Pathway analysis suggest function in epithelium formation (extracellular matrix).	Low but ubiquitous expression pattern.	Nothing
G6PC	Glucose-6-phosphatase (G6Pase) is a multi-subunit integral membrane protein of the endoplasmic reticulum that is composed of a catalytic subunit and transporters for G6P, inorganic phosphate, and glucose. This gene (G6PC) is one of the three glucose-6-phosphatase catalytic-subunit-encoding genes in human: G6PC, G6PC2 and G6PC3. Glucose-6-phosphatase catalyzes the hydrolysis of D-glucose 6-phosphate to D-glucose and orthophosphate and is a key enzyme in glucose homeostasis, functioning in gluconeogenesis and glycogenolysis. Mutations in this gene cause glycogen storage disease type I (GSD1). This disease, also known as von Gierke disease, is a metabolic disorder characterized by severe hypoglycemia associated with the accumulation of glycogen and fat in the liver and kidneys.	Very high in liver and small intestine.	Glycogen storage disease type I, also known as von Gierke disease, typically manifests during the first year of life with severe hypoglycemia and hepatomegaly caused by the accumulation of glycogen. Affected individuals exhibit growth retardation, delayed puberty, lactic acidemia, hyperlipidemia, hyperuricemia, and in adults a high incidence of hepatic adenomas. Without treatment, growth failure is common, due to chronically low insulin levels, persistent acidosis, chronic elevation of catabolic hormones, calorie insufficiency, and/or malabsorption.
NOX4	This gene encodes a member of the NOX-family of enzymes that functions as the catalytic subunit the NADPH oxidase complex. The encoded protein is localized to non-phagocytic cells where it acts as an oxygen sensor and catalyzes the reduction of molecular oxygen to various reactive oxygen species (ROS). The ROS generated by this protein have been implicated in numerous biological functions including signal transduction, cell differentiation and tumor cell growth. A pseudogene has been identified on the other arm of chromosome 11. Alternative splicing results in multiple transcript variants. Nox4 has anti-atherosclerotic functions in the mouse.	Very high expression in kidney.	Nothing.
UGGT2	UDP-glucose:glycoprotein glucosyltransferase (UGT) is a soluble protein of the endoplasmic reticulum (ER) that selectively reglucosylates unfolded glycoproteins, thus providing quality control for protein transport out of the ER.	Moderate but ubiquitous expression pattern. Higher expression levels in cardiomyocytes and the pituitary gland.	Nothing.
FLNB	Filamin B (FlnB) is an actin-binding protein thought to transduce signals from various membrane receptors and intracellular proteins onto the actin cytoskeleton. Formin1 (Fmn1) is an actin-nucleating protein, implicated in actin assembly and intracellular signaling. Human mutations in FLNB cause several skeletal disorders associated with dwarfism and early bone fusion. Mouse mutations in Fmn1 cause aberrant fusion of carpal digits. Hu et al (2014) report that FlnB and Fmn1 physically interact, are co-expressed in chondrocytes in the growth plate and share overlapping expression in the cell cytoplasm and nucleus.	High expression in colorectal adenocarcinoma, bronchial epithelial cells, and dendritic cells	Human mutations in FLNB cause several skeletal disorders associated with dwarfism and early bone fusion, including: atelosteogenesis types I and III, Boomerang dysplasia, Larsen syndrome, and spondylocarpotarsal synostosis syndrome.
B4GALNT3	B4GALNT3 transfers N-acetylgalactosamine (GalNAc) onto glucosyl residues to form N,N-prime-diacetyllactosediamine (LacdiNAc, or LDN), a unique terminal structure of cell surface N-glycans.	Low but ubiquitous expression pattern.	Nothing.
CCDC3	Also known as favine, this gene encodes a protein with lipogenic and adipogenic effects on adipocytes.	Nothing.	Nothing.

Supplementary Table 18. Single-variant association results in European-ancestry studies (discovery, validation, and combined) for variants implicated in significant gene-based results (Table 3 of the article). Effect allele frequency (EAF) and Beta are given for the Alternative (Alt) allele. In this table, we only considered variants with P<0.05 in the discovery analys

							GIANT discovery						Validation						Combined (discovery+validation)					
Chr	Pos (hg19)	rsID	Gene	VEP annotation	Ref	Alt	N	MAF	EAF	Beta	SE	P-value	N	MAF	EAF	Beta	SE	P-value	Het|2	N	MAF	EAF	Beta	SE	P-value	Het|2
2	241974013	rs200219556	*SNED1*	missense_variant	G	A	4E+05	0.0064	0.0064	0.072	0.014	4.97E-07	2E+05	0.0063	0.0063	0.048	0.019	0.011	0	6E+05	0.0063	0.0063	0.063	0.011	2.96E-08	0
2	241976210	rs201554730	*SNED1*	missense_variant	C	A	3E+05	0.0013	0.0013	0.098	0.034	0.004	1E+05	0.0007	0.0007	-0.032	0.111	0.774	0	5E+05	0.0011	0.0011	0.087	0.032	0.007	0
2	241991813	rs199813885	*SNED1*	missense_variant	A	T	4E+05	0.0011	0.0011	0.096	0.035	0.006	2E+05	0.0003	0.0003	0.052	0.089	0.561	4.3	6E+05	8.51E-04	8.51E-04	0.090	0.032	0.005	0
3	58104626	rs139875974	*FLNB*	missense_variant	G	T	4E+05	0.0011	0.0011	-0.174	0.035	5.93E-07	2E+05	0.0005	0.0005	-0.237	0.072	9.41E-04	0	6E+05	0.0009	0.0009	-0.186	0.031	2.90E-09	0
3	58116478	rs143831841	*FLNB*	missense_variant	C	G	4E+05	0.0008	0.0008	-0.155	0.041	1.51E-04	1E+05	0.0004	0.0004	-0.281	0.125	0.025	0	5E+05	0.0007	0.0007	-0.167	0.039	1.71E-05	0
8	75929305	rs199841663	*CRISPLD1*	missense_variant	T	G	4E+05	0.0002	0.0002	-0.230	0.092	0.012	2E+05	0.0003	0.0003	0.049	0.133	0.713	0	6E+05	2.58E-04	2.58E-04	-0.140	0.075	0.063	35.4
8	75929615	rs140591468	*CRISPLD1*	missense_variant	G	A	4E+05	0.0023	0.0023	-0.127	0.025	3.45E-07	2E+05	0.0004	0.0004	-0.024	0.104	0.815	36	5E+05	0.0017	0.0017	-0.122	0.024	5.43E-07	19.8
8	75937794	rs138426954	*CRISPLD1*	missense_variant	C	T	4E+05	2.60E-05	2.60E-05	-0.552	0.225	0.014	31017	1.61E-05	1.61E-05	-0.369	0.966	0.702	0	4E+05	2.52E-05	2.52E-05	-0.542	0.219	0.013	0
8	75941664	rs149361480	*CRISPLD1*	stop_gained	C	T	4E+05	4.47E-05	4.47E-05	-0.590	0.201	0.003	31017	8.06E-05	8.06E-05	-0.556	0.442	0.209	0	4E+05	4.74E-05	4.74E-05	-0.584	0.183	0.001	0
8	75926254	rs141389784	*CRISPLD1*	missense_variant	T	G	4E+05	1.40E-04	1.40E-04	-0.429	0.095	6.11E-06				Monomorphic										
10	13040481	rs139188420	*CCDC3*	missense_variant	C	T	4E+05	0.0001	0.0001	-0.476	0.113	2.42E-05	2E+05	0.0005	0.0005	-0.003	0.108	0.977	72.2	5E+05	0.0002	0.0002	-0.230	0.078	0.003	84.3
10	13040400	rs199848893	*CCDC3*	missense_variant	A	G	4E+05	0.0002	0.0002	-0.337	0.086	0.00009				Monomorphic										
11	89182666	rs139341533	*NOX4*	missense_variant	C	A	4E+05	0.0027	0.0027	-0.082	0.022	1.65E-04	2E+05	0.0042	0.0042	-0.105	0.023	4.30E-06	36.5	6E+05	0.0033	0.0033	-0.093	0.016	3.70E-09	18.7
11	89182686	rs56061986	*NOX4*	missense_variant	T	C	4E+05	0.0026	0.0026	-0.084	0.023	1.95E-04	2E+05	0.0023	0.0023	-0.047	0.035	0.181	40	6E+05	0.0025	0.0025	-0.073	0.019	1.14E-04	27
12	661265	rs200173452	*B4GALNT3*	missense_variant	C	T	4E+05	0.0002	0.0002	0.220	0.088	0.013	2E+05	0.0014	0.0014	0.217	0.045	1.48E-06	39.7	6E+05	0.0006	0.0006	0.218	0.040	5.89E-08	9.5
12	665822	rs145153320	*B4GALNT3*	missense_variant	C	T	4E+05	0.0005	0.0005	0.119	0.054	0.029	2E+05	0.0006	0.0006	0.195	0.075	0.010	0	5E+05	0.0005	0.0005	0.145	0.044	0.001	0
12	667217	rs143789073	*B4GALNT3*	missense_variant	G	A	4E+05	0.0004	0.0004	0.256	0.064	5.83E-05	2E+05	0.0005	0.0005	0.162	0.107	0.132	0	5E+05	0.0004	0.0004	0.232	0.055	2.38E-05	0
12	670520	rs149363012	*B4GALNT3*	missense_variant	C	T	4E+05	0.0180	0.0180	0.035	0.008	4.11E-05	2E+05	0.0228	0.0228	0.010	0.010	0.336	49.8	6E+05	0.0198	0.0198	0.024	0.007	1.75E-04	60.8
12	670531	rs141142525	*B4GALNT3*	missense_variant	G	A	4E+05	0.0004	0.0004	0.145	0.060	0.016	31017	0.0005	0.0005	0.002	0.179	0.992	0	4E+05	0.0004	0.0004	0.131	0.057	0.022	0
12	53553995	rs199797709	*CSAD*	missense_variant	G	A	4E+05	0.0001	0.0001	0.204	0.103	0.048	31017	4.84E-05	4.84E-05	-0.796	0.575	0.166	0	4E+05	0.0001	0.0001	0.173	0.101	0.088	65.9
12	53566174	rs149264090	*CSAD*	missense_variant	A	T	4E+05	0.0040	0.0040	0.092	0.019	7.86E-07	2E+05	0.0033	0.0033	-0.004	0.030	0.902	56.3	6E+05	0.0038	0.0038	0.065	0.016	3.61E-05	74.8
12	53566222	rs71455241	*CSAD*	splice_acceptor_variant	T	C	4E+05	0.0007	0.0007	0.126	0.042	0.003	2E+05	0.0008	0.0008	0.005	0.060	0.938	30.3	6E+05	0.0007	0.0007	0.086	0.035	0.013	52
12	53566324	rs149962027	*CSAD*	missense_variant	G	A	4E+05	0.0009	0.0009	0.112	0.037	0.002	2E+05	0.0008	0.0008	0.120	0.085	0.158	0	5E+05	0.0009	0.0009	0.113	0.034	7.66E-04	0
13	96511868	rs45473699	*UGGT2*	missense_variant	T	A	2E+05	0.0300	0.0300	0.034	0.009	8.37E-05	2E+05	0.0355	0.0355	0.024	0.009	0.006	8.9	4E+05	0.0326	0.0326	0.029	0.006	2.41E-06	0
13	96530020	rs199906236	*UGGT2*	missense_variant	C	A	4E+05	0.0002	0.0002	0.200	0.092	0.030	31017	8.06E-05	8.06E-05	0.761	0.434	0.079	0	4E+05	0.0002	0.0002	0.225	0.090	0.013	37.4
13	96546850	rs143508056	*UGGT2*	stop_gained	G	A	4E+05	0.0027	0.0027	0.080	0.022	2.97E-04	2E+05	0.0022	0.0022	0.088	0.036	0.015	0	6E+05	0.0025	0.0025	0.082	0.019	1.34E-05	0
13	96579526	rs147927483	*UGGT2*	missense_variant	C	T	4E+05	0.0001	0.0001	0.239	0.115	0.037	31017	1.61E-05	1.61E-05	0.366	0.988	0.711	0	4E+05	8.66E-05	8.66E-05	0.241	0.114	0.034	0
13	96601605	rs201688380	*UGGT2*	missense_variant	C	T	4E+05	0.0006	0.0006	0.097	0.045	0.033	31017	3.22E-05	3.22E-05	0.036	0.698	0.958	0	4E+05	5.96E-04	5.96E-04	0.097	0.045	0.033	0
13	96665697	rs148108950	*UGGT2*	missense_variant	G	A	4E+05	0.0051	0.0051	0.037	0.016	0.025	2E+05	0.0009	0.0009	-0.022	0.054	0.676	0	6E+05	0.0036	0.0036	0.032	0.016	0.042	0
16	83994249	rs62640906	*OSGIN1*	missense_variant	C	G	4E+05	0.0024	0.0024	-0.082	0.024	5.47E-04	2E+05	0.0015	0.0015	-0.029	0.035	0.402	0	6E+05	0.0021	0.0021	-0.065	0.020	8.52E-04	0
16	83998995	rs150791768	*OSGIN1*	missense_variant	G	A	3E+05	0.0076	0.0076	0.056	0.015	2.14E-04	2E+05	0.0073	0.0073	0.047	0.018	0.010	40.7	5E+05	0.0075	0.0075	0.052	0.012	6.82E-06	14.8
16	83999434	rs185728481	*OSGIN1*	missense_variant	C	T	4E+05	4.06E-05	4.06E-05	-0.838	0.187	7.78E-06	25296	1.98E-05	1.98E-05	0.046	0.965	0.962	0	4E+05	3.92E-05	3.92E-05	-0.806	0.184	1.19E-05	0
16	83999548	rs62640905	*OSGIN1*	missense_variant	T	C	3E+05	0.0279	0.0279	0.031	0.008	1.53E-04	2E+05	0.0271	0.0271	0.017	0.009	0.062	21.3	5E+05	0.0276	0.0276	0.025	0.006	4.87E-05	22.3
16	83999565	rs147251034	*OSGIN1*	missense_variant	G	A	4E+05	0.0059	0.0059	-0.061	0.015	5.33E-05	2E+05	0.0074	0.0074	-0.052	0.017	0.003	0	6E+05	0.0065	0.0065	-0.057	0.011	5.33E-07	0
17	41055964	rs1801175	*G6PC*	missense_variant	C	T	4E+05	0.0004	0.0004	-0.183	0.055	9.33E-04	2E+05	0.0002	0.0002	-0.242	0.106	0.022	0	6E+05	0.0004	0.0004	-0.196	0.049	6.53E-05	0
17	41062979	rs201961848	*G6PC*	missense_variant	G	T	4E+05	0.0015	0.0015	-0.107	0.031	5.29E-04	31017	6.45E-05	6.45E-05	0.585	0.496	0.238	0	4E+05	0.0014	0.0014	-0.105	0.031	7.11E-04	48.6
17	41063408	rs80356487	*G6PC*	stop_gained	C	T	4E+05	0.0003	0.0003	-0.271	0.065	3.34E-05	2E+05	0.0004	0.0004	0.148	0.083	0.075	0	6E+05	0.0003	0.0003	-0.111	0.051	0.030	87.6

Supplementary Table 19. ExomeSkip DEPICT results for height

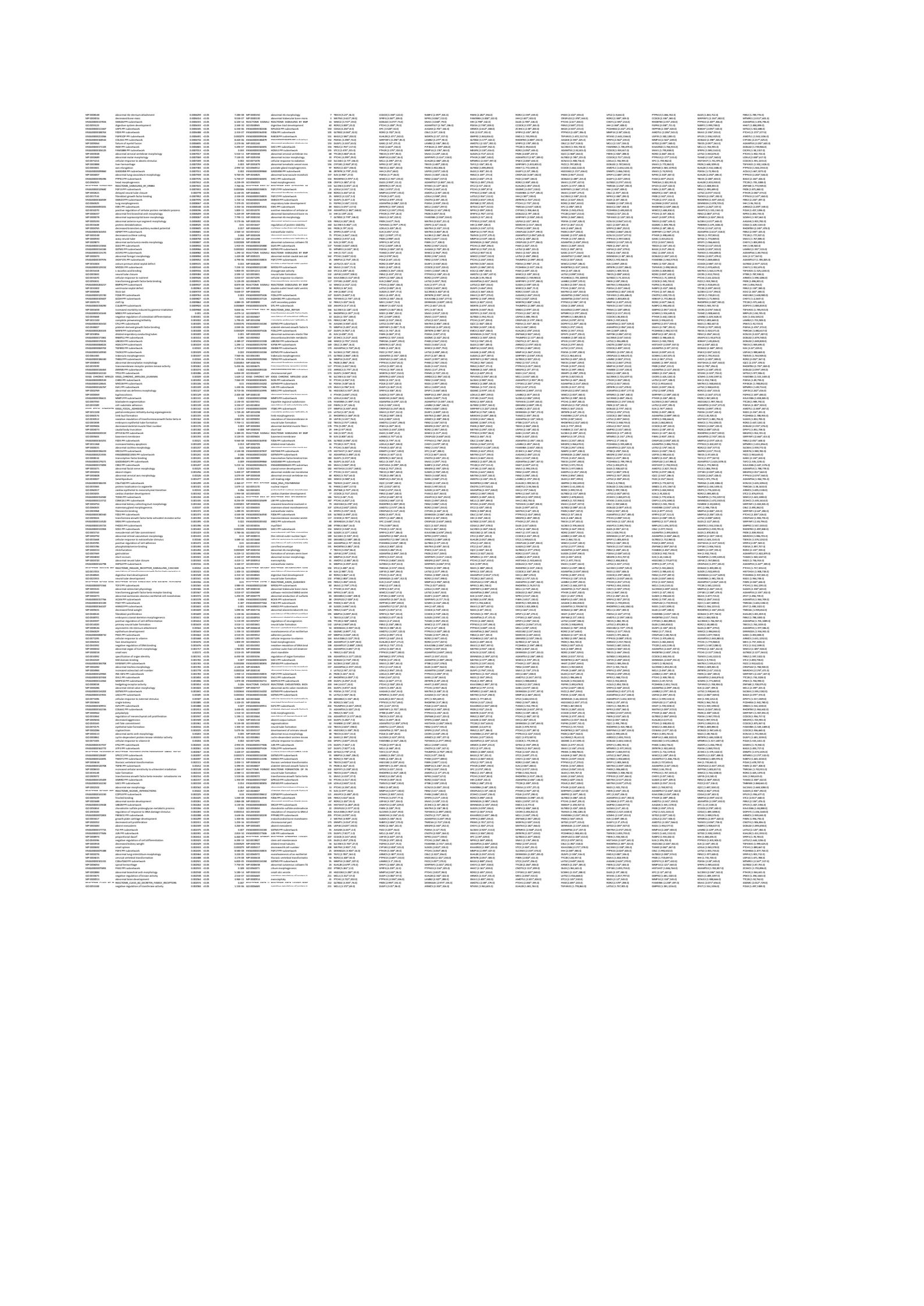
"Mixed-D-cadet" refers to the cluster formed here and from blood cell at. Fluidsome the role of immune cavitation in the mammin- and biofunctional substances of adult human health. Nature Genetics. 46. 1175-1186 (2014).

Reconstituted gene set Z-score columns indicate which height-associated GC genes have the highest z-score for pathway membership. In parentheses: (z-score, rank among all genes in that gene set); asterisk indicates z-score > 2.

Gene Ontology terms, manually curated or metadata for some sets (CHEA, KEGG) that allow enhanced annotation of pathways. Gene sets from MSigDB (C2:CP:KEGG, C5:BP, C5:CC, C5:MF) and the curated non-de-Tous **Curatedgenomics Notes** *for details).*

Full pathway membership data can be accessed at: http://www.broadinstitute.org/mpg/depictcm/_download/recontituted_gene/entryEGFL57-GPL96-GPL1261-GPL1355TermGene2Zscores-MSG_MF_CC_RT_MI_BP_KEGG_v.2.txt.gz

| Ontological gene set ID | Ontological gene set description | Nominal P value | Bonferroni adjusted P value | Observed gene set P value | Meta-analysis gene set description | Meta-analysis gene set size | Reconstituted gene set P score | Reconstituted gene set Z score | Reconstituted gene set P score | Reconstituted gene set Z score | Reconstituted gene set P score | Reconstituted gene set Z score



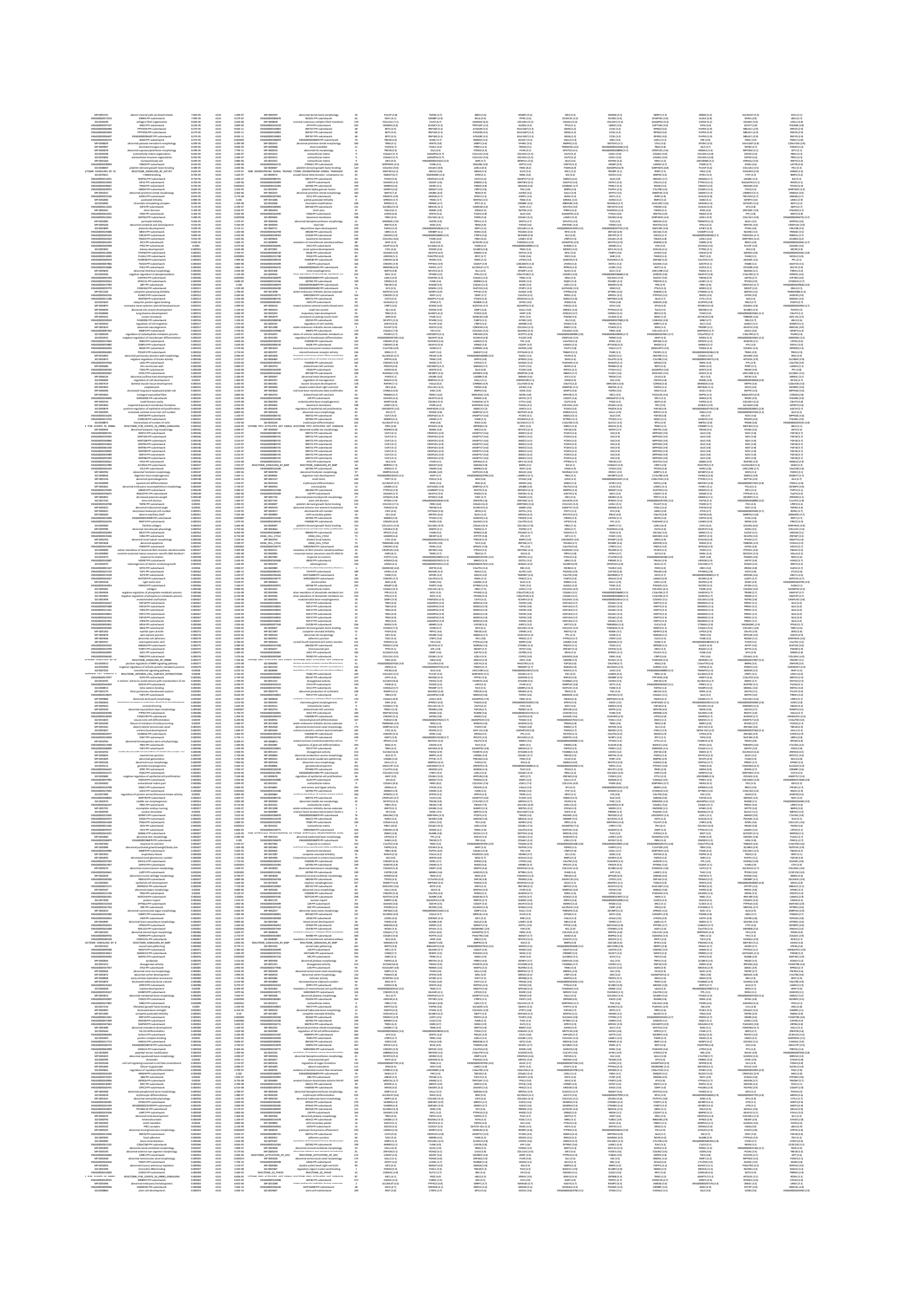
Supplementary Table 20. GWAS DEPICT results for height

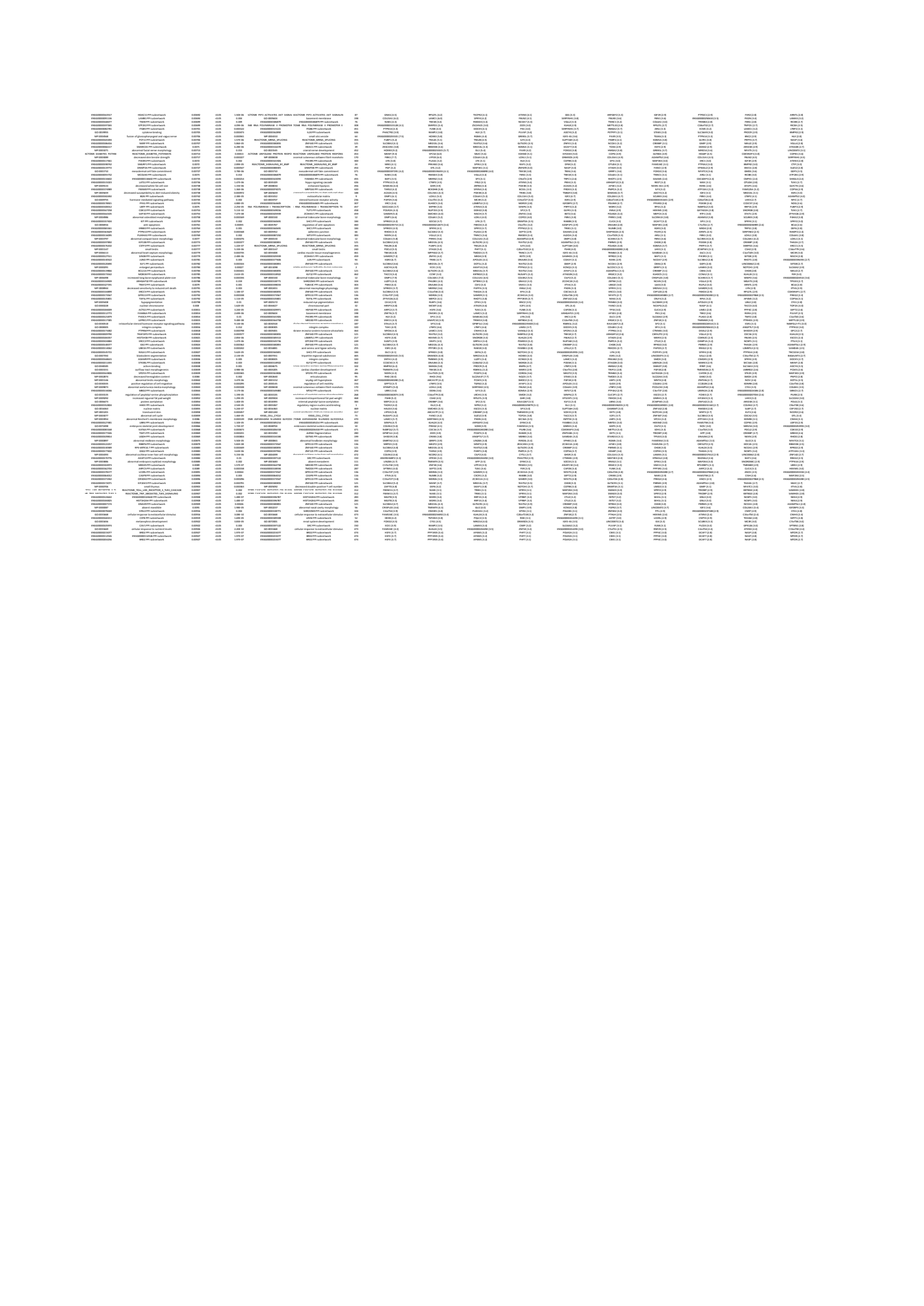
"Wood P-value" refers to the p-value for given gene set from Wood et al. Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, 46, 1173-1186 (2014)

Reconstituted gene set Z score columns indicate which height-associated GWAS genes have the highest z-score for pathway membership. In parentheses: z-score

Full pathway membership data can be accessed at: http://www.broadinstitute.org/mpg/depict/depict_download/reconstituted_genesets/GPL570-GPL96-GPL1261-GPL1355TermGeneZScores-MGI_MF_CC_RT_IW_BP_KEGG_z_z.txt.gz

Original gene set ID	Original gene set description	Nominal P value	False discovery rate	Wood P-value	Meta-gene set	Meta-gene set description	Meta-gene set rank	Reconstituted gene set Z score gene 1	Reconstituted gene set Z score gene 2	Reconstituted gene set Z score gene 3	Reconstituted gene set Z score gene 4	Reconstituted gene set Z score gene 5	Reconstituted gene set Z score gene 6	Reconstituted gene set Z score gene 7	Reconstituted gene set Z score gene 8	Reconstituted gene set Z score gene 9	Reconstituted gene set Z score gene 10
GO:0005667	transcription factor complex	5.54E-23	<0.01	3.20E-33	GO:0001067	regulatory region nucleic acid binding	1	FOXD2 (4.3)	SMAD6 (3.7)	ARID1B (3.6)	ISL1 (3.4)	PAX9 (3.4)	SMAD7 (3.1)	SDCCAG3 (3.1)	REST (3.0)	PRRX1 (3.0)	RBM15B (3.0)
MP:0001698	decreased embryo size	8.59E-20	<0.01	1.11E-24	MP:0011098	plete embryonic lethality during organoge	2	LIN28A (4.9)	CREBBP (4.3)	PTPN12 (3.6)	RYBP (3.5)	REST (3.3)	MED13L (3.2)	MAP3K3 (3.2)	SALL1 (3.0)	KIAA1267 (3.0)	KLF3 (2.9)
GO:0008134	transcription factor binding	2.89E-18	<0.01	4.68E-26	GO:0000989	cription factor binding transcription factor a	3	CREBBP (4.8)	RARA (4.3)	SMAD7 (4.1)	NCOR2 (3.8)	SMAD6 (3.7)	KLF3 (3.6)	TLE3 (3.6)	RPRD2 (3.5)	ZMIZ1 (3.5)	NFATC1 (3.4)
MP:0011098	complete embryonic lethality during organogenesis	3.45E-18	<0.01	4.85E-21	MP:0011098	plete embryonic lethality during organoge	2	SMAD6 (4.4)	CREBBP (4.2)	REST (4.0)	RAMP2 (3.7)	FN1 (3.5)	LIN28A (3.4)	LAMC1 (3.3)	DLC1 (3.3)	PTPN12 (3.2)	MAP3K3 (3.2)
ENSG00000005339	CREBBP PPI subnetwork	9.28E-18	<0.01	7.71E-21	GO:0000989	cription factor binding transcription factor a	3	TRIB1 (4.4)	EGR3 (4.4)	RARA (4.3)	KLF3 (4.2)	PLAG1 (4.0)	ENSG00000233101 (4.0)	HOXB3 (3.8)	CREBBP (3.7)	RB1 (3.6)	ZNFX1 (3.5)
GO:0043009	chordate embryonic development	6.45E-17	<0.01	2.05E-26	GO:0003002	regionalization	4	ENSG00000233101 (6.6)	HOXB3 (6.0)	LIN28A (3.6)	MEX3B (3.6)	FOXD2 (3.4)	TBX6 (3.3)	GREB1L (3.3)	BAHCC1 (3.2)	LIN28B (3.2)	FERD3L (3.2)
GO:0009792	embryo development ending in birth or egg hatching	7.22E-17	<0.01	3.26E-26	GO:0003002	regionalization	4	ENSG00000233101 (6.6)	HOXB3 (6.0)	MEX3B (3.6)	LIN28A (3.6)	TBX6 (3.4)	GREB1L (3.3)	LIN28B (3.3)	FOXD2 (3.3)	BAHCC1 (3.2)	FERD3L (3.2)
MP:0003984	embryonic growth retardation	5.10E-16	<0.01	3.89E-19	MP:0011098	plete embryonic lethality during organoge	2	LIN28A (4.5)	LAMC1 (4.2)	PTPN12 (4.1)	REST (3.8)	RYBP (3.6)	BMP2 (3.5)	SMAD6 (3.4)	DLC1 (3.4)	GATAD2A (3.3)	RAMP2 (3.3)
MP:0011092	complete embryonic lethality	9.63E-16	<0.01	6.15E-19	MP:0011098	plete embryonic lethality during organoge	2	KIAA1267 (3.5)	REST (3.4)	FRS2 (3.3)	PTPN12 (3.2)	CREBBP (3.2)	SMAD6 (3.1)	WDR26 (3.0)	CD2AP (2.9)	RTF1 (2.9)	ARFGEF2 (2.8)
MP:0001914	hemorrhage	1.56E-15	<0.01	8.54E-16	MP:0011098	plete embryonic lethality during organoge	2	RAMP2 (4.7)	FBN1 (4.5)	PLVAP (4.3)	LAMC1 (4.3)	FN1 (4.3)	SERPINH1 (4.2)	FBLN2 (4.2)	IGFBP4 (4.1)	LTBP1 (4.1)	GRK5 (4.0)
EGG_PATHWAYS_IN_CANCI	KEGG_PATHWAYS_IN_CANCER	2.22E-15	<0.01	2.47E-16	KEGG_CHRONIC_MYELOID_LEUKEMIA	KEGG_CHRONIC_MYELOID_LEUKEMIA	5	AXIN2 (4.6)	GLI2 (4.3)	LAMC1 (3.8)	LAMA5 (3.7)	SMAD3 (3.7)	SMAD7 (3.3)	IGFBP3 (3.3)	PTHLH (3.3)	WNT5A (3.3)	MAP3K1 (3.2)
MP:0000060	delayed bone ossification	2.51E-15	<0.01	8.26E-19	MP:0000150	abnormal rib morphology	6	COL24A1 (5.0)	FGFR2 (4.7)	COL10A1 (4.7)	DMP1 (4.5)	SCARA3 (4.5)	COL11A1 (4.4)	NFATC4 (4.3)	CRISPLD1 (4.3)	FAM101A (4.1)	SMAD6 (4.0)
ENSG00000100393	EP300 PPI subnetwork	4.89E-15	<0.01	3.42E-19	GO:0000989	cription factor binding transcription factor a	3	ENSG00000233101 (4.7)	TRIB1 (4.5)	HOXB3 (4.5)	ZMIZ1 (3.8)	SPRY2 (3.7)	MED13L (3.6)	RARA (3.6)	CREBBP (3.6)	EGR3 (3.5)	NAB1 (3.5)
GO:0048729	tissue morphogenesis	4.93E-15	<0.01	4.06E-20	GO:0002009	morphogenesis of an epithelium	7	THSD4 (3.7)	WNT5A (3.5)	WNT3 (3.3)	ENSG00000233101 (3.2)	WNT4 (3.2)	FOXD2 (3.1)	FOXL1 (3.1)	LAMA5 (3.0)	AXIN2 (2.9)	TBX6 (2.9)
MP:0011101	partial prenatal lethality	5.06E-15	<0.01	2.34E-18	MP:0011086	partial postnatal lethality	8	LIN28A (4.1)	LAMA5 (4.1)	AXIN2 (3.5)	IGFBP4 (3.3)	KIAA1267 (3.3)	SERPINH1 (3.3)	IGFBP3 (3.2)	SCUBE3 (3.1)	REST (2.9)	SPRY4 (2.7)
MP:0011090	partial perinatal lethality	6.26E-15	<0.01	2.78E-12	MP:0011086	partial postnatal lethality	8	IGFBP3 (4.8)	SMAD3 (4.6)	GRB10 (4.2)	IGF2 (4.1)	SMAD6 (3.6)	FBLN2 (3.6)	WNT5A (3.6)	FBLN5 (3.4)	ZNF536 (3.4)	PCSK5 (3.3)
GO:0019838	growth factor binding	9.37E-15	<0.01	2.60E-14	GO:0031012	extracellular matrix	9	COL15A1 (6.5)	FBN1 (6.1)	PLVAP (6.0)	COL6A1 (6.0)	LOXL1 (5.6)	SERPINH1 (5.2)	FBLN5 (5.0)	FN1 (4.8)	FBLN2 (4.8)	LAMC1 (4.6)
GO:0001501	skeletal system development	1.52E-14	<0.01	1.80E-20	GO:0048704	embryonic skeletal system morphogenesis	10	CILP2 (5.6)	COL10A1 (5.2)	DNM3OS (5.1)	MIR214 (5.0)	ENSG00000233101 (5.0)	SMOC2 (5.0)	FAM101A (4.9)	COL11A1 (4.8)	HOXB3 (4.8)	COPZ2 (4.5)
MP:0000097	short maxilla	1.59E-14	<0.01	4.23E-19	MP:0000088	short mandible	11	DMP1 (7.5)	PRRX1 (5.2)	COL24A1 (4.9)	PAX9 (4.9)	SCARA3 (4.7)	ESR1 (4.0)	MIR214 (3.8)	NFATC4 (3.5)	CRISPLD1 (3.4)	PCOLCE2 (3.3)
MP:0005508	abnormal skeleton morphology	3.83E-14	<0.01	1.12E-15	MP:0000130	abnormal trabecular bone morphology	12	FGFR2 (5.7)	FAM101A (5.4)	COL6A1 (5.2)	COL9A2 (5.1)	COL10A1 (4.9)	WWP2 (4.4)	ENPP2 (4.3)	FN1 (4.2)	COL11A1 (4.1)	SCARA3 (4.1)
MP:0000088	short mandible	4.37E-14	<0.01	3.26E-19	MP:0000088	short mandible	11	DMP1 (7.0)	TRPS1 (6.1)	PRRX1 (5.2)	COL10A1 (4.8)	FAM101A (4.7)	CRISPLD1 (4.6)	PAX9 (4.4)	CILP2 (4.3)	FGFR2 (4.1)	TBX4 (4.1)
MP:0000445	short snout	6.31E-14	<0.01	1.35E-18	MP:0000088	short mandible	11	DMP1 (5.9)	SCUBE3 (5.5)	FGFR2 (5.5)	CRISPLD1 (5.4)	SCARA3 (4.9)	COL9A2 (4.9)	NFATC4 (4.6)	PRRX1 (4.6)	WWP2 (4.6)	FAM101A (4.6)
ENSG00000170365	SMAD1 PPI subnetwork	7.01E-14	<0.01	1.93E-19	ENSG00000166949	SMAD3 PPI subnetwork	13	GLTSCR1 (4.4)	ARID1B (4.0)	KIAA1267 (3.9)	SMAD7 (3.7)	MIB1 (3.7)	TRIM32 (3.6)	EZH1 (3.4)	BMPR2 (3.4)	CRLF3 (3.3)	KLF11 (3.1)
MP:0000914	exencephaly	8.20E-14	<0.01	1.04E-16	MP:0000914	exencephaly	14	LIN28A (4.4)	SALL1 (4.0)	REST (3.9)	GLI2 (3.7)	NEK4 (3.7)	WNT5A (3.7)	STK36 (3.5)	PTPN14 (3.4)	DMRTA2 (3.3)	UNC119B (3.3)
GO:0048598	embryonic morphogenesis	8.78E-14	<0.01	6.76E-20	GO:0003002	regionalization	4	ENSG00000233101 (6.1)	HOXB3 (5.0)	TBX6 (3.9)	FOXD2 (3.6)	GLIS1 (3.5)	NFATC4 (3.4)	TBX18 (3.4)	LIN28B (3.4)	GRRP1 (3.3)	HMGA2 (3.3)
GO:0003705	II distal enhancer sequence-specific DNA binding transcrip	1.33E-13	<0.01	4.52E-20	GO:0001067	regulatory region nucleic acid binding	1	ISL1 (4.6)	HHIP (4.3)	FOXL1 (4.1)	FOXD2 (4.0)	BMP2 (3.7)	ENSG00000237424 (3.6)	ZNF536 (3.4)	ARID1B (3.3)	TBX4 (3.3)	TBX2 (3.3)
MP:0011108	partial embryonic lethality during organogenesis	1.62E-13	<0.01	1.72E-20	MP:0011098	plete embryonic lethality during organoge	2	ISL1 (4.5)	EML4 (3.9)	ECM1 (3.8)	IGF2 (3.7)	SMAD6 (3.6)	DLC1 (3.6)	LAMA5 (3.5)	LRP5 (3.4)	LIN28A (3.4)	KLF3 (3.4)
MP:0011099	omplete lethality throughout fetal growth and developme	1.84E-13	<0.01	7.81E-18	MP:0011098	plete embryonic lethality during organoge	2	KLF3 (3.7)	HLX (3.6)	PLVAP (3.6)	MED13L (3.5)	ECE1 (3.2)	NFIC (3.0)	ETV6 (3.0)	MLXIP (2.9)	RYBP (2.9)	GRB10 (2.9)
GO:0035239	tube morphogenesis	1.99E-13	<0.01	5.36E-18	GO:0002009	morphogenesis of an epithelium	7	THSD4 (3.3)	ADAMTS19 (3.2)	FOXD2 (3.2)	STK36 (3.1)	DCBLD1 (3.1)	ECM1 (3.1)	AXIN2 (3.0)	WNT5A (3.0)	LIN28A (2.9)	WNT3 (2.9)
MP:0000428	abnormal craniofacial morphology	2.14E-13	<0.01	8.16E-18	MP:0000914	exencephaly	14	GLI2 (4.3)	NFATC4 (4.2)	ZNF536 (3.9)	FGFR2 (3.9)	AXIN2 (3.6)	RGMA (3.3)	HHIP (3.3)	LIN28A (3.1)	NOG (3.1)	FGF18 (3.0)
ENSG00000175387	SMAD2 PPI subnetwork	2.43E-13	<0.01	1.31E-16	ENSG00000166949	SMAD3 PPI subnetwork	13	GLTSCR1 (4.1)	SMAD7 (3.7)	CREBBP (3.5)	SMAD3 (3.3)	IGF1R (3.1)	FBXW11 (3.0)	TNPO1 (3.0)	NUMB (3.0)	BMPR2 (3.0)	TRIM32 (2.9)
ENSG00000171681	ATF7IP PPI subnetwork	2.49E-13	<0.01	2.28E-17	ENSG00000169016	E2F6 PPI subnetwork	15	GH2 (4.5)	SEC16A (3.5)	NISCH (3.5)	COL15A1 (3.1)	ADAM12 (3.0)	ZC3H11A (3.0)	PTPRG (3.0)	PLVAP (3.0)	STARD13 (3.0)	RAMP2 (3.0)
GO:0060021	palate development	2.55E-13	<0.01	1.62E-20	MP:0009890	cleft secondary palate	16	MIR214 (4.9)	C7orf58 (4.6)	NFATC4 (4.5)	DNM3OS (4.1)	TBX2 (3.4)	PAX9 (3.3)	MPPED2 (3.2)	SCUBE3 (3.1)	TBX4 (3.1)	CHCHD7 (2.9)
GO:0001701	in utero embryonic development	2.88E-13	<0.01	1.87E-25	MP:0011098	plete embryonic lethality during organoge	2	P4HA2 (3.4)	LIN28A (3.2)	DOT1L (3.2)	PCGF5 (3.1)	DCBLD1 (3.0)	POLG (2.9)	MIER3 (2.6)	MED13L (2.4)	MEX3B (2.4)	CREBBP (2.3)
MP:0008803	abnormal placental labyrinth vasculature morphology	2.95E-13	<0.01	4.27E-18	MP:0001716	abnormal placenta labyrinth morphology	17	CREBBP (3.5)	DNM2 (2.9)	PTPN12 (2.9)	NEK4 (2.8)	PBRM1 (2.8)	LIN28A (2.7)	FLNB (2.7)	TRPC4AP (2.7)	LAMC1 (2.7)	ZC3H11A (2.6)
MP:0003229	abnormal vitelline vasculature morphology	4.31E-13	<0.01	1.67E-15	MP:0011098	plete embryonic lethality during organoge	2	RAMP2 (5.5)	SMAD6 (4.6)	PLVAP (4.5)	ADCY4 (4.2)	TRIOBP (3.8)	EDNRB (3.8)	IGFBP3 (3.8)	DLC1 (3.7)	ECE1 (3.7)	LAMC1 (3.6)
MP:0002151	abnormal neural tube morphology/development	4.81E-13	<0.01	1.31E-16	MP:0000914	exencephaly	14	SALL1 (4.7)	WNT5A (4.2)	SMAD6 (3.7)	WNT3 (3.7)	STK36 (3.5)	WDR19 (3.5)	ADAMTS19 (3.5)	LIN28A (3.4)	BMP2 (3.2)	KIAA1267 (3.1)
MP:0000150	abnormal rib morphology	4.82E-13	<0.01	1.23E-17	MP:0000150	abnormal rib morphology	6	HOXB3 (5.7)	GDF5 (5.2)	DMP1 (5.2)	WWP2 (4.8)	HMGA2 (4.7)	FAM101A (4.7)	COL9A2 (4.7)	ENSG00000233101 (4.6)	VGLL2 (4.4)	PRRX1 (4.3)
GO:0051216	cartilage development	4.99E-13	<0.01	1.96E-19	GO:0060350	endochondral bone morphogenesis	18	COL9A2 (6.4)	CILP2 (6.3)	COL10A1 (5.7)	SMOC2 (5.5)	FAM101A (5.3)	GDF5 (5.2)	CRISPLD1 (4.7)	ANGPTL7 (4.6)	WWP2 (4.5)	CYTL1 (4.3)
MP:0011109	partial lethality throughout fetal growth and development	5.67E-13	<0.01	1.23E-18	MP:0011098	plete embryonic lethality during organoge	2	LAMA5 (4.3)	NCOR2 (3.8)	SMAD6 (3.7)	IGF2 (3.5)	PAPPA (3.5)	LRP5 (3.5)	IGFBP4 (3.3)	GLTSCR1 (3.3)	WNT5A (3.2)	DAB2 (3.2)
GO:0060562	epithelial tube morphogenesis	7.22E-13	<0.01	4.06E-19	GO:0002009	morphogenesis of an epithelium	7	STK36 (3.5)	THSD4 (3.5)	SALL1 (3.1)	ECM1 (2.9)	WNT3 (2.9)	ADAMTS19 (2.9)	PTPRG (2.8)	WNT5A (2.8)	LIN28A (2.8)	DCBLD1 (2.7)
GO:0035295	tube development	8.10E-13	<0.01	7.30E-18	GO:0002009	morphogenesis of an epithelium	7	TBX2 (3.6)	DCBLD1 (3.3)	FGF18 (3.2)	FOXD2 (3.1)	LAMA5 (3.1)	ADAMTS19 (3.0)	HHIP (2.9)	AXIN2 (2.9)	THSD4 (2.9)	FOXL1 (2.9)
GO:0002009	morphogenesis of an epithelium	1.47E-12	<0.01	2.33E-17	GO:0002009	morphogenesis of an epithelium	7	THSD4 (3.7)	LAMA5 (3.6)	WNT5A (3.3)	WNT4 (3.3)	FOXD2 (3.3)	ENSG00000233101 (3.2)	FOXL1 (3.1)	TBX2 (3.1)	WNT3 (3.0)	GLIS1 (3.0)
MP:0003419	delayed endochondral bone ossification	2.22E-12	<0.01	5.80E-17	MP:0005306	abnormal phalanx morphology	19	CRISPLD1 (5.1)	FGFR2 (4.9)	COL10A1 (4.8)	FAM101A (4.7)	GDF5 (4.5)	CYTL1 (4.4)	COL9A2 (4.4)	SMOC2 (4.2)	TBX18 (4.1)	IGF2 (4.0)
GO:0048705	skeletal system morphogenesis	2.74E-12	<0.01	3.38E-18	GO:0048704	embryonic skeletal system morphogenesis	10	ENSG00000233101 (8.1)	HOXB3 (6.9)	MIR214 (5.5)	DNM3OS (5.1)	CILP2 (5.0)	FAM101A (4.4)	COL9A2 (4.0)	TBX18 (3.9)	COL10A1 (3.9)	NFATC4 (3.8)
MP:0000074	abnormal neurocranium morphology	2.91E-12	<0.01	8.67E-15	MP:0010029	abnormal basicranium morphology	20	TRPS1 (5.9)	DMP1 (5.9)	FGFR2 (4.8)	CRISPLD1 (4.7)	PRRX1 (4.3)	FAM101A (4.0)	GDF5 (4.0)	SCARA3 (4.0)	COL10A1 (3.9)	COL9A2 (3.9)
MP:0011091	complete prenatal lethality	3.12E-12	<0.01	5.58E-14	MP:0011098	plete embryonic lethality during organoge	2	LIN28A (5.2)	CA14 (4.3)	FN1 (3.5)	CREBBP (3.3)	GLTSCR1 (3.3)	BMP2 (3.3)	NT5DC2 (3.3)	WNT3 (3.3)	KIAA1267 (3.0)	FLNB (2.9)
MP:0000266	abnormal heart morphology	3.22E-12	<0.01	1.71E-14	MP:0000267	abnormal heart development	21	TMOD1 (3.8)	TNNC1 (3.8)	PDE3A (3.5)	FBLN2 (3.3)	TRIM63 (3.2)	LTBP2 (3.2)	BMP2 (3.1)	CORO6 (3.1)	ENSG00000238018 (3.1)	PLAG1 (3.1)
ENSG00000129965	INS-IGF2 PPI subnetwork	3.41E-12	<0.01	1.93E-13	ENSG00000158815	FGF17 PPI subnetwork	22	ENPP2 (5.1)	SLC16A9 (4.3)	SERPINE2 (3.9)	PRRX1 (3.9)	PLVAP (3.5)	PTPRG (3.4)	FBLN5 (3.3)	SEPP1 (3.3)	ESR1 (3.3)	LOXL1 (3.1)
ENSG00000166949	SMAD3 PPI subnetwork	4.04E-12	<0.01	1.72E-14	ENSG00000166949	SMAD3 PPI subnetwork	13	GATAD2A (4.2)	GH2 (3.9)	CREBBP (3.8)	SMAD7 (3.7)	NCOR2 (3.5)	RARA (3.5)	ARID1B (3.4)	TRIB1 (3.4)	SP2 (3.4)	SENP6 (3.3)
ENSG00000105810	CDK6 PPI subnetwork	4.06E-12	<0.01	9.33E-12	REACTOME_G1_PHASE	REACTOME_G1_PHASE	23	PLAG1 (4.3)	DLEU2 (3.9)	ENSG00000240280 (3.6)	ABCA17P (3.1)	CDKN2C (2.9)	CTBP2 (2.9)	RB1 (2.9)	GSS (2.9)	FRS2 (2.8)	LINC00462 (2.8)
GO:0061138	morphogenesis of a branching epithelium	4.33E-12	<0.01	4.28E-15	GO:0002009	morphogenesis of an epithelium	7	THSD4 (4.9)	ENSG00000247735 (3.8)	FOXD2 (3.8)	HHIP (3.6)	ARSJ (3.6)	ENSG00000237424 (3.4)	ENSG00000248890 (3.3)	IGFBP4 (3.2)	SALL1 (3.0)	DCBLD1 (2.9)
GO:0060429	epithelium development	5.52E-12	<0.01	1.33E-15	GO:0002009	morphogenesis of an epithelium	7	LYPD3 (4.4)	PPL (3.6)	WNT4 (3.6)	ENSG00000247735 (3.5)	ECM1 (3.1)	LAMA5 (3.0)	HOXB3 (3.0)	ENSG00000233101 (3.0)	WNT5A (3.0)	THSD4 (2.9)
MP:0009703	decreased birth body size	6.48E-12	<0.01	2.76E-20	MP:0011086	partial postnatal lethality	8	REST (3.8)	NOG (3.6)	FAM101A (3.6)	CREBBP (3.4)	EML4 (3.4)	CDKN1B (3.2)	NCOA1 (3.1)	KLF3 (3.0)	SCAPER (2.9)	HMGA2 (2.8)
MP:0000435	shortened head	1.03E-11	<0.01	3.44E-17	MP:0000088	short mandible	11	PRRX1 (5.5)	COL9A2 (4.7)	FAM101A (4.6)	COL10A1 (4.4)	TRPS1 (3.8)	C7orf58 (3.7)	WNT5A (3.7)	FOXD2 (3.5)	GDF5 (3.5)	SOX5 (3.5)
GO:0046332	SMAD binding	1.04E-11	<0.01	5.23E-15	REACTOME_SIGNALING_BY_BMP	REACTOME_SIGNALING_BY_BMP	24	SMAD7 (7.0)	SMAD6 (4.9)	BMPR2 (4.2)	FN1 (4.1)	SPRY2 (3.6)	PTPN12 (3.6)	MAP3K3 (3.4)	ID4 (3.4)	SOCS5 (3.3)	CREBBP (3.2)
GO:0048568	embryonic organ development	1.14E-11	<0.01	5.10E-19	GO:0003002	regionalization	4	ENSG00000233101 (8.2)	HOXB3 (6.5)	FOXD2 (3.8)	AXIN2 (3.2)	TBX18 (3.1)	MEX3B (3.1)	IGF2-AS (3.1)	ABP1 (3.0)	FOXE3 (3.0)	TBX6 (2.9)
MP:0009890	cleft secondary palate	1.19E-11	<0.01	2.38E-16	MP:0009890	cleft secondary palate	16	PRRX1 (5.5)	PAX9 (5.2)	MIR214 (5.1)	TRPS1 (4.9)	WNT5A (4.7)	DNM3OS (4.5)	C7orf58 (4.4)	NFATC4 (4.1)	FOXD2 (4.1)	CRISPLD1 (3.9)
MP:0001718	abnormal visceral yolk sac morphology	1.20E-11	<0.01	4.57E-15	MP:0011098	plete embryonic lethality during organoge	2	LIN28A (4.7)	BMP2 (3.8)	SMAD6 (3.3)	EML4 (3.3)	RAD54L2 (3.3)	OTUD4 (3.2)	FBN1 (3.2)	IGF2 (3.1)	BMPR2 (3.0)	FN1 (3.0)
MP:0011086	partial postnatal lethality	1.99E-11	<0.01	3.80E-12	MP:0011086	partial postnatal lethality	8	GLI2 (4.5)	IGF2 (4.3)	NOTCH1 (4.2)	IGFBP3 (4.1)	HMGA2 (4.1)	HOXB3 (3.9)	NHLH1 (3.8)	ZMIZ1 (3.6)	SPRY4 (3.5)	PTPRG (3.4)
ENSG00000163513	TGFBR2 PPI subnetwork	2.08E-11	<0.01	3.81E-13	GO:0005072	growth factor beta receptor, cytoplasmic m	25	SMAD7 (5.0)	SMAD6 (4.3)	PROCR (4.0)	APP (3.9)	LTBP2 (3.5)	SCARA3 (3.5)	SMAD3 (3.5)	IGFBP4 (3.5)	RAMP2 (3.4)	MXD4 (3.2)
MP:0001614	abnormal blood vessel morphology	2.22E-11	<0.01	8.48E-12	GO:0001568	blood vessel development	26	PLVAP (6.0)	COL15A1 (5.3)	RAMP2 (5.0)	ADCY4 (4.8)	APOLD1 (4.2)	SEMA3G (4.1)	ECE1 (4.0)	NFATC4 (3.8)	IGFBP3 (3.8)	ADAMTS2 (3.8)
GO:0001763	morphogenesis of a branching structure	2.32E-11	<0.01	5.78E-14	GO:0002009	morphogenesis of an epithelium	7	THSD4 (4.4)	HHIP (3.9)	ENSG00000247735 (3.9)	FOXD2 (3.8)	ARSJ (3.6)	ENSG00000237424 (3.5)	TBX2 (3.3)	ENSG00000248890 (3.3)	SPRED1 (3.2)	ADAMTS19 (3.2)
MP:0000137	abnormal vertebrae morphology	2.68E-11	<0.01	1.54E-15	MP:0000150	abnormal rib morphology	6	HOXB3 (6.5)	ENSG00000233101 (5.9)	FAM101A (5.1)	COL11A1 (5.0)	FGFR2 (5.0)	CYTL1 (4.4)	COL10A1 (4.4)	COL9A2 (4.2)	CILP2 (4.1)	WNT5A (4.0)
GO:0034504	protein localization to nucleus	2.75E-11	<0.01	1.17E-17	GO:0051170	nuclear import	27	DLEU2 (3.6)	RSBN1L (3.3)	ZNFX1 (2.8)	BCL6 (2.8)	MEPCE (2.6)	ENSG00000196355 (2.6)	FSD1L (2.6)	CHD8 (2.6)	ENSG00000252498 (2.6)	SMAD3 (2.5)
MP:0000432	abnormal head morphology	3.66E-11	<0.01	1.49E-15	MP:0000914	exencephaly	14	FGFR2 (5.4)	LIN28A (5.4)	SCUBE3 (3.7)	WWP2 (3.6)	ID4 (3.4)	WNT3 (3.3)	GLIS1 (3.3)	COL10A1 (3.3)	DMP1 (3.3)	IGF1R (3.3)
MP:0000107	abnormal frontal bone morphology	3.67E-11	<0.01	2.56E-15	MP:0010029	abnormal basicranium morphology	20	NFATC4 (5.1)	FOXD2 (5.0)	WNT5A (4.6)	SALL1 (4.2)	BMP2 (4.0)	DMP1 (3.9)	FGFR2 (3.8)	PRRX1 (3.8)	KLHL29 (3.8)	SMAD6 (3.5)
ENSG00000114166	KAT2B PPI subnetwork	4.12E-11	<0.01	3.78E-20	ENSG00000196226	HIST1H2BB PPI subnetwork	28	CDKN1B (4.1)	CREBBP (4.0)	ARID1B (3.9)	POLR2A (3.9)	H1FX (3.6)	HEXIM1 (3.5)	MEPCE (3.4)	REST (3.2)	MED13L (3.0)	RPS27L (2.8)
ENSG00000141646	SMAD4 PPI subnetwork	4.12E-11	<0.01	1.17E-15	ENSG00000166949	SMAD3 PPI subnetwork	13	SMAD7 (4.4)	KIAA1267 (3.6)	EGR3 (3.6)	MAP3K3 (3.5)	DIS3L2 (3.3)	TNPO1 (3.3)	RB1 (3.1)	STK25 (3.0)	RPRD2 (3.0)	ARID1B (3.0)
GO:0007507	heart development	5.49E-11	<0.01	4.08E-15	GO:0003205	cardiac chamber development	29	MYH7B (5.2)	TBX18 (4.2)	ADAMTS19 (3.8)	ENSG00000238018 (3.3)	FGF18 (3.3)	PDE3A (3.1)	GREB1L (3.1)	SMAD6 (3.1)	XRRA1 (3.1)	FAM101A (3.0)
MP:0004462	small basisphenoid bone	5.87E-11	<0.01	8.86E-17	MP:0000088	short mandible	11	SCARA3 (5.1)	FOXD2 (4.7)	TBX18 (4.5)	SCUBE3 (4.5)	ENSG00000248890 (4.2)	GMDS (4.0)	NFATC1 (4.0)	TRPS1 (3.9)	BMP6 (3.8)	FAM101A (3.8)
GO:0048736	appendage development	6.39E-11	<0.01	1.43E-18	GO:0035108	limb morphogenesis	30	NFATC4 (4.2)	TBX18 (4.0)	DNM3OS (3.9)	TRPS1 (3.9)	MIR214 (3.8)	CRISPLD1 (3.6)	SCUBE3 (3.4)	PRRX1 (3.4)	PLAG1 (3.2)	CILP2 (3.2)
GO:0060173	limb development	6.39E-11	<0.01	1.43E-18	GO:0035108	limb morphogenesis	30	NFATC4 (4.2)	TBX18 (4.0)	DNM3OS (3.9)	TRPS1 (3.9)	MIR214 (3.8)	CRISPLD1 (3.6)	SCUBE3 (3.4)	PRRX1 (3.4)	PLAG1 (3.2)	CILP2 (3.2)
MP:0000157	abnormal sternum morphology	6.87E-11	<0.01	3.49E-14	MP:0000150	abnormal rib morphology	6	HOXB3 (6.2)	ENSG00000233101 (4.8)	RGMA (3.9)	FOXD2 (3.9)	HMGA2 (3.9)	GDF5 (3.8)	NOG (3.8)	SALL1 (3.6)	ENSG00000231160 (3.4)	GLI2 (3.4)
MP:0011089	complete perinatal lethality	7.32E-11	<0.01	8.68E-14	MP:0011087	complete neonatal lethality	31	RGMA (4.7)	NOTCH1 (4.3)	FGF18 (4.1)	ID4 (3.8)	HOXB3 (3.7)	IGFBP3 (3.7)	EPHB1 (3.6)	TGFB2 (3.5)	FGFR2 (3.3)	NOG (3.3)
MP:0000352	decreased cell proliferation	7.33E-11	<0.01	1.25E-16	GO:0044427	chromosomal part	32	ATAD5 (3.8)	CREBBP (3.3)	PBRM1 (3.3)	REST (3.2)	ENSG00000171658 (3.2)	RFC1 (3.1)	NQO1 (3.0)	KCTD9 (3.0)	FANCI (3.0)	TOP2A (2.9)
GO:0040008	regulation of growth	7.44E-11	<0.01	1.18E-14	GO:0001558	regulation of cell growth	33	CSH2 (5.3)	ENSG00000246985 (5.2)	GH2 (5.1)	FSHB (3.9)	PCOLCE2 (3.5)	ESR1 (3.3)	FBXO31 (3.2)	CYTL1 (2.9)	B4GALNT3 (2.9)	HES7 (2.9)
GO:0048732	gland development	8.01E-11	<0.01	5.38E-16	GO:0002009	morphogenesis of an epithelium	7	ENSG00000233101 (3.6)	WNT4 (3.5)	ESR1 (3.4)	PAPPA (3.4)	PDLIM4 (3.3)	ENSG00000235300 (3.3)	GH2 (3.3)	CSH2 (3.2)	ANO1 (3.2)	FSHB (3.0)
GO:0005520	insulin-like growth factor binding	8.83E-11	<0.01	7.78E-10	ENSG00000092969	TGFB2 PPI subnetwork	34	COL8A1 (6.4)	LTBP2 (5.2)	FBN1 (5.0)	LOXL1 (4.8)	IGFBP4 (4.5)	FN1 (4.4)	EFEMP1 (4.4)	SMOC2 (4.3)	TGFB2 (4.2)	FBLN2 (4.1)
MP:0002109	abnormal limb morphology	9.49E-11	<0.01	2.34E-13	MP:0000150	abnormal rib morphology	6	DMP1 (5.1)	PRRX1 (4.8)	NFATC4 (4.5)	FGFR2 (4.4)	FAM101A (4.0)	BMP2 (3.9)	SCARA3 (3.7)	TRPS1 (3.5)	SMAD6 (3.4)	CRISPLD1 (3.3)
MP:0000559	abnormal femur morphology	1.06E-10	<0.01	1.52E-14	MP:0000130	abnormal trabecular bone morphology	12	COL11A1 (7.3)	CILP2 (6.3)	COL9A2 (5.4)	COL10A1 (5.3)	DMP1 (4.8)	FAM101A (4.7)	TRPS1 (4.4)	COL6A1 (4.3)	MSRB3 (3.9)	CRISPLD1 (3.9)
MP:0000260	abnormal angiogenesis	1.10E-10	<0.01	1.15E-11	MP:0004787	abnormal dorsal aorta morphology	35	ADCY4 (6.2)	PLVAP (6.1)	RAMP2 (4.9)	COL15A1 (4.9)	PXDN (4.5)	FBN1 (4.3)	IGFBP4 (4.3)	ECE1 (4.3)	APOLD1 (3.9)	SEMA3G (3.8)
GO:0044212	transcription regulatory region DNA binding	1.14E-10	<0.01	4.28E-17	GO:0001067	regulatory region nucleic acid binding	1	TLE3 (4.5)	ISL1 (4.2)	RARA (4.0)	TRIB1 (4.0)	FOXD2 (3.9)	TBX2 (3.9)	SMAD6 (3.8)	NOTCH1 (3.8)	KIAA1267 (3.8)	REST (3.7)
KEGG_PROSTATE_CANCER	KEGG_PROSTATE_CANCER	1.18E-10	<0.01	2.85E-14	KEGG_CHRONIC_MYELOID_LEUKEMIA	KEGG_CHRONIC_MYELOID_LEUKEMIA	5	FRS2 (3.7)	MIER3 (3.5)	NFIC (3.4)	SETD8 (3.2)	MAP3K1 (3.2)	PBRM1 (3.2)	TAOK2 (2.9)	VGLL4 (2.8)	ZBTB38 (2.7)	SPRED1 (2.7)
MP:0011087	complete neonatal lethality	1.21E-10	<0.01	1.44E-12	MP:0011087	complete neonatal lethality	31	ISL1 (4.5)	FGFR2 (4.2)	NOG (4.2)	IGF2 (3.9)	RGMA (3.8)	PRRX1 (3.5)	ID4 (3.5)	WNT5A (3.4)	NHLH1 (3.3)	GLI2 (3.3)
TGF_BETA_SIGNALING_PA	KEGG_TGF_BETA_SIGNALING_PATHWAY	1.27E-10	<0.01	3.84E-15	REACTOME_SIGNALING_BY_BMP	REACTOME_SIGNALING_BY_BMP	24	SMAD7 (8.1)	SMAD6 (7.9)	ID4 (5.9)	AXIN2 (5.3)	BMP6 (5.2)	BMPR2 (4.7)	BMP2 (4.7)	LTBP2 (4.6)	COL8A1 (4.0)	CCDC3 (3.6)
GO:0008285	negative regulation of cell proliferation	1.45E-10	<0.01	4.32E-17	GO:0050678	regulation of epithelial cell proliferation	36	TRIOBP (3.0)	AFAP1 (3.0)	SERPINE2 (2.9)	ENSG00000228290 (2.7)	BMP6 (2.6)	TBX4 (2.5)	FBLN2 (2.4)	TRIB1 (2.4)	RGP1 (2.4)	C5orf56 (2.3)
MP:0001785	edema	1.46E-10	<0.01	3.27E-11	MP:0000267	abnormal heart development	21	RAMP2 (5.8)	PLVAP (4.9)	ADCY4 (4.3)	ECE1 (4.0)	BMP2 (3.7)	SMAD6 (3.7)	GRB10 (3.5)	PTPN14 (3.5)	LRP5 (3.4)	SEMA3G (3.4)
MP:0000167	decreased chondrocyte cell number	1.48E-10	<0.01	2.27E-11	MP:0004359	short ulna	37	FGFR2 (5.3)	NOG (4.9)	TGFB2 (4.7)	FAM101A (4.1)	C9orf3 (4.0)	WNT5A (4.0)	HMGA2 (3.5)	GLIS1 (3.5)	SMAD3 (3.4)	ENPP2 (3.1)
GO:0002062	chondrocyte differentiation	1.83E-10	<0.01	3.01E-15	GO:0032330	regulation of chondrocyte differentiation	38	COL9A2 (6.8)	GDF5 (6.2)	CILP2 (5.8)	WWP2 (5.6)	SMOC2 (5.1)	FAM101A (5.0)	COL10A1 (4.8)	CRISPLD1 (4.8)	SCUBE3 (4.5)	ANGPTL7 (4.3)
GO:0003682	chromatin binding	1.89E-10	<0.01	6.38E-17	ENSG00000116478	HDAC1 PPI subnetwork	39	BAHCC1 (4.1)	RPRD2 (3.8)	CREBBP (3.6)	MEPCE (3.6)	FOXD2 (3.6)	KIAA1267 (3.4)	TLE3 (3.4)	REST (3.4)	RSBN1L (3.3)	ARID1B (3.3)
GO:0000981	-specific DNA binding RNA polymerase II transcription fact	1.97E-10	<0.01	1.52E-13	GO:0000982	proximal region sequence-specific DNA b	40	TRIB1 (4.9)	TBX2 (4.7)	ISL1 (4.7)	EGR3 (4.2)	ID4 (4.0)	RARA (3.9)	LHX3 (3.9)	KLF3 (3.6)	SMAD7 (3.5)	FOXD2 (3.5)
MP:0000111	cleft palate	2.04E-10	<0.01	3.39E-14	MP:0009890	cleft secondary palate	16	PAX9 (5.2)	FOXD2 (4.9)	FAM101A (4.4)	NFATC4 (4.2)	PRRX1 (4.0)	IGF2 (4.0)	SCUBE3 (4.0)	IGF1R (3.8)	ZNF462 (3.7)	WNT5A (3.7)
GO:0060349	bone morphogenesis	2.22E-10	<0.01	3.30E-18	GO:0060350	endochondral bone morphogenesis	18	CILP2 (6.3)	COL10A1 (4.6)	COL11A1 (4.5)	CRISPLD1 (4.3)	FAM101A (4.3)	COL9A2 (4.1)	SMOC2 (4.0)	DNM3OS (4.0)	MIR214 (3.9)	TRPS1 (3.8)
GO:0001067	regulatory region nucleic acid binding	2.53E-10	<0.01	1.25E-16	GO:0001067	regulatory region nucleic acid binding	1	TLE3 (4.5)	ISL1 (4.2)	TRIB1 (4.1)	RARA (4.0)	NOTCH1 (4.0)	FOXD2 (3.9)	TBX2 (3.8)	KIAA1267 (3.8)	SMAD7 (3.7)	SMAD6 (3.7)
GO:0000975	regulatory region DNA binding	2.53E-10	<0.01	1.25E-16	GO:0001067	regulatory region nucleic acid binding	1	TLE3 (4.5)	ISL1 (4.2)	TRIB1 (4.1)	RARA (4.0)	NOTCH1 (4.0)	FOXD2 (3.9)	TBX2 (3.8)	KIAA1267 (3.8)	SMAD7 (3.7)	SMAD6 (3.7)
GO:0000122	tive regulation of transcription from RNA polymerase II pro	2.57E-10	<0.01	1.51E-19	GO:0001067	regulatory region nucleic acid binding	1	RSBN1L (3.6)	CDKN1B (3.5)	PAX9 (3.5)	KIAA1267 (3.5)	C1orf51 (3.4)	MPPED2 (3.1)	BAHCC1 (3.0)	ZBTB4 (3.0)	FOXD2 (2.9)	ENSG00000217612 (2.8)
MP:0003723	abnormal long bone morphology	2.66E-10	<0.01	3.11E-13	MP:0004359	short ulna	37	DMP1 (7.1)	COL6A1 (6.4)	COL11A1 (6.0)	COL10A1 (5.9)	COL9A2 (5.1)	FAM101A (4.5)	SCARA3 (4.4)	FGFR2 (4.4)	SERPINH1 (4.3)	COL24A1 (4.3)
MP:0000079	abnormal basioccipital bone morphology	2.68E-10	<0.01	2.53E-11	MP:0000106	abnormal basisphenoid bone morphology	41	HOXB3 (5.5)	FGFR2 (4.3)	FAM101A (4.0)	RGMA (3.7)	PAX9 (3.6)	CRISPLD1 (3.6)	DNM3OS (3.5)	TBX18 (3.4)	FOXD2 (3.4)	SALL1 (3.3)
MP:0000547	short limbs	3.40E-10	<0.01	2.79E-13	MP:0003662	mal long bone epiphyseal plate proliferativ	42	COL10A1 (7.5)	COL9A2 (6.1)	CYTL1 (5.9)	COL11A1 (5.7)	CILP2 (5.6)	CRISPLD1 (5.3)	FAM101A (5.2)	BMP2 (5.1)	FGFR2 (4.4)	DMP1 (4.3)
GO:0048754	branching morphogenesis of a tube	3.73E-10	<0.01	9.71E-15	GO:0002009	morphogenesis of an epithelium	7	THSD4 (4.2)	ENSG00000248890 (4.0)	FOXD2 (3.9)	ENSG00000237424 (3.9)	B4GALNT3 (3.8)	ENSG00000224514 (3.6)	HHIP (3.6)	SALL1 (3.5)	ENSG00000247735 (3.5)	TBX2 (3.4)
MP:0000556	abnormal hindlimb morphology	4.17E-10	<0.01	2.87E-11	MP:0000088	short mandible	11	DMP1 (6.1)	CILP2 (5.3)	COL10A1 (4.9)	FGFR2 (4.3)	COL24A1 (4.0)	SCUBE3 (4.0)	PAX9 (3.7)	COL11A1 (3.7)	BMP2 (3.6)	TBX4 (3.5)
ENSG00000157933	SKI PPI subnetwork	4.18E-10	<0.01	5.35E-13	GO:0005072	growth factor beta receptor, cytoplasmic m	25	SMAD7 (5.8)	NFIC (4.5)	SPIN1 (4.1)	NCOR2 (4.0)	SMAD6 (4.0)	SNORD58C (3.5)	ZBTB4 (3.5)	ARID1B (3.5)	ZMIZ1 (3.5)	CREBBP (3.2)
MP:0004607	abnormal cervical atlas morphology	4.33E-10	<0.01	1.56E-15	MP:0003048	abnormal cervical vertebrae morphology	43	PAX9 (4.8)	FOXD2 (4.6)	ENSG00000231160 (4.0)	FAM101A (4.0)	NOG (3.8)	MIR214 (3.3)	RCN2 (3.3)	HMGA2 (3.2)	MPPED2 (3.1)	CYTL1 (3.0)
MP:0000550	abnormal forelimb morphology	5.51E-10	<0.01	7.01E-14	GO:0035108	limb morphogenesis	30	DMP1 (5.1)	ISL1 (4.6)	BMP2 (4.3)	NFATC4 (4.2)	CRISPLD1 (4.1)	SMAD6 (4.0)	C7orf58 (4.0)	PRRX1 (3.9)	FGFR2 (3.8)	MOXD1 (3.6)
_CHRONIC_MYELOID_LEUK	KEGG_CHRONIC_MYELOID_LEUKEMIA	5.52E-10	<0.01	1.62E-12	KEGG_CHRONIC_MYELOID_LEUKEMIA	KEGG_CHRONIC_MYELOID_LEUKEMIA	5	FRS2 (4.4)	MXD4 (4.0)	TP53 (3.2)	MAP3K1 (3.2)	GATAD2A (3.1)	SMAD3 (3.1)	SLC44A2 (3.0)	ZBTB4 (3.0)	RPS27L (2.9)	RNF169 (2.9)
G_SMALL_CELL_LUNG_CAN	KEGG_SMALL_CELL_LUNG_CANCER	7.56E-10	<0.01	5.13E-12	KEGG_CHRONIC_MYELOID_LEUKEMIA	KEGG_CHRONIC_MYELOID_LEUKEMIA	5	LAMC1 (5.3)	PXDN (3.7)	MAP3K1 (3.7)	PLEKHA1 (3.3)	LAMA5 (3.3)	COL15A1 (3.0)	CSF2 (3.0)	MOXD1 (2.9)	DAAM1 (2.9)	DRAM1 (2.8)
ENSG00000120738	EGR1 PPI subnetwork	7.78E-10	<0.01	1.07E-12	GO:0001067	regulatory region nucleic acid binding	1	TRIB1 (4.3)	FOXD2 (3.3)	DET1 (3.2)	STAU1 (3.1)	PAX9 (2.9)	SP3 (2.8)	DOT1L (2.8)	NFIC (2.8)	MANF (2.8)	EGR3 (2.7)
MP:0001255	decreased body height	7.88E-10	<0.01	4.20E-18	MP:0003662	mal long bone epiphyseal plate proliferativ	42	COL10A1 (4.7)	SMOC2 (3.9)	COL6A1 (3.8)	BMP6 (3.5)	CHRDL2 (3.5)	PRRX1 (3.5)	CRISPLD1 (3.4)	SOX8 (3.3)	ENPP2 (3.3)	CYP27A1 (3.3)
MP:0003055	abnormal long bone epiphyseal plate morphology	8.09E-10	<0.01	4.75E-11	MP:0003662	mal long bone epiphyseal plate proliferativ	42	COL10A1 (8.4)	COL9A2 (8.0)	CILP2 (6.9)	DMP1 (6.5)	CYTL1 (5.9)	WWP2 (5.4)	COL11A1 (5.4)	SMOC2 (5.2)	TRPS1 (4.9)	CRISPLD1 (4.8)
GO:0009968	negative regulation of signal transduction	8.67E-10	<0.01	4.13E-12	GO:0030111	regulation of Wnt receptor signaling pathw	44	SPRY4 (3.9)	SPRED1 (3.4)	SH3PXD2A (3.3)	FBLN2 (3.2)	COL10A1 (3.1)	CILP2 (3.0)	SPRY2 (3.0)	HMGA2 (2.9)	MOXD1 (2.9)	DLC1 (2.7)
MP:0002113	abnormal skeleton development	8.98E-10	<0.01	4.84E-14	MP:0003662	mal long bone epiphyseal plate proliferativ	42	COL9A2 (5.1)	FGFR2 (5.0)	COL11A1 (4.7)	FAM101A (4.7)	COL10A1 (4.1)	PCSK5 (4.1)	SMOC2 (4.0)	GDF5 (4.0)	NOG (3.9)	CILP2 (3.7)
GO:0030326	embryonic limb morphogenesis	9.59E-10	<0.01	8.86E-16	GO:0035108	limb morphogenesis	30	NFATC4 (4.9)	TBX18 (3.6)	GLIS1 (3.5)	DNM3OS (3.5)	TRPS1 (3.4)	PRRX1 (3.3)	LIN28B (3.2)	PLAG1 (3.2)	SALL1 (3.1)	MIR214 (3.1)
GO:0035113	embryonic appendage morphogenesis	9.59E-10	<0.01	8.86E-16	GO:0035108	limb morphogenesis	30	NFATC4 (4.9)	TBX18 (3.6)	GLIS1 (3.5)	DNM3OS (3.5)	TRPS1 (3.4)	PRRX1 (3.3)	LIN28B (3.2)	PLAG1 (3.2)	SALL1 (3.1)	MIR214 (3.1)
ENSG00000101665	SMAD7 PPI subnetwork	1.01E-09	<0.01	2.44E-15	ENSG00000166949	SMAD3 PPI subnetwork	13	SMAD7 (5.0)	SMAD6 (5.0)	BMPR2 (4.2)	PTPN12 (3.8)	ID4 (3.6)	MAP3K3 (3.5)	SMAD3 (3.3)	ZMIZ1 (3.3)	FRS2 (3.2)	FBXO30 (3.1)
MP:0004355	short radius	1.13E-09	<0.01	4.31E-11	MP:0004359	short ulna	37	TBX4 (5.8)	NFATC4 (5.6)	TBX18 (5.2)	BNC2 (4.9)	FAM101A (4.8)	TRPS1 (4.8)	ARSJ (4.6)	COL11A1 (4.4)	ADAMTSL1 (4.1)	CRISPLD1 (4.0)
ENSG00000092203	TOX4 PPI subnetwork	1.14E-09	<0.01	2.03E-17	ENSG00000169016	E2F6 PPI subnetwork	15	ZNF652 (4.0)	RPRD2 (3.9)	MIB1 (3.8)	MARK3 (3.5)	RBM15B (3.5)	CCDC50 (3.4)	ZNF76 (3.4)	OTUD4 (3.3)	PDIK1L (3.1)	PBRM1 (3.1)
MP:0004200	decreased fetal size	1.21E-09	<0.01	2.33E-15	MP:0011087	complete neonatal lethality	31	IGF2 (4.4)	SMAD3 (3.6)	MARK3 (3.6)	NOG (3.4)	FGFR2 (3.3)	RGMA (3.2)	LRP5 (3.2)	BMP2 (3.1)	SERPINH1 (3.1)	CRISPLD1 (3.1)
MP:0000161	scoliosis	1.21E-09	<0.01	1.47E-11	MP:0000150	abnormal rib morphology	6	WWP2 (4.9)	MIR214 (4.5)	FAM134C (3.3)	GLI2 (2.8)	APP (2.8)	SERPINE2 (2.8)	COL6A1 (2.7)	CREB5 (2.7)	KCTD9 (2.7)	ENSG00000182329 (2.6)
MP:0004599	abnormal vertebral arch morphology	1.22E-09	<0.01	5.83E-11	MP:0000150	abnormal rib morphology	6	HOXB3 (6.6)	FOXD2 (6.2)	TBX18 (5.5)	ENSG00000237424 (4.6)	ENSG00000233101 (4.5)	SALL1 (4.0)	RGMA (3.8)	TGFB2 (3.5)	FAM101A (3.5)	CYTL1 (3.5)
ENSG00000100395	L3MBTL2 PPI subnetwork	1.26E-09	<0.01	6.45E-19	ENSG00000169016	E2F6 PPI subnetwork	15	MARK3 (3.8)	ZNF652 (3.7)	RNPS1 (3.5)	RBM15B (3.5)	LCORL (3.3)	RPRD2 (3.2)	GPBP1L1 (3.2)	SPIN1 (3.0)	ARID1B (3.0)	SENP3 (2.9)
MP:0000049	abnormal middle ear morphology	1.52E-09	<0.01	2.45E-13	MP:0000049	abnormal middle ear morphology	45	PAX9 (5.2)	SALL1 (5.1)	HOXB3 (4.8)	ISL1 (4.3)	DMP1 (4.2)	FGF18 (4.2)	PTPN14 (4.0)	TGFB2 (3.4)	GREB1L (3.4)	FGFR2 (3.2)
ENSG00000139687	RB1 PPI subnetwork	1.53E-09	<0.01	1.93E-11	ENSG00000116478	HDAC1 PPI subnetwork	39	DTL (4.2)	ZNF367 (3.8)	ATAD5 (3.6)	PPP4C (3.4)	SUZ12 (3.4)	ARID1B (3.4)	SMCHD1 (3.3)	ATXN3 (3.3)	NUSAP1 (3.1)	MAP3K1 (3.1)
MP:0002764	short tibia	1.56E-09	<0.01	4.81E-11	MP:0004359	short ulna	37	COL10A1 (6.8)	COL11A1 (5.4)	CRISPLD1 (4.7)	BNC2 (4.5)	COL9A2 (4.3)	DMP1 (4.3)	GFPT2 (4.0)	TRPS1 (4.0)	SMOC2 (3.9)	PCSK5 (3.8)
MP:0000120	malocclusion	1.61E-09	<0.01	3.77E-17	MP:0005358	abnormal incisor morphology	46	PRRX1 (4.3)	SMAD6 (3.8)	BMP2 (3.6)	SPRED1 (3.4)	MPPED2 (3.4)	DMRTA2 (3.3)	NPR2 (3.3)	ADAMTS19 (3.3)	LOXL1 (3.1)	SH3PXD2A (3.0)
GO:0061035	regulation of cartilage development	1.70E-09	<0.01	3.49E-17	GO:0032330	regulation of chondrocyte differentiation	38	SMOC2 (4.9)	CRISPLD1 (4.8)	FAM101A (3.6)	PCSK5 (3.5)	BNC2 (3.4)	NOG (3.3)	BANF2 (3.2)	GDF5 (3.2)	CHRDL2 (3.2)	COL9A2 (3.1)
GO:0030879	mammary gland development	1.71E-09	<0.01	4.51E-13	GO:0060443	mammary gland morphogenesis	47	ESR1 (5.6)	ANO1 (4.9)	ENSG00000250406 (4.2)	TRPS1 (3.6)	ENSG00000234028 (3.5)	PDLIM4 (3.3)	PHLDB3 (3.2)	ENSG00000235300 (2.9)	ENSG00000248463 (2.8)	CRISPLD1 (2.7)
ENSG00000132153	DHX30 PPI subnetwork	1.73E-09	<0.01	5.18E-16	ENSG00000130803	ZNF317 PPI subnetwork	48	POLG (3.8)	RPRD2 (3.5)	ZNF652 (3.4)	FXR2 (3.4)	FBXO30 (3.4)	ZNF18 (3.4)	ZNF142 (3.3)	SSH2 (3.1)	KIAA1267 (3.1)	RTF1 (3.1)
ENSG00000105329	TGFB1 PPI subnetwork	1.87E-09	<0.01	6.26E-12	ENSG00000092969	TGFB2 PPI subnetwork	34	LTBP2 (6.9)	FN1 (6.2)	COL10A1 (6.0)	FBN1 (5.9)	SMAD7 (5.7)	COL8A1 (5.7)	COL6A1 (5.4)	CILP2 (5.1)	FBLN2 (5.1)	LOXL1 (5.0)
MP:0001954	respiratory distress	1.88E-09	<0.01	4.39E-11	MP:0011087	complete neonatal lethality	31	HOXB3 (5.6)	NOG (4.7)	SCUBE3 (3.9)	RGMA (3.8)	FGFR2 (3.6)	WNT5A (3.6)	COL6A1 (3.6)	COL9A2 (3.5)	FGF18 (3.5)	HLX (3.5)
REACTOME_PI3K_CASCAD	REACTOME_PI3K_CASCADE	1.91E-09	<0.01	6.17E-13	GO:0071774	response to fibroblast growth factor stimuli	49	MYH7B (4.5)	FRS2 (4.2)	GNA12 (3.5)	CLOCK (3.4)	XRRA1 (3.3)	MAP3K3 (3.2)	PLAG1 (3.2)	RORA (3.1)	SPTBN1 (3.1)	PPARD (3.1)
MP:0010876	decreased bone volume	1.95E-09	<0.01	1.78E-10	MP:0010869	decreased bone trabecula number	50	ENSG00000227388 (4.0)	PRRX1 (3.7)	CBFA2T2 (3.5)	GMDS (3.4)	SCARA3 (3.3)	SOCS5 (3.3)	SMOX (3.2)	COL15A1 (3.1)	IGF2 (3.1)	IGFBP3 (3.1)
ENSG00000177485	ZBTB33 PPI subnetwork	2.07E-09	<0.01	1.29E-19	ENSG00000169016	E2F6 PPI subnetwork	15	RBM15B (3.5)	ZNF652 (3.5)	RNPS1 (3.5)	SENP3 (3.3)	RPRD2 (3.3)	CCDC50 (3.3)	MEAF6 (3.2)	LRP5 (3.1)	SUZ12 (3.0)	FUBP3 (3.0)
ENSG00000169016	E2F6 PPI subnetwork	2.10E-09	<0.01	1.60E-19	ENSG00000169016	E2F6 PPI subnetwork	15	ZNF652 (4.2)	RBM15B (3.9)	MARK3 (3.7)	RNPS1 (3.2)	MEAF6 (3.2)	TLE3 (3.1)	RPRD2 (3.0)	ARID1B (3.0)	CCDC50 (3.0)	SETD8 (3.0)
MP:0004359	short ulna	2.16E-09	<0.01	4.71E-13	MP:0004359	short ulna	37	TBX4 (6.7)	FAM101A (5.4)	TRPS1 (5.1)	COL9A2 (5.0)	COL10A1 (4.9)	NFATC4 (4.9)	BNC2 (4.5)	COL11A1 (4.5)	TBX18 (4.5)	GDF5 (4.4)
GO:0035107	appendage morphogenesis	2.31E-09	<0.01	1.42E-16	GO:0035108	limb morphogenesis	30	NFATC4 (4.2)	TRPS1 (3.9)	TBX18 (3.8)	DNM3OS (3.3)	PRRX1 (3.3)	CRISPLD1 (3.2)	PLAG1 (3.2)	MIR214 (3.1)	LIN28B (3.1)	MPPED2 (3.1)
GO:0035108	limb morphogenesis	2.31E-09	<0.01	1.42E-16	GO:0035108	limb morphogenesis	30	NFATC4 (4.2)	TRPS1 (3.9)	TBX18 (3.8)	DNM3OS (3.3)	PRRX1 (3.3)	CRISPLD1 (3.2)	PLAG1 (3.2)	MIR214 (3.1)	LIN28B (3.1)	MPPED2 (3.1)
MP:0002116	abnormal craniofacial bone morphology	2.37E-09	<0.01	6.61E-15	MP:0000088	short mandible	11	WWP2 (5.5)	CRISPLD1 (5.5)	DMP1 (5.4)	COL9A2 (5.4)	FAM101A (5.3)	SCARA3 (5.2)	CILP2 (4.9)	TRPS1 (4.4)	PAX9 (4.2)	FOXD2 (4.2)
MP:0000163	abnormal cartilage morphology	2.37E-09	<0.01	1.91E-13	MP:0010029	abnormal basicranium morphology	20	CILP2 (6.9)	COL11A1 (6.9)	DMP1 (6.0)	COL10A1 (5.8)	FAM101A (5.8)	WWP2 (5.4)	COL9A2 (5.4)	GDF5 (5.3)	FGFR2 (5.1)	CYTL1 (5.0)
MP:0008271	abnormal bone ossification	2.48E-09	<0.01	2.60E-12	MP:0000130	abnormal trabecular bone morphology	12	DMP1 (6.4)	WWP2 (5.2)	SCUBE3 (4.9)	COL9A2 (4.9)	COL11A1 (4.8)	FAM101A (4.5)	COL10A1 (4.3)	FAM46A (4.2)	CRISPLD1 (4.2)	TRPS1 (4.0)
MP:0005108	abnormal ulna morphology	2.58E-09	<0.01	1.87E-15	GO:0035108	limb morphogenesis	30	SALL1 (6.1)	TBX4 (5.3)	WNT5A (4.2)	FGFR2 (4.1)	NFATC4 (4.0)	IGF2-AS (3.8)	FAM101A (3.7)	GLIS1 (3.6)	AXIN2 (3.3)	DCBLD1 (3.1)
GO:0007179	transforming growth factor beta receptor signaling pathwa	2.64E-09	<0.01	8.43E-15	GO:0090092	brane receptor protein serine/threonine k	51	ENSG00000197291 (3.8)	BMPR2 (3.6)	LTBP2 (3.6)	SMAD7 (3.4)	KIAA1267 (3.2)	GH2 (3.1)	COL8A1 (3.1)	LOXL1 (3.0)	GAL3ST4 (3.0)	ZBTB4 (2.9)
ENSG00000205250	E2F4 PPI subnetwork	2.73E-09	<0.01	3.26E-13	ENSG00000189308	LIN54 PPI subnetwork	52	TAF6 (4.2)	BCL7A (3.6)	MCM7 (3.6)	MEPCE (3.3)	SETD8 (3.2)	FAM53B (3.1)	RAD54L2 (3.1)	LCORL (3.1)	FANCI (3.0)	PSMC3IP (2.9)
GO:0007389	pattern specification process	2.83E-09	<0.01	3.86E-15	GO:0003002	regionalization	4	ENSG00000233101 (6.6)	HOXB3 (5.7)	FOXD2 (4.2)	TBX6 (4.0)	GRRP1 (3.6)	ENSG00000237424 (3.5)	EPHB1 (3.3)	MIR214 (3.2)	IGF2-AS (3.2)	HMGA2 (3.2)
GO:0007178	mbrane receptor protein serine/threonine kinase signaling	3.02E-09	<0.01	3.21E-14	GO:0090092	brane receptor protein serine/threonine k	51	NOG (3.6)	SMAD7 (3.5)	LTBP1 (3.4)	GREB1L (3.3)	COL8A1 (3.3)	PRKAB2 (3.2)	PAPPA (3.2)	FBLN2 (3.1)	BMPR2 (3.1)	TBX6 (3.0)
ENSG00000167244	IGF2 PPI subnetwork	3.04E-09	<0.01	7.72E-06	H_FACTOR_IGF_ACTIVITY_BY_INSULIN	WTH_FACTOR_IGF_ACTIVITY_BY_INSULIN-LI	53	IGF2 (7.9)	ITIH3 (4.6)	WNT4 (4.4)	PDLIM4 (4.0)	FBLN2 (3.8)	ADAMTSL1 (3.8)	FBLN5 (3.7)	MOXD1 (3.6)	ECE1 (3.5)	GRB10 (3.5)
MP:0000351	increased cell proliferation	3.25E-09	<0.01	7.82E-13	GO:0004861	lin-dependent protein kinase inhibitor acti	54	RPS27L (5.7)	AFAP1 (3.8)	DRAM1 (3.8)	FRS2 (3.7)	SERPINE2 (3.6)	FBN1 (3.5)	PRRX1 (3.5)	IGFBP3 (3.3)	FBLN2 (2.8)	GAL3ST4 (2.7)
MP:0006027	impaired lung alveolus development	3.27E-09	<0.01	8.90E-11	GO:0030323	respiratory tube development	55	TBX4 (4.4)	COL6A1 (4.2)	DCBLD1 (3.7)	HOXB3 (3.6)	DLC1 (3.5)	LOXL1 (3.5)	RGMA (3.4)	ITGB8 (3.3)	SPON1 (3.3)	TGFB2 (3.1)
MP:0003109	short femur	3.29E-09	<0.01	1.84E-10	MP:0000130	abnormal trabecular bone morphology	12	DMP1 (8.7)	COL11A1 (8.5)	COL10A1 (7.3)	COL24A1 (6.4)	CILP2 (6.2)	COL9A2 (5.8)	TRPS1 (5.1)	FAM101A (4.8)	WWP2 (4.4)	COPZ2 (4.2)
MP:0003054	spina bifida	3.34E-09	<0.01	1.42E-09	MP:0000914	exencephaly	14	WNT3 (4.7)	DMRTA2 (3.8)	AXIN2 (3.5)	RGMA (3.3)	PTPN14 (3.2)	KIAA1267 (3.2)	NFATC4 (3.2)	KLHDC5 (3.1)	SERPINH1 (2.9)	WNT5A (2.8)
MP:0001716	abnormal placenta labyrinth morphology	3.38E-09	<0.01	5.04E-16	MP:0001716	abnormal placenta labyrinth morphology	17	MAP3K1 (3.4)	FN1 (3.0)	GNA12 (3.0)	AVL9 (2.9)	REST (2.9)	WNT5A (2.9)	SLC16A3 (2.8)	LAMC1 (2.8)	IGFBP3 (2.7)	RXRA (2.7)
ENSG00000138696	BMPR1B PPI subnetwork	3.44E-09	<0.01	1.31E-14	REACTOME_SIGNALING_BY_BMP	REACTOME_SIGNALING_BY_BMP	24	XPA (4.5)	SMAD6 (4.1)	SMAD7 (3.5)	KLF11 (3.3)	DCBLD1 (3.3)	BMPR2 (3.2)	ID4 (3.2)	CABLES1 (3.1)	MIB1 (3.0)	AXIN2 (3.0)
GO:0090092	ansmembrane receptor protein serine/threonine kinase si	3.48E-09	<0.01	1.43E-16	GO:0090092	brane receptor protein serine/threonine k	51	NOG (3.8)	MSRB3 (3.7)	SMAD7 (3.6)	PAPPA (3.6)	PCSK5 (3.5)	TMEM136 (3.4)	ENSG00000237424 (3.3)	LTBP1 (3.3)	BMP6 (3.2)	GREB1L (3.2)
MP:0000930	wavy neural tube	3.62E-09	<0.01	1.02E-12	MP:0011098	plete embryonic lethality during organoge	2	MIER3 (3.9)	MSRB3 (3.7)	ID4 (3.4)	WDR19 (3.3)	MAP3K3 (3.1)	BMP2 (3.0)	UBN1 (3.0)	TBX4 (3.0)	FNIP1 (3.0)	PTPN12 (2.9)
MP:0003935	abnormal craniofacial development	3.62E-09	<0.01	1.36E-13	MP:0002237	abnormal nasal cavity morphology	56	FGFR2 (3.8)	NFATC4 (3.5)	DMRTA2 (3.5)	GLI2 (3.4)	LAMA5 (3.3)	ADAMTS19 (3.1)	PPL (3.1)	CRISPLD1 (3.0)	EFEMP1 (3.0)	ISL1 (3.0)
ENSG00000129152	MYOD1 PPI subnetwork	3.76E-09	<0.01	7.23E-10	ENSG00000122180	MYOG PPI subnetwork	57	SMAD6 (7.0)	SMAD7 (4.9)	ID4 (3.9)	PLEKHH3 (3.7)	KLF3 (3.6)	TBX2 (3.5)	RB1 (3.5)	BMPR2 (3.5)	ZMIZ1 (3.5)	BMP2 (3.3)
GO:0030278	regulation of ossification	3.81E-09	<0.01	4.49E-17	GO:0045667	regulation of osteoblast differentiation	58	SCARA3 (3.5)	DMP1 (3.5)	CYTL1 (3.5)	CRISPLD1 (3.4)	SMOC2 (3.3)	ENSG00000185294 (3.1)	ID4 (3.1)	GREB1L (3.0)	TRPS1 (3.0)	MIER3 (3.0)
ENSG00000151090	THRB PPI subnetwork	3.95E-09	<0.01	1.50E-12	ENSG00000091831	ESR1 PPI subnetwork	59	CREBBP (4.8)	GPBP1L1 (3.8)	AP3D1 (3.5)	CBX1 (3.5)	CHRDL2 (3.0)	ZMIZ1 (2.9)	SP3 (2.9)	DDX42 (2.9)	RBL2 (2.8)	KBTBD4 (2.8)
MP:0002114	abnormal axial skeleton morphology	4.03E-09	<0.01	2.61E-15	MP:0000150	abnormal rib morphology	6	BMP2 (4.8)	FAM101A (4.8)	DMP1 (4.6)	COL9A2 (4.4)	FGFR2 (4.4)	TRPS1 (4.2)	WWP2 (4.0)	ID4 (4.0)	NFATC1 (3.8)	CRISPLD1 (3.8)
MP:0002187	abnormal fibula morphology	4.46E-09	<0.01	6.23E-14	MP:0004359	short ulna	37	TBX4 (7.5)	TBX18 (4.4)	COL9A2 (4.3)	FAM101A (4.0)	ANGPTL7 (4.0)	SMAD6 (3.9)	TGFB2 (3.9)	GMDS (3.7)	HHIP (3.6)	COL10A1 (3.5)
ACTOME_SIGNALING_BY_PI	REACTOME_SIGNALING_BY_PDGF	4.49E-09	<0.01	4.77E-10	OME_DOWNSTREAM_SIGNAL_TRANSD	CTOME_DOWNSTREAM_SIGNAL_TRANSDUC	60	COL6A1 (6.0)	COL15A1 (5.8)	FBN1 (5.5)	PXDN (4.9)	LOXL1 (4.5)	COL11A1 (4.4)	FAM101A (4.3)	ADAMTS2 (4.2)	SMOC2 (3.8)	FN1 (3.7)
MP:0000141	abnormal vertebral body morphology	4.52E-09	<0.01	4.40E-14	MP:0000150	abnormal rib morphology	6	FAM101A (7.5)	WWP2 (6.1)	COL9A2 (6.0)	CILP2 (5.6)	CYTL1 (5.4)	COL11A1 (4.8)	SCUBE3 (4.7)	RGMA (4.5)	COL10A1 (4.4)	CRISPLD1 (4.3)
MP:0001286	abnormal eye development	4.57E-09	<0.01	2.86E-14	MP:0002237	abnormal nasal cavity morphology	56	ID4 (4.1)	SOX8 (4.0)	SALL1 (3.6)	FOXE3 (3.5)	NR2E3 (3.5)	FOXD2 (3.4)	CA14 (3.1)	TGFB2 (3.1)	WNT5A (3.1)	ADAMTS19 (3.1)
ENSG00000126351	THRA PPI subnetwork	4.60E-09	<0.01	1.15E-10	ENSG00000182093	WRB PPI subnetwork	61	ZNFX1 (5.1)	ZMIZ1 (4.7)	RARA (4.3)	NFIC (4.2)	SAMD9 (3.9)	ATF7IP (3.8)	HMGA2 (3.5)	CREBBP (3.4)	DDX6 (3.3)	PTPN12 (3.3)
MP:0001719	absent vitelline blood vessels	4.84E-09	<0.01	2.48E-11	MP:0011098	plete embryonic lethality during organoge	2	SMAD6 (5.4)	PLVAP (4.9)	RAMP2 (4.5)	GRRP1 (4.4)	TBX2 (4.4)	ADCY4 (4.2)	EDNRB (4.1)	PDE3A (3.6)	HLX (3.5)	SMAD7 (3.5)
MP:0000929	open neural tube	5.26E-09	<0.01	2.81E-12	MP:0000914	exencephaly	14	LIN28A (5.5)	SALL1 (3.9)	GLTSCR1 (3.6)	LIN28B (3.5)	ID4 (3.4)	WNT5A (3.4)	WNT3 (3.4)	AXIN2 (3.4)	TRPS1 (3.3)	TMEM165 (3.2)
ENSG00000124151	NCOA3 PPI subnetwork	5.67E-09	<0.01	3.22E-11	ENSG00000084676	NCOA1 PPI subnetwork	62	NFIC (4.8)	ZCCHC24 (4.1)	KLF3 (3.7)	TRIB1 (3.5)	PLEKHH3 (3.5)	RARA (3.3)	CREBBP (3.2)	TRIOBP (3.1)	CBX6 (2.9)	ANO1 (2.8)
ENSG00000183741	CBX6 PPI subnetwork	5.84E-09	<0.01	2.26E-17	ENSG00000169016	E2F6 PPI subnetwork	15	RBM15B (4.1)	RNPS1 (3.5)	ZNF652 (3.4)	BCL7A (3.4)	GLYR1 (3.2)	SPIN1 (3.1)	ARID1B (3.1)	MARK3 (3.1)	RPRD2 (3.0)	MEAF6 (3.0)
MP:0001732	postnatal growth retardation	5.85E-09	<0.01	6.00E-11	MP:0011086	partial postnatal lethality	8	KCNJ16 (3.5)	SCUBE3 (3.5)	ZMIZ1 (3.4)	CTBP2 (3.3)	NFAT5 (3.2)	STARD13 (3.2)	NFIC (3.1)	ENPP2 (3.0)	GNAS (2.9)	ANO1 (2.9)
GO:0017147	Wnt-protein binding	5.94E-09	<0.01	1.87E-12	ENSG00000085741	WNT11 PPI subnetwork	63	SMOC2 (5.6)	PCSK5 (4.7)	CRISPLD1 (4.7)	GLI2 (4.4)	CILP2 (4.0)	FBLN2 (3.9)	COL15A1 (3.6)	FGFR2 (3.6)	NOV (3.6)	FBLN5 (3.5)
MP:0002884	abnormal branchial arch morphology	6.29E-09	<0.01	5.18E-14	MP:0004310	small otic vesicle	64	SALL1 (3.6)	SMAD6 (3.2)	FGF18 (3.1)	ABP1 (3.0)	SLC25A13 (2.9)	IGFBP3 (2.8)	NFATC4 (2.7)	RPIA (2.7)	RAMP2 (2.6)	PTPN12 (2.6)
GO:0016049	cell growth	6.34E-09	<0.01	1.21E-11	GO:0001558	regulation of cell growth	33	SLC22A5 (3.6)	ENSG00000235713 (3.4)	ENSG00000246985 (3.3)	PAPPA (3.1)	CYTL1 (3.1)	COL8A1 (3.0)	CILP2 (3.0)	NOV (2.9)	SLC39A13 (2.9)	SERPINE2 (2.8)
ENSG00000206279	DAXX PPI subnetwork	6.68E-09	<0.01	1.44E-08	ENSG00000206206	DAXX PPI subnetwork	65	ARID1B (4.4)	ZNFX1 (4.3)	PPP4C (3.8)	PIK3R1 (3.6)	CREBBP (3.4)	PTPRJ (3.4)	STAT1 (3.3)	CELF1 (3.0)	PCGF5 (2.9)	RNF169 (2.8)
ENSG00000206206	DAXX PPI subnetwork	6.68E-09	<0.01	1.44E-08	ENSG00000206206	DAXX PPI subnetwork	65	ARID1B (4.4)	ZNFX1 (4.3)	PPP4C (3.8)	PIK3R1 (3.6)	CREBBP (3.4)	PTPRJ (3.4)	STAT1 (3.3)	CELF1 (3.0)	PCGF5 (2.9)	RNF169 (2.8)
ENSG00000204209	DAXX PPI subnetwork	6.68E-09	<0.01	1.44E-08	ENSG00000206206	DAXX PPI subnetwork	65	ARID1B (4.4)	ZNFX1 (4.3)	PPP4C (3.8)	PIK3R1 (3.6)	CREBBP (3.4)	PTPRJ (3.4)	STAT1 (3.3)	CELF1 (3.0)	PCGF5 (2.9)	RNF169 (2.8)
KEGG_ADHERENS_JUNCTIO	KEGG_ADHERENS_JUNCTION	6.76E-09	<0.01	3.98E-08	GO:0005912	adherens junction	66	FLNB (4.6)	PTPN12 (4.1)	RRAS2 (4.1)	PTPRG (3.8)	SH3D19 (3.8)	EPB41L2 (3.7)	LUZP1 (3.5)	ANKFN1 (3.5)	PTPN14 (3.4)	SPTBN1 (3.4)
MP:0004251	failure of heart looping	7.33E-09	<0.01	1.44E-11	MP:0000267	abnormal heart development	21	SMAD6 (4.1)	AXIN2 (3.8)	RSBN1L (3.5)	CACNA2D2 (3.5)	TBX4 (3.3)	BMP2 (2.9)	RBM15B (2.8)	TMOD1 (2.7)	ECE1 (2.7)	MEX3B (2.7)
MP:0004471	short nasal bone	7.62E-09	<0.01	1.70E-13	MP:0000088	short mandible	11	TBX4 (7.7)	COL24A1 (6.7)	DMP1 (6.6)	FGFR2 (5.7)	COL9A2 (4.7)	AXIN2 (4.7)	TGFB2 (4.5)	HHIP (4.3)	FAM101A (3.9)	CYTL1 (3.9)
GO:0060070	canonical Wnt receptor signaling pathway	7.71E-09	<0.01	4.02E-13	GO:0030111	regulation of Wnt receptor signaling pathw	44	AXIN2 (4.1)	PTHLH (3.6)	ENSG00000196355 (3.5)	FAM101A (3.4)	CRISPLD1 (3.3)	WNT4 (3.1)	PCSK5 (3.0)	TBX6 (3.0)	VANGL2 (2.9)	ZNF354C (2.9)
MP:0002086	abnormal extraembryonic tissue morphology	7.73E-09	<0.01	2.26E-14	MP:0011098	plete embryonic lethality during organoge	2	REST (4.1)	CTBP2 (3.9)	SERPINH1 (3.5)	NFAT5 (3.4)	OTUD4 (3.2)	PTPN12 (3.2)	LAMC1 (3.2)	NCOR2 (3.2)	MED13L (3.1)	RAD54L2 (3.0)
ENSG00000214528	ENSG00000214528 PPI subnetwork	8.26E-09	<0.01	2.43E-11	ENSG00000143995	MEIS1 PPI subnetwork	67	HOXB3 (6.4)	ENSG00000233101 (4.7)	SALL1 (4.5)	IGF2BP2 (3.6)	IGF2-AS (3.6)	FOXD2 (3.5)	ISL1 (3.3)	VGLL2 (3.3)	ENSG00000238199 (3.2)	MSRB3 (3.0)
GO:0060541	respiratory system development	8.39E-09	<0.01	3.08E-17	GO:0030323	respiratory tube development	55	TBX4 (5.0)	RSPO1 (4.0)	HHIP (3.7)	FGF18 (3.3)	N4BP2L2 (3.3)	SH3PXD2A (3.2)	DCBLD1 (3.2)	AXIN2 (3.0)	PAPPA (2.9)	PCSK5 (2.8)
GO:0022612	gland morphogenesis	9.00E-09	<0.01	4.99E-14	GO:0060443	mammary gland morphogenesis	47	THSD4 (3.9)	PDLIM4 (3.8)	ENSG00000250406 (3.3)	TRPS1 (3.3)	KLHDC5 (3.1)	SMAD3 (3.1)	ARSJ (3.0)	ANO1 (3.0)	SPRED1 (3.0)	HHIP (2.9)
GO:2000027	regulation of organ morphogenesis	9.69E-09	<0.01	9.96E-16	GO:0002009	morphogenesis of an epithelium	7	CYS1 (3.9)	SPRY2 (3.3)	PDLIM4 (3.5)	MOXD1 (3.4)	SALL1 (3.3)	IGF2-AS (3.3)	GLIS1 (3.3)	ENSG00000197291 (3.3)	LINC00472 (3.2)	DNM3OS (3.2)
GO:0008301	DNA binding, bending	9.87E-09	<0.01	2.08E-18	GO:0003690	double-stranded DNA binding	68	FOXD2 (6.0)	FOXL1 (5.2)	ENSG00000237424 (4.9)	PAX9 (4.6)	IGF2BP3 (3.4)	TBX18 (3.3)	HHIP (3.2)	DMRTA2 (3.1)	C20orf144 (3.1)	ARID1B (3.1)
MP:0000154	rib fusion	9.94E-09	<0.01	1.92E-13	MP:0000150	abnormal rib morphology	6	HOXB3 (5.2)	NFATC4 (4.8)	PAX9 (4.7)	IGF2 (4.5)	HMGA2 (4.5)	ENSG00000233101 (4.3)	PRRX1 (4.1)	IGFBP4 (3.9)	TBX6 (3.8)	WNT3 (3.6)
ENSG00000091831	ESR1 PPI subnetwork	1.09E-08	<0.01	3.35E-16	ENSG00000091831	ESR1 PPI subnetwork	59	CREBBP (3.7)	RPRD2 (3.7)	NCOR2 (3.6)	PIK3R1 (3.6)	ARID1B (3.5)	RARA (3.3)	KLF3 (3.3)	ECE1 (3.3)	SMARCD2 (3.3)	NFIC (3.3)
MP:0005105	abnormal middle ear ossicle morphology	1.11E-08	<0.01	5.91E-12	MP:0000049	abnormal middle ear morphology	45	SALL1 (6.0)	FGFR2 (5.6)	WNT5A (5.2)	CRISPLD1 (4.9)	PRRX1 (4.6)	DMP1 (4.6)	NFATC4 (4.4)	HMGA2 (4.3)	TRPS1 (4.3)	IGFBP3 (4.1)
ENSG00000143995	MEIS1 PPI subnetwork	1.12E-08	<0.01	3.08E-11	ENSG00000143995	MEIS1 PPI subnetwork	67	HOXB3 (6.1)	SALL1 (5.0)	ENSG00000233101 (4.5)	IGF2-AS (3.7)	IGF2BP2 (3.5)	FOXD2 (3.5)	VGLL2 (3.3)	ISL1 (3.2)	ENSG00000238199 (3.2)	B3GNT7 (3.0)
ENSG00000015153	YAF2 PPI subnetwork	1.13E-08	<0.01	5.58E-18	ENSG00000169016	E2F6 PPI subnetwork	15	RBM15B (4.4)	MARK3 (3.7)	RPRD2 (3.4)	ZNF652 (3.4)	SPIN1 (3.3)	RNPS1 (3.2)	H1FX (3.1)	BCL7A (3.1)	MEAF6 (3.1)	FUBP1 (3.0)
MP:0000455	abnormal maxilla morphology	1.27E-08	<0.01	1.04E-11	MP:0009890	cleft secondary palate	16	DMP1 (5.4)	FGFR2 (4.6)	FOXD2 (4.5)	TRPS1 (4.5)	WNT5A (4.4)	PRRX1 (4.4)	COL11A1 (4.3)	SALL1 (4.1)	NFATC4 (4.0)	CRISPLD1 (3.9)
ENSG00000183337	BCOR PPI subnetwork	1.49E-08	<0.01	2.69E-17	ENSG00000169016	E2F6 PPI subnetwork	15	SP3 (3.8)	ZNF76 (3.7)	SUZ12 (3.3)	RBM15B (3.2)	GLTSCR1 (3.1)	SOCS5 (3.1)	CABLES2 (3.1)	ZBTB20 (3.0)	SETD8 (2.9)	MARK3 (2.9)
ENSG00000120693	SMAD9 PPI subnetwork	1.49E-08	<0.01	2.46E-17	ENSG00000166949	SMAD3 PPI subnetwork	13	GH2 (4.5)	SMAD7 (4.4)	SMAD6 (4.0)	BMPR2 (3.6)	POLG (3.2)	ZMIZ1 (3.2)	FAM134C (3.1)	MIB1 (3.0)	DYM (2.8)	HSD17B1 (2.8)
MP:0001634	internal hemorrhage	1.57E-08	<0.01	8.87E-12	FORMATION_OF_FIBRIN_CLOT_CLOTTI	E_FORMATION_OF_FIBRIN_CLOT_CLOTTING	69	LTBP1 (4.9)	C9 (3.8)	ERC1 (3.6)	NFATC4 (3.6)	DNM3 (3.0)	PTPN12 (3.0)	ERGIC2 (2.9)	TBX2 (2.9)	ITIH1 (2.8)	HP (2.8)
GO:0060348	bone development	1.58E-08	<0.01	8.10E-17	GO:0060350	endochondral bone morphogenesis	18	CILP2 (5.6)	SMOC2 (4.8)	COL11A1 (4.6)	COL10A1 (4.5)	CRISPLD1 (4.4)	FAM101A (3.9)	DNM3OS (3.8)	COPZ2 (3.7)	MIR214 (3.7)	PCSK5 (3.6)
GO:0010171	body morphogenesis	1.61E-08	<0.01	3.31E-14	GO:0060323	head morphogenesis	70	MIR214 (4.6)	ANKFN1 (3.2)	NFATC4 (3.2)	DNM3OS (3.0)	C9orf3 (2.9)	PDLIM4 (2.9)	CRISPLD1 (2.8)	EPS15P1 (2.8)	ENSG00000243224 (2.7)	PTPDC1 (2.7)
MP:0002135	abnormal kidney morphology	1.62E-08	<0.01	3.51E-11	MP:0002705	dilated renal tubules	71	THSD4 (4.2)	SEMA3G (4.0)	CYS1 (3.9)	PAPPA (3.9)	TBX2 (3.7)	RAMP2 (3.7)	PRKG1 (3.5)	TBX4 (3.5)	LTBP1 (3.5)	HHIP (3.2)
MP:0002115	abnormal limb bone morphology	1.63E-08	<0.01	1.76E-08	MP:0005306	abnormal phalanx morphology	19	TBX18 (6.2)	COL9A2 (6.0)	WWP2 (5.8)	CRISPLD1 (5.7)	PRRX1 (5.6)	COL11A1 (5.3)	FGFR2 (5.0)	DMP1 (5.0)	TRPS1 (4.9)	COL10A1 (4.7)
ENSG00000161955	TNFSF13 PPI subnetwork	1.73E-08	<0.01	6.90E-10	GO:0005031	mor necrosis factor-activated receptor activ	72	CCR10 (3.7)	NOV (2.8)	UBXN2A (2.8)	LRCH1 (2.7)	ZBTB20 (2.7)	LTBP2 (2.6)	SMAD7 (2.6)	ITGB8 (2.6)	RORA (2.5)	COL8A1 (2.4)
GO:0001944	vasculature development	2.00E-08	<0.01	1.10E-08	GO:0001568	blood vessel development	26	ADCY4 (5.3)	PLVAP (4.7)	RAMP2 (4.6)	APOLD1 (4.6)	IGFBP3 (4.0)	COL15A1 (3.8)	GRRP1 (3.8)	ADAM12 (3.8)	PXDN (3.7)	LTBP2 (3.6)
MP:0005621	abnormal cell physiology	2.03E-08	<0.01	3.59E-16	KEGG_CELL_CYCLE	KEGG_CELL_CYCLE	73	AP3B1 (3.1)	ZNFX1 (3.0)	NCOA7 (3.0)	SMAD3 (2.9)	SAMHD1 (2.7)	RPS27L (2.7)	FNIP1 (2.7)	ARFGEF2 (2.6)	YEATS2 (2.6)	AFAP1 (2.5)
MP:0003036	vertebral transformation	2.09E-08	<0.01	2.38E-11	MP:0004618	thoracic vertebral transformation	74	HOXB3 (7.3)	ENSG00000233101 (6.5)	FOXD2 (4.6)	SALL1 (4.0)	AXIN2 (3.9)	PLAG1 (3.8)	LIN28B (3.6)	ENSG00000237424 (3.6)	GRRP1 (3.2)	ANKRD13B (3.1)
MP:0003743	abnormal facial morphology	2.11E-08	<0.01	2.76E-11	MP:0011087	complete neonatal lethality	31	HOXB3 (5.4)	GREB1L (4.7)	ENSG00000233101 (4.4)	GLI2 (4.4)	LIN28A (4.1)	FGFR2 (3.5)	RSBN1L (3.4)	RGMA (3.3)	NOG (3.3)	COL11A1 (3.1)
ENSG00000142208	AKT1 PPI subnetwork	2.15E-08	<0.01	6.39E-10	ENSG00000105221	AKT2 PPI subnetwork	75	MAP3K3 (4.2)	NUMB (3.5)	BAP1 (3.3)	RYBP (3.3)	DLEU2 (3.1)	CREBBP (3.0)	SSH2 (3.0)	MED13L (3.0)	ARID1B (2.9)	SMCHD1 (2.8)
ENSG00000129473	BCL2L2 PPI subnetwork	2.15E-08	<0.01	4.63E-07	ENSG00000186879	ENSG00000186879 PPI subnetwork	76	LOXL1 (3.9)	NCOA7 (3.7)	TBX18 (3.5)	FRK (3.3)	COL6A1 (3.1)	ATP2B1 (3.0)	APH1A (3.0)	FBN1 (2.9)	RILPL2 (2.9)	TMEM129 (2.8)
ENSG00000186350	RXRA PPI subnetwork	2.17E-08	<0.01	3.09E-13	ENSG00000091831	ESR1 PPI subnetwork	59	ZMIZ1 (4.6)	EGR3 (3.7)	CREBBP (3.5)	GLTSCR1 (3.5)	KLF11 (3.3)	SP2 (3.2)	SMAD3 (3.1)	NFIC (3.1)	TRIB1 (3.1)	CRADD (3.0)
ENSG00000112658	SRF PPI subnetwork	2.18E-08	<0.01	1.05E-12	GO:0001067	regulatory region nucleic acid binding	1	REST (4.2)	RAPSN (3.9)	RARA (3.6)	CHRNB1 (3.5)	MLXIP (3.4)	C1orf105 (3.3)	ETV6 (3.3)	ZC3H11A (3.1)	CLIC1P1 (3.1)	RB1 (3.1)
ENSG00000169083	AR PPI subnetwork	2.23E-08	<0.01	8.94E-17	ENSG00000091831	ESR1 PPI subnetwork	59	PBRM1 (4.0)	PPP6R3 (3.9)	TP53 (3.6)	SBNO1 (3.6)	ARID1B (3.6)	REST (3.5)	FRS2 (3.4)	MED13L (3.4)	ATF7IP (3.4)	MAP3K1 (3.3)
MP:0004810	decreased hematopoietic stem cell number	2.23E-08	<0.01	1.01E-11	MP:0008813	reased common myeloid progenitor cell nu	77	ENSG00000238018 (3.3)	CYTL1 (3.2)	NFAT5 (3.2)	ETV6 (3.2)	CXCR1 (3.1)	MIER3 (3.1)	REST (3.1)	SOCS2 (3.1)	DRAM1 (3.1)	GRRP1 (3.0)
MP:0008973	decreased erythroid progenitor cell number	2.27E-08	<0.01	9.17E-14	MP:0008813	reased common myeloid progenitor cell nu	77	MEX3B (3.7)	MIER3 (3.6)	MED13L (3.5)	SOCS2 (3.4)	SLC25A37 (3.3)	TLE3 (3.2)	DRAM1 (2.8)	RPGRIP1 (2.8)	KLF3 (2.8)	ZMIZ1 (2.8)
MP:0003560	osteoarthritis	2.28E-08	<0.01	1.42E-10	MP:0003662	mal long bone epiphyseal plate proliferativ	42	COL10A1 (12.8)	CILP2 (10.9)	COL11A1 (8.1)	COL9A2 (8.0)	LTBP2 (7.3)	ANGPTL7 (6.0)	COL8A1 (5.7)	WWP2 (5.0)	SMOC2 (5.0)	CRISPLD1 (4.9)
ENSG00000137834	SMAD6 PPI subnetwork	2.57E-08	<0.01	6.10E-14	REACTOME_SIGNALING_BY_BMP	REACTOME_SIGNALING_BY_BMP	24	SMAD6 (5.7)	SMAD7 (4.6)	AXIN2 (3.3)	SMAD3 (3.2)	PRKAB2 (3.2)	CBFA2T2 (3.2)	ZMIZ1 (3.1)	SPIN1 (3.1)	TULP4 (2.9)	OTUD4 (2.9)
MP:0003446	renal hypoplasia	2.66E-08	<0.01	3.42E-12	MP:0004936	d branching involved in ureteric bud morph	78	THSD4 (5.1)	IGFBP4 (5.0)	IGF2-AS (4.8)	HMGA2 (4.7)	SALL1 (4.6)	DNM3OS (4.5)	IGF2 (4.1)	LTBP1 (4.1)	MOXD1 (4.0)	MIR214 (3.9)
GO:0001503	ossification	2.67E-08	<0.01	7.74E-14	GO:0045667	regulation of osteoblast differentiation	58	DMP1 (7.8)	COL24A1 (6.7)	CILP2 (4.6)	SCARA3 (4.5)	COL10A1 (4.4)	CRISPLD1 (4.3)	COPZ2 (4.0)	COL11A1 (3.7)	FAM101A (3.5)	COL9A2 (3.4)
GO:0032330	regulation of chondrocyte differentiation	2.69E-08	<0.01	6.21E-16	GO:0032330	regulation of chondrocyte differentiation	38	BANF2 (4.5)	BNC2 (4.5)	SMOC2 (4.3)	CRISPLD1 (4.1)	PRKG2 (3.5)	FAM101A (3.5)	CHRDL2 (3.4)	SH3D19 (3.4)	C9orf3 (3.3)	GDF5 (3.3)
GO:0021915	neural tube development	2.87E-08	<0.01	3.62E-14	GO:0001841	neural tube formation	79	WNT3 (3.8)	STK36 (3.8)	LIN28B (3.8)	VANGL2 (3.6)	TMEM74 (3.4)	DMRTA2 (3.3)	ENSG00000229212 (3.2)	RBM15B (3.1)	NHLH1 (3.0)	AXIN2 (3.0)
MP:0002110	abnormal digit morphology	2.99E-08	<0.01	1.14E-10	MP:0005306	abnormal phalanx morphology	19	NFATC4 (5.0)	FGFR2 (4.8)	TRPS1 (4.5)	PRRX1 (4.3)	CRISPLD1 (3.8)	SCARA3 (3.8)	MOXD1 (3.7)	TBX4 (3.6)	WNT5A (3.5)	COL10A1 (3.3)
ENSG00000056661	PCGF2 PPI subnetwork	3.00E-08	<0.01	2.66E-16	ENSG00000169016	E2F6 PPI subnetwork	15	RNPS1 (3.8)	RPRD2 (3.3)	MARK3 (3.2)	RBM15B (3.2)	MEAF6 (3.1)	ZNF652 (3.0)	FUBP3 (3.0)	SPIN1 (2.9)	SUZ12 (2.9)	TLE3 (2.9)
ENSG00000131788	PIAS3 PPI subnetwork	3.09E-08	<0.01	4.20E-08	ENSG00000131788	PIAS3 PPI subnetwork	80	ESR1 (5.2)	ARID1B (4.9)	NFATC1 (3.9)	ZNFX1 (3.7)	PLAG1 (3.7)	SMAD7 (3.7)	DYM (3.2)	EZH1 (3.2)	SNORD58C (3.0)	TRIOBP (3.0)
MP:0005104	abnormal tarsal bone morphology	3.17E-08	<0.01	2.91E-11	MP:0005306	abnormal phalanx morphology	19	FOXD2 (4.4)	TBX4 (4.4)	TBX18 (4.3)	GDF5 (3.9)	ANGPTL7 (3.9)	TRPS1 (3.7)	FKBP5 (3.7)	ENSG00000224186 (3.7)	ZCCHC24 (3.5)	GMDS (3.4)
MP:0003048	abnormal cervical vertebrae morphology	3.21E-08	<0.01	5.51E-11	MP:0003048	abnormal cervical vertebrae morphology	43	FOXD2 (4.9)	HOXB3 (4.7)	PAX9 (4.7)	VGLL2 (3.8)	HMGA2 (3.5)	CYTL1 (3.4)	MPPED2 (3.3)	ENSG00000233101 (3.3)	ENSG00000231160 (3.3)	NOG (3.2)
ENSG00000175029	CTBP2 PPI subnetwork	3.31E-08	<0.01	9.51E-16	ENSG00000206215	ENSG00000206215 PPI subnetwork	81	MEAF6 (3.5)	CCDC50 (3.4)	TRIOBP (3.3)	TMEM57 (3.2)	NFIC (3.1)	RPRD2 (3.1)	SETD8 (3.0)	MAST2 (3.0)	FRS2 (3.0)	ATAD2B (2.9)
ENSG00000198176	TFDP1 PPI subnetwork	3.44E-08	<0.01	4.02E-15	ENSG00000206215	ENSG00000206215 PPI subnetwork	81	LCORL (4.0)	SETD8 (4.0)	PBRM1 (3.8)	ENSG00000212673 (3.7)	SUZ12 (3.3)	BCL7A (3.2)	MIER3 (3.2)	CDKN2C (3.0)	GLTSCR1 (3.0)	ZNF3 (3.0)
MP:0004618	thoracic vertebral transformation	3.54E-08	<0.01	2.45E-11	MP:0004618	thoracic vertebral transformation	74	HOXB3 (11.1)	ENSG00000233101 (9.5)	HMGA2 (3.9)	FOXD2 (3.5)	PLAG1 (3.5)	LIN28B (3.5)	DNM3OS (3.1)	MIR214 (3.1)	SALL1 (3.1)	TLE3 (3.1)
MP:0004076	abnormal vitelline vascular remodeling	3.56E-08	<0.01	7.35E-12	MP:0004787	abnormal dorsal aorta morphology	35	PLVAP (4.1)	SMAD6 (4.0)	ADCY4 (4.0)	MAP3K3 (4.0)	BMPR2 (3.9)	RAMP2 (3.9)	PXDN (3.2)	PHACTR2 (3.2)	ECE1 (3.1)	PXMP4 (3.0)
ENSG00000116478	HDAC1 PPI subnetwork	3.66E-08	<0.01	1.21E-14	ENSG00000116478	HDAC1 PPI subnetwork	39	ARID1B (4.1)	CREBBP (3.5)	CDKN1B (3.4)	NFIC (3.4)	H1FX (3.4)	RARA (3.3)	KIAA1267 (3.3)	NUP153 (3.2)	MEPCE (3.2)	TP53 (3.2)
GO:0033365	protein localization to organelle	3.86E-08	<0.01	1.67E-13	GO:0051170	nuclear import	27	TRIP11 (3.2)	N4BP2L2-IT1 (3.2)	VPS13C (3.1)	ARFGEF2 (3.0)	ENSG00000241170 (3.0)	RALGAPA2 (2.8)	TMEM129 (2.7)	TRIM4 (2.6)	SHPRH (2.6)	PCGF5 (2.5)
MP:0005358	abnormal incisor morphology	4.08E-08	<0.01	1.26E-13	MP:0005358	abnormal incisor morphology	46	DMP1 (5.6)	FGFR2 (4.6)	PRRX1 (4.0)	NFATC4 (3.5)	COL24A1 (3.5)	SMAD6 (3.4)	GLIS1 (3.4)	WNT5A (3.3)	VANGL2 (3.3)	PTPRG (3.2)
MP:0004686	decreased length of long bones	4.11E-08	<0.01	2.67E-12	MP:0003662	mal long bone epiphyseal plate proliferativ	42	COL9A2 (7.6)	COL10A1 (6.9)	DMP1 (6.7)	WWP2 (5.9)	CILP2 (5.4)	FAM101A (5.2)	COL11A1 (5.0)	CRISPLD1 (4.9)	SOX5 (4.6)	FGFR2 (4.6)
MP:0001722	pale yolk sac	4.15E-08	<0.01	5.57E-11	MP:0011098	plete embryonic lethality during organoge	2	SMAD6 (4.3)	KLF3 (3.9)	TBX2 (3.4)	GATAD2A (3.3)	CREBBP (3.2)	EML4 (3.1)	CMIP (3.1)	ZMIZ1 (3.1)	CRLF3 (2.9)	NCOR2 (2.9)
ENSG00000140464	PML PPI subnetwork	4.15E-08	<0.01	1.12E-13	ENSG00000116478	HDAC1 PPI subnetwork	39	SAMD9 (4.1)	ZNFX1 (4.0)	SMCHD1 (3.7)	SSH2 (3.6)	TRIB1 (3.2)	RNF169 (3.1)	RARA (3.0)	MED13L (3.0)	YEATS2 (3.0)	RHOT1 (3.0)
MP:0004616	lumbar vertebral transformation	4.24E-08	<0.01	8.53E-11	MP:0004618	thoracic vertebral transformation	74	HOXB3 (4.9)	HMGA2 (3.9)	SALL1 (3.3)	LIN28B (3.2)	BAHCC1 (3.1)	SENP6 (3.0)	SOCS2 (3.0)	FKBP5 (2.9)	MIR214 (2.8)	TBX18 (2.8)
GO:0042813	Wnt-activated receptor activity	4.33E-08	<0.01	5.38E-12	ENSG00000085741	WNT11 PPI subnetwork	63	SMOC2 (5.6)	CILP2 (4.7)	GLI2 (4.3)	ANGPTL7 (4.2)	NOV (4.1)	CRISPLD1 (4.1)	PCSK5 (3.8)	FBLN5 (3.8)	FOXD2 (3.6)	ID4 (3.4)
ENSG00000106004	HOXA5 PPI subnetwork	4.34E-08	<0.01	2.07E-08	GO:0003002	regionalization	4	HOXB3 (8.8)	ENSG00000233101 (6.1)	ISL1 (5.1)	ENSG00000226688 (3.5)	NFATC4 (3.4)	MIR214 (3.3)	HMGA2 (3.2)	SPON1 (3.1)	IGF2BP3 (3.1)	RGMA (3.1)
MP:0001577	anemia	4.50E-08	<0.01	3.66E-10	MP:0000245	abnormal erythropoiesis	82	RHCE (7.6)	RHD (7.6)	SLC25A37 (6.9)	ETV6 (4.0)	SMOX (3.5)	ECE1 (3.2)	NFATC1 (3.0)	ARHGEF12 (2.9)	DOT1L (2.9)	CISH (2.7)
MP:0005269	abnormal occipital bone morphology	4.63E-08	<0.01	1.04E-08	MP:0010029	abnormal basicranium morphology	20	GDF5 (6.3)	WWP2 (5.1)	FGFR2 (4.8)	GMDS (4.6)	ID4 (4.4)	DMP1 (4.3)	SMAD6 (4.1)	SCARA3 (3.8)	FAM101A (3.8)	BMP6 (3.6)
ENSG00000070018	LRP6 PPI subnetwork	4.66E-08	<0.01	3.20E-13	ENSG00000085741	WNT11 PPI subnetwork	63	SPRY4 (5.1)	PRKG1 (4.5)	TGFB2 (4.0)	ID4 (3.8)	SPRY2 (3.8)	CRISPLD1 (3.7)	MPPED2 (3.5)	ADAMTS19 (3.2)	PTPRG (3.2)	HEXIM1 (3.1)
MP:0000433	microcephaly	4.68E-08	<0.01	2.92E-13	MP:0009890	cleft secondary palate	16	FOXD2 (4.0)	L3MBTL3 (3.5)	ENSG00000207034 (3.4)	CCDC50 (3.1)	TBX18 (2.8)	GREB1L (2.7)	SMAD3 (2.6)	SMCHD1 (2.6)	SMAD6 (2.6)	CEP192 (2.5)
MP:0000029	abnormal malleus morphology	4.78E-08	<0.01	1.91E-10	MP:0005106	abnormal incus morphology	83	NFATC4 (5.5)	PRRX1 (5.3)	WNT5A (4.9)	FGFR2 (4.7)	SALL1 (4.5)	DMP1 (4.3)	BMP2 (4.0)	SCARA3 (4.0)	TRPS1 (3.9)	COL10A1 (3.8)
ENSG00000185591	SP1 PPI subnetwork	4.82E-08	<0.01	7.05E-13	ENSG00000116478	HDAC1 PPI subnetwork	39	NCOR2 (4.3)	TRIB1 (4.2)	EGR3 (4.0)	NFATC1 (4.0)	NFIC (3.9)	RARA (3.7)	KIAA1267 (3.7)	CREBBP (3.6)	ARID1B (3.6)	REST (3.6)
ENSG00000180628	PCGF5 PPI subnetwork	4.92E-08	<0.01	2.43E-16	ENSG00000169016	E2F6 PPI subnetwork	15	RNPS1 (4.1)	RBM15B (3.6)	STAU1 (3.4)	FUBP1 (3.2)	VANGL2 (3.1)	SPIN1 (3.1)	ARID1B (3.1)	MARK3 (3.1)	TLE3 (3.0)	RQCD1 (2.9)
KEGG_COLORECTAL_CANCE	KEGG_COLORECTAL_CANCER	4.94E-08	<0.01	4.76E-09	KEGG_CHRONIC_MYELOID_LEUKEMIA	KEGG_CHRONIC_MYELOID_LEUKEMIA	5	GATAD2A (3.5)	FBXW11 (3.5)	MAP3K1 (3.3)	MXD4 (3.3)	VGLL4 (3.3)	MAX (3.1)	SPRED1 (3.1)	WDR82 (3.0)	APOLD1 (3.0)	SPIN1 (3.0)
G_WNT_SIGNALING_PATH	KEGG_WNT_SIGNALING_PATHWAY	4.95E-08	<0.01	3.14E-11	ENSG00000107404	DVL1 PPI subnetwork	84	AXIN2 (7.2)	SPRY2 (3.7)	BMP2 (3.6)	GLI2 (3.4)	WNT4 (3.3)	FBXW11 (3.1)	ADAMTS19 (3.1)	PTHLH (3.1)	MYH7B (3.0)	WNT5A (3.0)
GO:0019900	kinase binding	5.14E-08	<0.01	1.64E-09	GO:0019901	protein kinase binding	85	LIMD2 (3.7)	RRAS2 (3.5)	PPP6R3 (3.4)	SSH2 (3.4)	MAP3K3 (3.0)	TRPC4AP (2.9)	PPM1M (2.9)	FAM134C (2.8)	SEPT2 (2.8)	CDC42EP3 (2.8)
ENSG00000122691	TWIST1 PPI subnetwork	5.15E-08	<0.01	2.95E-13	ENSG00000113196	HAND1 PPI subnetwork	86	ENSG00000233101 (4.8)	ISL1 (4.7)	HOXB3 (3.9)	IGF2-AS (3.8)	PRRX1 (3.6)	C1orf105 (3.6)	NFATC1 (3.4)	RAPSN (3.4)	TBX18 (3.2)	VGLL2 (3.1)
ACTOME_PI3KAKT_ACTIVAT	REACTOME_PI3KAKT_ACTIVATION	5.26E-08	<0.01	6.70E-10	CTOME_PIP3_ACTIVATES_AKT_SIGNAL	EACTOME_PIP3_ACTIVATES_AKT_SIGNALIN	87	FRS2 (4.3)	MAP3K3 (3.8)	YPEL3 (3.5)	ZBTB38 (3.3)	CREBBP (3.3)	PLEKHH3 (3.2)	ENSG00000207034 (3.1)	INO80E (3.0)	APOLD1 (3.0)	KLF11 (3.0)
MP:0001787	pericardial edema	5.28E-08	<0.01	1.73E-08	MP:0011098	plete embryonic lethality during organoge	2	SMAD6 (3.8)	GFPT2 (3.1)	LIN28A (2.9)	ERC1 (2.8)	GRK5 (2.8)	RAB28 (2.7)	C20orf144 (2.7)	WDR19 (2.7)	SNAP47 (2.6)	PAPPA (2.5)
MP:0006395	abnormal epiphyseal plate morphology	5.32E-08	<0.01	2.24E-10	MP:0003662	mal long bone epiphyseal plate proliferativ	42	COL10A1 (6.6)	COL9A2 (6.5)	FGFR2 (5.6)	CILP2 (5.0)	SCUBE3 (4.7)	WWP2 (4.3)	FAM101A (3.9)	CYTL1 (3.9)	BNC2 (3.8)	DMP1 (3.8)
MP:0005352	small cranium	5.33E-08	<0.01	2.00E-11	MP:0004359	short ulna	37	DMP1 (6.6)	PRRX1 (4.5)	COL9A2 (4.3)	COL6A1 (4.2)	COL11A1 (4.0)	NFATC4 (4.0)	TRPS1 (3.8)	COL24A1 (3.6)	FAM101A (3.4)	SCARA3 (3.4)
ENSG00000107882	SUFU PPI subnetwork	5.36E-08	<0.01	1.82E-16	GO:0008589	regulation of smoothened signaling pathwa	88	HHIP (5.1)	GLI2 (3.7)	TAOK2 (3.3)	BNC2 (3.0)	CBX6 (3.0)	SCUBE3 (3.0)	PLAG1 (2.9)	NFATC4 (2.9)	RAF1 (2.9)	APH1A (2.8)
MP:0002270	abnormal pulmonary alveolus morphology	5.39E-08	<0.01	1.67E-10	MP:0003209	bnormal pulmonary elastic fiber morpholo	89	TBX4 (5.0)	FBN1 (4.3)	DRAM1 (4.2)	FN1 (4.2)	ABCA3 (4.1)	DAB2 (4.1)	LOXL1 (4.0)	COL6A1 (4.0)	LTBP2 (3.9)	PXDN (3.9)
ENSG00000125084	WNT1 PPI subnetwork	5.44E-08	<0.01	5.24E-13	ENSG00000085741	WNT11 PPI subnetwork	63	CRISPLD1 (4.6)	SMAD6 (3.7)	ID4 (3.7)	SMOC2 (3.6)	PTHLH (3.3)	GRRP1 (3.3)	CILP2 (3.3)	MPPED2 (3.2)	TRPS1 (3.2)	GLI2 (3.1)
GO:0042826	histone deacetylase binding	5.52E-08	<0.01	1.22E-11	ENSG00000116478	HDAC1 PPI subnetwork	39	ZMIZ1 (4.1)	EPB41L2 (3.9)	RBL2 (3.8)	EZH1 (3.4)	ZEB2 (3.1)	KIAA1267 (3.1)	TSC22D4 (3.1)	PLAG1 (3.0)	KLF3 (2.9)	HLX (2.9)
MP:0010418	perimembraneous ventricular septal defect	5.65E-08	<0.01	1.22E-10	MP:0000284	double outlet heart right ventricle	90	BMP6 (5.0)	IGF2 (4.6)	HHIP (4.6)	SMAD6 (4.5)	TBX4 (4.2)	WNT5A (4.2)	PAPPA (3.8)	PCSK5 (3.8)	AXIN2 (3.8)	GLI2 (3.6)
ENSG00000131759	RARA PPI subnetwork	5.73E-08	<0.01	6.09E-11	ENSG00000091831	ESR1 PPI subnetwork	59	MED13L (4.1)	ARNTL (4.0)	ZMIZ1 (4.0)	NCOA1 (4.0)	GLTSCR1 (3.7)	CREBBP (3.5)	ATF7IP (3.4)	PBRM1 (3.3)	SP3 (3.2)	FKBP5 (3.2)
MP:0005195	abnormal posterior eye segment morphology	5.85E-08	<0.01	7.00E-11	MP:0005193	abnormal anterior eye segment morpholog	91	TGFB2 (4.4)	COL11A1 (4.3)	PTPN14 (3.9)	SOX8 (3.8)	COL9A2 (3.4)	FOXE3 (3.4)	CHRNB1 (3.3)	CILP2 (3.3)	COL10A1 (3.3)	IGF2-AS (3.2)
MP:0000274	enlarged heart	5.85E-08	<0.01	2.49E-07	MP:0002753	dilated heart left ventricle	92	TMOD1 (4.8)	TNNC1 (4.7)	MYH7B (3.6)	PDE3A (3.6)	TRIM63 (3.5)	ENSG00000238018 (3.4)	MIR133A1 (3.3)	IGF1R (3.3)	MYPN (3.3)	NEXN (3.1)
MP:0002427	disproportionate dwarf	5.90E-08	<0.01	1.76E-13	MP:0003662	mal long bone epiphyseal plate proliferativ	42	COL10A1 (9.4)	CILP2 (8.8)	COL9A2 (8.6)	COL11A1 (7.9)	WWP2 (6.5)	FAM101A (6.0)	DMP1 (5.6)	CYTL1 (5.4)	CRISPLD1 (5.2)	SCUBE3 (4.8)
GG_BASAL_CELL_CARCINO	KEGG_BASAL_CELL_CARCINOMA	5.94E-08	<0.01	1.50E-12	ENSG00000104332	SFRP1 PPI subnetwork	93	AXIN2 (7.6)	GLI2 (6.7)	WNT5A (5.3)	SCUBE3 (5.0)	HHIP (4.7)	ENSG00000248890 (4.6)	PCSK5 (4.4)	WNT4 (4.2)	FGFR2 (4.1)	VANGL2 (4.1)
GO:0000988	protein binding transcription factor activity	6.00E-08	<0.01	5.54E-16	GO:0000989	cription factor binding transcription factor a	3	CREBBP (4.8)	RPRD2 (4.6)	KIAA1267 (4.2)	SP2 (4.2)	RARA (3.4)	RBM15B (3.4)	POLR2A (3.4)	MED13L (3.4)	GLTSCR1 (3.3)	SMAD7 (3.3)
ENSG00000141027	NCOR1 PPI subnetwork	6.19E-08	<0.01	9.71E-13	ENSG00000116478	HDAC1 PPI subnetwork	39	CREBBP (4.2)	NFIC (3.7)	RYBP (3.6)	ZMIZ1 (3.6)	ARID1B (3.5)	MED13L (3.4)	NCOR2 (3.3)	SP2 (3.3)	ZHX2 (3.2)	SP3 (3.2)
ENSG00000113658	SMAD5 PPI subnetwork	6.32E-08	<0.01	4.15E-11	REACTOME_SIGNALING_BY_BMP	REACTOME_SIGNALING_BY_BMP	24	SMAD7 (5.4)	BMPR2 (5.3)	SMAD6 (5.3)	ID4 (4.0)	ZMIZ1 (3.7)	GLTSCR1 (3.5)	LUZP1 (3.3)	FBXO30 (3.2)	BMP6 (3.2)	PCOLCE2 (3.0)
GO:0001558	regulation of cell growth	6.36E-08	<0.01	1.59E-10	GO:0001558	regulation of cell growth	33	ENSG00000246985 (3.5)	SERPINE2 (3.4)	GMNC (3.4)	COL8A1 (3.3)	CILP2 (3.2)	SLC22A5 (3.2)	PAPPA (3.1)	CYTL1 (3.1)	ZBTB4 (3.1)	PDLIM4 (2.8)
GO:0060350	endochondral bone morphogenesis	6.43E-08	<0.01	8.76E-14	GO:0060350	endochondral bone morphogenesis	18	CILP2 (6.3)	COL9A2 (5.3)	COL10A1 (5.2)	FAM101A (4.9)	CRISPLD1 (4.2)	COL11A1 (4.2)	ENSG00000257194 (4.2)	DNM3OS (4.0)	SMOC2 (3.9)	DMP1 (3.8)
MP:0003409	decreased width of hypertrophic chondrocyte zone	6.46E-08	<0.01	2.69E-11	MP:0003662	mal long bone epiphyseal plate proliferativ	42	SCARA3 (4.8)	COL9A2 (4.4)	COL10A1 (4.4)	BMP2 (4.3)	COL6A1 (4.1)	COPZ2 (4.0)	BMP6 (3.9)	DMP1 (3.9)	CYTL1 (3.8)	NPR2 (3.8)
ENSG00000100888	CHD8 PPI subnetwork	6.55E-08	<0.01	5.31E-16	ENSG00000130803	ZNF317 PPI subnetwork	48	RPRD2 (4.5)	KIAA1267 (4.2)	RNF169 (4.1)	CREBBP (3.9)	FXR2 (3.6)	RNF25 (3.5)	DET1 (3.4)	DDX6 (3.3)	CHD8 (3.3)	MED13L (3.2)
ENSG00000089094	KDM2B PPI subnetwork	6.70E-08	<0.01	1.62E-16	ENSG00000169016	E2F6 PPI subnetwork	15	RNPS1 (4.2)	RBM15B (3.4)	STAU1 (3.2)	MARK3 (3.1)	FUBP1 (3.1)	MEAF6 (3.0)	ZNF652 (3.0)	MIB1 (2.9)	RQCD1 (2.9)	SPIN1 (2.9)
GO:0060443	mammary gland morphogenesis	6.71E-08	<0.01	3.06E-13	GO:0060443	mammary gland morphogenesis	47	ESR1 (4.8)	THSD4 (3.7)	SH3PXD2A (3.6)	ENSG00000241170 (3.4)	KLHDC5 (3.3)	PDLIM4 (3.3)	ENSG00000250406 (3.3)	ENSG00000235300 (3.3)	C7orf58 (3.3)	ANO1 (3.1)
MP:0002932	abnormal joint morphology	6.91E-08	<0.01	8.59E-11	MP:0003662	mal long bone epiphyseal plate proliferativ	42	COL10A1 (5.8)	COL6A1 (5.4)	CILP2 (5.3)	PRRX1 (4.6)	FN1 (4.4)	LOXL1 (4.3)	FBN1 (4.2)	SMOC2 (4.1)	BNC2 (4.1)	ADAMTS2 (4.1)
ENSG00000033800	PIAS1 PPI subnetwork	7.13E-08	<0.01	3.42E-12	ENSG00000131788	PIAS3 PPI subnetwork	80	ESR1 (3.7)	KIAA1267 (3.4)	SMAD7 (3.3)	RARA (3.1)	PLAG1 (3.0)	EML4 (3.0)	IGF1R (2.9)	SALL1 (2.9)	NFATC1 (2.9)	ARID1B (2.8)
ENSG00000177606	JUN PPI subnetwork	7.26E-08	<0.01	2.81E-10	ENSG00000177606	JUN PPI subnetwork	94	TRIB1 (5.8)	EGR3 (5.6)	MED13L (4.0)	ETV6 (4.0)	NFIC (3.6)	KLF3 (3.6)	RB1 (3.3)	RYBP (3.2)	HLX (3.1)	RARA (2.9)
MP:0002875	decreased erythrocyte cell number	7.31E-08	<0.01	2.86E-09	MP:0002640	reticulocytosis	95	RHCE (8.4)	RHD (8.0)	SLC25A37 (6.7)	NQO1 (3.5)	BMP6 (3.0)	EDNRB (3.0)	ARHGEF12 (2.9)	KLF3 (2.9)	CMIP (2.9)	SMOX (2.8)
MP:0003667	hemangiosarcoma	7.60E-08	<0.01	9.08E-10	MP:0002038	carcinoma	96	RPS27L (3.9)	FAF1 (3.3)	SNAP47 (3.3)	RHOD (3.2)	PIK3R3 (3.0)	PHLDB3 (3.0)	WDR26 (2.8)	PDIK1L (2.7)	NQO1 (2.6)	RNF169 (2.6)
MP:0011088	partial neonatal lethality	7.61E-08	<0.01	5.16E-07	MP:0011086	partial postnatal lethality	8	GNAS (4.2)	IGF2 (4.1)	WNT5A (3.9)	FGFR2 (3.6)	NOG (3.5)	ENSG00000233101 (3.5)	EDNRB (3.3)	PTHLH (3.3)	FAM101A (3.3)	PAPPA (3.3)
GO:0050678	regulation of epithelial cell proliferation	7.64E-08	<0.01	2.03E-13	GO:0050678	regulation of epithelial cell proliferation	36	ENSG00000247735 (3.4)	SMOC2 (3.2)	SH3PXD2A (3.2)	PCSK5 (3.0)	EDNRB (2.8)	SH3D19 (2.7)	RAMP2 (2.6)	NOG (2.6)	FGFR2 (2.6)	JMJD4 (2.6)
GO:0016055	Wnt receptor signaling pathway	8.27E-08	<0.01	6.85E-14	GO:0030111	regulation of Wnt receptor signaling pathw	44	AXIN2 (5.0)	TBX6 (3.6)	L3MBTL3 (3.4)	PTHLH (3.4)	VANGL2 (3.4)	ENSG00000196355 (3.3)	WNT4 (3.1)	FGFR2 (3.1)	FAM101A (3.1)	WNT3 (3.0)
MP:0000063	decreased bone mineral density	8.40E-08	<0.01	3.85E-10	MP:0000130	abnormal trabecular bone morphology	12	DMP1 (6.4)	SERPINH1 (4.4)	IGFBP4 (4.1)	DAB2 (4.0)	WWP2 (3.9)	COL6A1 (3.9)	COL9A2 (3.8)	BMP2 (3.5)	COL10A1 (3.4)	ENPP2 (3.4)
MP:0000267	abnormal heart development	8.43E-08	<0.01	5.24E-09	MP:0000267	abnormal heart development	21	LIN28A (5.2)	SMAD6 (5.1)	ADAMTS19 (4.4)	RAMP2 (4.1)	BMP2 (3.7)	DLC1 (3.7)	SALL1 (3.6)	IGF2 (3.2)	ZMIZ1 (3.1)	FILIP1 (3.0)
MP:0000784	forebrain hypoplasia	8.56E-08	<0.01	5.33E-12	MP:0000783	abnormal forebrain morphology	97	DMRTA2 (6.6)	RLBP1 (4.8)	GLI2 (3.8)	NOTCH1 (3.3)	SLCO1C1 (3.3)	IGF2BP3 (3.1)	TTLL4 (3.1)	PPARD (3.0)	NFAT5 (2.9)	SOX8 (2.8)
MP:0000295	trabecula carnea hypoplasia	9.02E-08	<0.01	2.90E-10	MP:0011098	plete embryonic lethality during organoge	2	REST (4.3)	CLIC1P1 (3.6)	TNNC1 (3.3)	SAMD4A (3.3)	RNF169 (3.2)	RARA (3.1)	PRKAB2 (3.0)	MYH7B (3.0)	NFIC (2.9)	IGFBP4 (2.9)
ENSG00000156374	PCGF6 PPI subnetwork	9.02E-08	<0.01	2.05E-16	ENSG00000169016	E2F6 PPI subnetwork	15	RNPS1 (4.3)	RBM15B (3.3)	SETD8 (3.2)	MARK3 (3.2)	SPIN1 (3.1)	STAU1 (3.0)	ZNF652 (3.0)	BCL7A (3.0)	MEAF6 (2.8)	FUBP3 (2.8)
GO:0004713	protein tyrosine kinase activity	9.10E-08	<0.01	4.54E-08	REACTOME_SIGNALLING_BY_NGF	REACTOME_SIGNALLING_BY_NGF	98	MAP3K3 (3.8)	MAP2K4 (3.8)	MLXIP (3.6)	BAP1 (3.6)	GIT1 (3.5)	CABLES2 (3.3)	SMAD3 (3.2)	PHACTR2 (3.2)	SSH2 (3.0)	WDR26 (3.0)
GO:0051170	nuclear import	9.15E-08	<0.01	8.75E-14	GO:0051170	nuclear import	27	DLEU2 (3.5)	FSD1L (2.8)	ENSG00000228290 (2.7)	BCL6 (2.7)	CHD8 (2.7)	ZNFX1 (2.7)	TOX4 (2.6)	ENSG00000237424 (2.6)	SMAD3 (2.6)	ENSG00000182873 (2.5)
MP:0004255	abnormal spongiotrophoblast layer morphology	9.64E-08	<0.01	3.18E-16	MP:0001716	abnormal placenta labyrinth morphology	17	IGF2 (4.2)	HSD17B1 (4.0)	GH2 (3.8)	ZBTB7C (3.4)	CSH2 (3.3)	DIRC3 (3.3)	SLC16A3 (3.1)	DNM2 (3.1)	RARA (3.0)	SOX15 (3.0)
ENSG00000162616	DNAJB4 PPI subnetwork	9.85E-08	<0.01	2.80E-07	ENSG00000186879	ENSG00000186879 PPI subnetwork	76	TBX18 (3.7)	NAB1 (3.5)	RWDD3 (3.5)	LOXL1 (3.4)	MAX (3.4)	SSH2 (3.3)	C5orf51 (3.2)	KCTD9 (3.0)	FBN1 (3.0)	KLHDC5 (2.8)
MP:0010124	decreased bone mineral content	1.03E-07	<0.01	1.14E-07	MP:0000130	abnormal trabecular bone morphology	12	COL6A1 (5.8)	ANO1 (4.7)	COL11A1 (4.2)	LOXL1 (3.9)	SERPINH1 (3.9)	COL15A1 (3.9)	FBN1 (3.9)	ENPP2 (3.8)	PRRX1 (3.8)	DNM3OS (3.8)
GO:0001568	blood vessel development	1.03E-07	<0.01	5.21E-08	GO:0001568	blood vessel development	26	ADCY4 (5.4)	RAMP2 (4.7)	APOLD1 (4.7)	PLVAP (4.7)	IGFBP3 (4.1)	PXDN (3.8)	GRRP1 (3.7)	COL15A1 (3.6)	LOXL1 (3.5)	LTBP2 (3.5)
GO:0071495	cellular response to endogenous stimulus	1.05E-07	<0.01	1.15E-09	GO:0071375	ellular response to peptide hormone stimul	99	ESR1 (3.4)	FERD3L (3.3)	OR2S2 (3.3)	C20orf118 (3.2)	KLHL24 (3.1)	CSH2 (3.1)	ENSG00000157837 (2.9)	ADAMTS2 (2.9)	EPS15P1 (2.8)	ENSG00000182873 (2.8)
GO:0042733	embryonic digit morphogenesis	1.12E-07	<0.01	3.24E-12	GO:0035108	limb morphogenesis	30	NFATC4 (4.4)	NEK4 (3.9)	ADAMTS19 (3.5)	GLIS1 (3.4)	PRRX1 (3.4)	UNC119B (3.1)	TRIM4 (3.1)	KLHDC5 (3.0)	WNT5A (2.8)	SALL1 (2.8)
ENSG00000171720	HDAC3 PPI subnetwork	1.15E-07	<0.01	2.24E-13	ENSG00000116478	HDAC1 PPI subnetwork	39	ARID1B (4.2)	TLE3 (3.9)	UBN1 (3.6)	ETV6 (3.5)	VGLL4 (3.4)	MED13L (3.4)	RARA (3.4)	NFIC (3.4)	CREBBP (3.3)	SETD8 (3.3)
ENSG00000115289	PCGF1 PPI subnetwork	1.22E-07	<0.01	8.33E-17	ENSG00000169016	E2F6 PPI subnetwork	15	RNPS1 (4.2)	RBM15B (3.4)	ZNF652 (3.3)	STAU1 (3.1)	MEAF6 (3.0)	OTUD4 (3.0)	UBE2Z (3.0)	FUBP1 (2.9)	ZNF76 (2.9)	MARK3 (2.9)
ENSG00000143033	MTF2 PPI subnetwork	1.22E-07	<0.01	2.88E-10	MP:0004618	thoracic vertebral transformation	74	HOXB3 (4.2)	ENSG00000233101 (4.0)	SENP6 (3.7)	HMGA2 (3.1)	CCR10 (2.9)	ARID1B (2.9)	ENSG00000231160 (2.9)	IGF2BP2 (2.8)	RCN2 (2.7)	PDLIM4 (2.7)
MP:0000562	polydactyly	1.26E-07	<0.01	1.51E-10	GO:0035108	limb morphogenesis	30	WDR19 (5.2)	NFATC4 (4.6)	STK36 (4.0)	CROCC (3.7)	TBX4 (3.7)	IGF2BP2 (3.5)	GLI2 (3.5)	AXIN2 (3.4)	NEK4 (3.4)	SPRED1 (3.4)
ENSG00000133740	E2F5 PPI subnetwork	1.28E-07	<0.01	3.92E-11	ENSG00000189308	LIN54 PPI subnetwork	52	LCORL (4.3)	CDKN2C (4.1)	ZNF367 (3.7)	FANCI (3.6)	CENPO (3.5)	E2F1 (3.4)	CCNF (3.3)	DTL (3.3)	MEPCE (3.3)	CDKN1B (3.2)
ENSG00000010803	SCMH1 PPI subnetwork	1.30E-07	<0.01	8.02E-14	ENSG00000206215	ENSG00000206215 PPI subnetwork	81	RPRD2 (3.6)	PDIK1L (3.5)	RBM15B (3.4)	SOCS5 (3.3)	LCORL (3.3)	ZNF76 (3.2)	BCL7A (3.1)	RARA (3.0)	OTUD4 (2.9)	MARK3 (2.9)
ENSG00000150093	ITGB1 PPI subnetwork	1.32E-07	<0.01	5.18E-08	ENSG00000150093	ITGB1 PPI subnetwork	100	LAMC1 (6.5)	COL6A1 (6.2)	COL15A1 (6.1)	SERPINH1 (5.9)	LOXL1 (5.7)	FBN1 (5.5)	PXDN (5.0)	LTBP2 (4.9)	FN1 (4.8)	FBLN2 (4.0)
MP:0000160	kyphosis	1.33E-07	<0.01	3.19E-10	MP:0000150	abnormal rib morphology	6	VGLL2 (5.8)	RAPSN (5.1)	CHRNB1 (4.4)	COL8A1 (4.2)	WWP2 (4.0)	MYPN (3.8)	COL11A1 (3.6)	COL9A2 (3.4)	CORO6 (3.2)	PRRX1 (3.2)
MP:0000106	abnormal basisphenoid bone morphology	1.35E-07	<0.01	6.52E-12	MP:0000106	abnormal basisphenoid bone morphology	41	SALL1 (5.3)	FOXD2 (4.9)	WNT5A (4.8)	CRISPLD1 (4.7)	ID4 (4.7)	KCNG3 (4.7)	ISL1 (4.3)	DMP1 (4.1)	KCNK2 (3.9)	MIR214 (3.7)
MP:0004174	abnormal spine curvature	1.37E-07	<0.01	1.35E-10	MP:0000150	abnormal rib morphology	6	RGMA (4.6)	VGLL2 (4.0)	CNKSR1 (3.8)	MAST2 (3.6)	NFATC4 (3.5)	SMAD3 (3.3)	DNM3OS (3.3)	NOG (3.3)	MYPN (3.2)	MIR214 (3.2)





Supplementary Table 21. ExomeChip PASCAL results for height

Full pathway membership data can be accessed at: http://www.broadinstitute.org/mpg/depict/depict_download/reconstituted_genesets/GPL570-GPL96-GPL1261-GPL1355TermGeneZScores-MGI_MF_CC_RT_IW_BP_KEGG_z_z.txt.gz

Only results with FDR <0.05 are presented. Pascal genescore top corresponds to the 10 genes most strongly associated with height in a given gene set.

Original gene set ID	Original gene set description	Meta-gene set	Meta-gene set description	Nominal P value	False discovery rate	Pascal genescore top 1	Pascal genescore top 2	Pascal genescore top 3	Pascal genescore top 4	Pascal genescore top 5	Pascal genescore top 6	Pascal genescore top 7	Pascal genescore top 8	Pascal genescore top 9	Pascal genescore top 10
MP:0002932	abnormal joint morphology	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	3.85E-12	<0.01	GDF5 (1.769e-166)	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	SSC5D (1.610e-14)	MFGE8 (1.226e-13)	COL11A1 (1.646e-10)
MP:0000163	abnormal cartilage morphology	MP:0010029	abnormal basicranium morphology	1.28E-11	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	CHSY1 (1.007e-34)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)
MP:0005508	abnormal skeleton morphology	MP:0000130	abnormal trabecular bone morphology	1.89E-11	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	TBX4 (1.743e-13)
MP:0004359	short ulna	MP:0004359	short ulna	2.25E-11	<0.01	GDF5 (1.769e-166)	HMGA2 (4.991e-98)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)
MP:0008271	abnormal bone ossification	MP:0000130	abnormal trabecular bone morphology	2.81E-11	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	CHSY1 (1.007e-34)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	GHR (3.331e-16)
MP:0003419	delayed endochondral bone ossification	MP:0005306	abnormal phalanx morphology	3.13E-11	<0.01	GDF5 (1.769e-166)	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	ID4 (1.034e-25)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)
MP:0003055	ıbnormal long bone epiphyseal plate morpholog	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	3.20E-11	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	GHR (3.331e-16)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	LOXL4 (1.426e-11)
ENSG00000139219	COL2A1 PPI subnetwork	GO:0031012	extracellular matrix	3.40E-11	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	IL11 (2.040e-57)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	MFGE8 (1.226e-13)
GO:0005578	proteinaceous extracellular matrix	GO:0031012	extracellular matrix	5.00E-11	<0.01	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	COL7A1 (8.882e-15)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)
GO:0031012	extracellular matrix	GO:0031012	extracellular matrix	5.66E-11	<0.01	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	MFGE8 (1.226e-13)
MP:0000150	abnormal rib morphology	MP:0000150	abnormal rib morphology	8.22E-11	<0.01	GDF5 (1.769e-166)	HMGA2 (4.991e-98)	ACAN (3.868e-71)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	SLC8A3 (9.990e-11)
MP:0003120	abnormal tracheal cartilage morphology	MP:0000088	short mandible	9.87E-11	<0.01	GDF5 (1.769e-166)	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	GPR126 (2.783e-34)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)
ENSG00000092969	TGFB2 PPI subnetwork	ENSG00000092969	TGFB2 PPI subnetwork	1.46E-10	<0.01	ACAN (3.868e-71)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	MFGE8 (1.226e-13)	LAMB2 (2.200e-13)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)
GO:0005201	extracellular matrix structural constituent	GO:0031012	extracellular matrix	2.10E-10	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)
MP:0003560	osteoarthritis	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	2.31E-10	<0.01	GDF5 (1.769e-166)	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	GPR126 (2.783e-34)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	MFGE8 (1.226e-13)
GO:0030934	anchoring collagen	GO:0031012	extracellular matrix	3.14E-10	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	CRISPLD2 (4.572e-11)
MP:0000164	abnormal cartilage development	MP:0010029	abnormal basicranium morphology	4.29E-10	<0.01	GDF5 (1.769e-166)	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	ID4 (1.034e-25)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	CYTL1 (4.018e-17)
MP:0004989	decreased osteoblast cell number	MP:0000130	abnormal trabecular bone morphology	7.18E-10	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	CHSY1 (1.007e-34)	ID4 (1.034e-25)	MATN3 (2.666e-23)	KCNJ15 (9.461e-20)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	SLC8A3 (9.990e-11)
GO:0005581	collagen	GO:0031012	extracellular matrix	1.05E-09	<0.01	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	COL7A1 (8.882e-15)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	CRISPLD2 (4.572e-11)
ENSG00000119699	TGFB3 PPI subnetwork	ENSG00000092969	TGFB2 PPI subnetwork	1.55E-09	<0.01	ACAN (3.868e-71)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	LAMB2 (2.200e-13)	LATS2 (6.856e-12)
MP:0004351	short humerus	MP:0004359	short ulna	1.55E-09	<0.01	HMGA2 (4.991e-98)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	GHR (3.331e-16)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)
ENSG00000105329	TGFB1 PPI subnetwork	ENSG00000092969	TGFB2 PPI subnetwork	1.87E-09	<0.01	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	ID4 (1.034e-25)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	LAMB2 (2.200e-13)
MP:0000559	abnormal femur morphology	MP:0000130	abnormal trabecular bone morphology	2.36E-09	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	LOXL4 (1.426e-11)	SLC8A3 (9.990e-11)
MP:0000131	abnormal long bone epiphysis morphology	MP:0010029	abnormal basicranium morphology	3.65E-09	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	DUSP1 (5.151e-14)	COL9A2 (5.762e-14)	MFGE8 (1.226e-13)	LATS2 (6.856e-12)
MP:0008277	abnormal sternum ossification	MP:0000150	abnormal rib morphology	4.03E-09	<0.01	GDF5 (1.769e-166)	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	FGFR4 (7.881e-64)	CHSY1 (1.007e-34)	C14orf39 (4.983e-31)	TBX15 (3.226e-24)	TET2 (7.234e-24)	ZNF354C (6.439e-15)	COL9A2 (5.762e-14)
ENSG00000142798	HSPG2 PPI subnetwork	GO:0031012	extracellular matrix	4.94E-09	<0.01	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	LATS2 (6.856e-12)	SNAI1 (1.391e-11)	CRISPLD2 (4.572e-11)	PAPPA (1.177e-10)	COL11A1 (1.646e-10)	SFRP4 (1.517e-09)
GO:0044420	extracellular matrix part	GO:0031012	extracellular matrix	6.69E-09	<0.01	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	COL7A1 (8.882e-15)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)
GO:0048705	skeletal system morphogenesis	GO:0048704	embryonic skeletal system morphogenesis	7.53E-09	<0.01	GDF5 (1.769e-166)	HMGA2 (4.991e-98)	ACAN (3.868e-71)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	IL11RA (5.211e-13)	ADAMTS10 (1.248e-11)	GLT8D2 (2.621e-09)
MP:0000074	abnormal neurocranium morphology	MP:0010029	abnormal basicranium morphology	8.10E-09	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	ID4 (1.034e-25)	MATN3 (2.666e-23)	COL9A2 (5.762e-14)	PIGC (6.716e-12)	SNAI1 (1.391e-11)	COL11A1 (1.646e-10)
MP:0003723	abnormal long bone morphology	MP:0004359	short ulna	8.30E-09	<0.01	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	LOXL4 (1.426e-11)	SLC8A3 (9.990e-11)
MP:0005353	abnormal patella morphology	MP:0004359	short ulna	9.55E-09	<0.01	GDF5 (1.769e-166)	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)
MP:0005587	abnormal Meckel's cartilage morphology	MP:0000088	short mandible	9.57E-09	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	SIX6 (5.246e-43)	FBN2 (2.465e-32)	C14orf39 (4.983e-31)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)
GO:0005518	collagen binding	GO:0031012	extracellular matrix	9.80E-09	<0.01	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	CYTL1 (4.018e-17)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)
MP:0000547	short limbs	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	1.03E-08	<0.01	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	SNAI1 (1.391e-11)	LOXL4 (1.426e-11)	SLC8A3 (9.990e-11)
MP:0000157	abnormal sternum morphology	MP:0000150	abnormal rib morphology	1.13E-08	<0.01	GDF5 (1.769e-166)	ADAMTS17 (2.835e-129	HMGA2 (4.991e-98)	FBN2 (2.465e-32)	ID4 (1.034e-25)	TBX15 (3.226e-24)	LATS2 (6.856e-12)	PDLIM4 (1.237e-10)	TTC28 (3.793e-10)	ROR2 (8.806e-10)
GO:0019838	growth factor binding	GO:0031012	extracellular matrix	1.28E-08	<0.01	ACAN (3.868e-71)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	LRP5 (1.354e-14)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	LAMB2 (2.200e-13)	LATS2 (6.856e-12)
ENSG00000077942	FBLN1 PPI subnetwork	GO:0031012	extracellular matrix	1.37E-08	<0.01	MTMR11 (5.149e-81)	ADAMTSL3 (1.781e-78)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	LRP5 (1.354e-14)	SSC5D (1.610e-14)	PKD1 (3.930e-14)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	ADAMTS10 (1.248e-11)
GO:0030199	collagen fibril organization	MP:0008438	abnormal cutaneous collagen fibril morphology	1.41E-08	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	SFRP4 (1.517e-09)
MP:0000088	short mandible	MP:0000088	short mandible	1.45E-08	<0.01	GDF5 (1.769e-166)	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	SNAI1 (1.391e-11)
MP:0000445	short snout	MP:0000088	short mandible	1.56E-08	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	CHSY1 (1.007e-34)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	SNAI1 (1.391e-11)	SLC8A3 (9.990e-11)
MP:0004471	short nasal bone	MP:0000088	short mandible	1.62E-08	<0.01	ADAMTS17 (2.835e-129	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)
ENSG00000163453	IGFBP7 PPI subnetwork	GO:0031012	extracellular matrix	2.29E-08	<0.01	ACAN (3.868e-71)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)	SFRP4 (1.517e-09)
GO:0002062	chondrocyte differentiation	GO:0032330	regulation of chondrocyte differentiation	2.36E-08	<0.01	GDF5 (1.769e-166)	ADAMTS17 (2.835e-129	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	LOXL4 (1.426e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)
MP:0000060	delayed bone ossification	MP:0000150	abnormal rib morphology	2.49E-08	<0.01	ADAMTS17 (2.835e-129	ACAN (3.868e-71)	PTCH1 (3.154e-47)	CHSY1 (1.007e-34)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	SLC8A3 (9.990e-11)
ENSG00000087245	MMP2 PPI subnetwork	ENSG00000149968	MMP3 PPI subnetwork	2.65E-08	<0.01	ACAN (3.868e-71)	IL11 (2.040e-57)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	DUSP1 (5.151e-14)	COL9A2 (5.762e-14)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	SNAI1 (1.391e-11)
MP:0000443	abnormal snout morphology	MP:0010029	abnormal basicranium morphology	2.92E-08	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	ID4 (1.034e-25)	TBX15 (3.226e-24)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	LOXL4 (1.426e-11)	SUSD5 (6.052e-07)	COL27A1 (7.444e-07)
GO:0050840	extracellular matrix binding	GO:0005604	basement membrane	2.96E-08	<0.01	ACAN (3.868e-71)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	LAMB2 (2.200e-13)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)
MP:0000435	shortened head	MP:0000088	short mandible	2.98E-08	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	COL9A2 (5.762e-14)	FRZB (4.484e-10)	GLT8D2 (2.621e-09)	COL10A1 (5.366e-08)	SUSD5 (6.052e-07)
MP:0000162	lordosis	MP:0010029	abnormal basicranium morphology	2.98E-08	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	MFGE8 (1.226e-13)	LOXL4 (1.426e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)
MP:0010103	small thoracic cage	MP:0010029	abnormal basicranium morphology	3.37E-08	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	ID4 (1.034e-25)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	CREB3L2 (5.230e-17)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	LOXL4 (1.426e-11)	COL11A1 (1.646e-10)
GO:0030198	extracellular matrix organization	GO:0031012	extracellular matrix	3.60E-08	<0.01	ACAN (3.868e-71)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	SSC5D (1.610e-14)	PKD1 (3.930e-14)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	LAMB2 (2.200e-13)	ADAMTS10 (1.248e-11)	CRISPLD2 (4.572e-11)
GO:0043062	extracellular structure organization	GO:0031012	extracellular matrix	3.60E-08	<0.01	ACAN (3.868e-71)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	SSC5D (1.610e-14)	PKD1 (3.930e-14)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	LAMB2 (2.200e-13)	ADAMTS10 (1.248e-11)	CRISPLD2 (4.572e-11)
GO:0005539	glycosaminoglycan binding	GO:0005539	glycosaminoglycan binding	3.68E-08	<0.01	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)
GO:0001871	pattern binding	GO:0005539	glycosaminoglycan binding	4.66E-08	<0.01	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	SERPINA1 (6.951e-45)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)
GO:0030247	polysaccharide binding	GO:0005539	glycosaminoglycan binding	4.66E-08	<0.01	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	SERPINA1 (6.951e-45)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)
ENSG00000149968	MMP3 PPI subnetwork	ENSG00000149968	MMP3 PPI subnetwork	5.09E-08	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	IL11 (2.040e-57)	LOXL2 (3.110e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	LOXL4 (1.426e-11)	CRISPLD2 (4.572e-11)	PAPPA (1.177e-10)
MP:0004686	decreased length of long bones	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	8.03E-08	<0.01	ACAN (3.868e-71)	FNDC3B (2.855e-67)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	GHR (3.331e-16)	COL9A2 (5.762e-14)	MFGE8 (1.226e-13)	LOXL4 (1.426e-11)	SLC8A3 (9.990e-11)
MP:0000558	abnormal tibia morphology	MP:0004359	short ulna	8.50E-08	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	LOXL4 (1.426e-11)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)
MP:0000137	abnormal vertebrae morphology	MP:0000150	abnormal rib morphology	8.79E-08	<0.01	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	PTPN13 (1.744e-18)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	AXIN2 (1.070e-11)	SNAI1 (1.391e-11)
GO:0005583	fibrillar collagen	GO:0048407	platelet-derived growth factor binding	9.03E-08	<0.01	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	SFRP4 (1.517e-09)
MP:0010029	abnormal basicranium morphology	MP:0010029	abnormal basicranium morphology	9.06E-08	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	ID4 (1.034e-25)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	SNAI1 (1.391e-11)
MP:0004509	abnormal pelvic girdle bone morphology	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	9.49E-08	<0.01	ACAN (3.868e-71)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	LOXL4 (1.426e-11)	COL11A1 (1.646e-10)
TOME SIGNALING BY	REACTOME_SIGNALING_BY_PDGF	WNSTREAM SIGNAL	REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION	9.94E-08	<0.01	ACAN (3.868e-71)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	SLC35E3 (1.128e-09)	LTBP3 (1.192e-08)	MMP14 (3.438e-08)
ENSG00000115414	FN1 PPI subnetwork	GO:0031012	extracellular matrix	1.16E-07	<0.01	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	LOXL2 (3.110e-19)	SSC5D (1.610e-14)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	CRISPLD2 (4.572e-11)	FRZB (4.484e-10)	ITIH4 (4.941e-09)	DKK3 (8.789e-09)
GF BETA SIGNALING P	KEGG_TGF_BETA_SIGNALING_PATHWAY	TOME SIGNALING BY	REACTOME_SIGNALING_BY_BMP	1.36E-07	<0.01	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	ID4 (1.034e-25)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	AXIN2 (1.070e-11)	SNAI1 (1.391e-11)	PAPPA (1.177e-10)	SFRP4 (1.517e-09)
MP:0002113	abnormal skeleton development	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	1.36E-07	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	GHR (3.331e-16)	COL9A2 (5.762e-14)	LATS2 (6.856e-12)	SNAI1 (1.391e-11)
GO:0051216	cartilage development	GO:0060350	endochondral bone morphogenesis	1.41E-07	<0.01	GDF5 (1.769e-166)	ADAMTS17 (2.835e-129	ACAN (3.868e-71)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	LOXL4 (1.426e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)
MP:0000141	abnormal vertebral body morphology	MP:0000150	abnormal rib morphology	1.64E-07	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	CYTL1 (4.018e-17)	LRP5 (1.354e-14)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	COL11A1 (1.646e-10)	FRZB (4.484e-10)
MP:0003662	ıormal long bone epiphyseal plate proliferative z	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	1.69E-07	<0.01	ACAN (3.868e-71)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	GHR (3.331e-16)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	MFGE8 (1.226e-13)	LOXL4 (1.426e-11)	CRISPLD2 (4.572e-11)	SLC8A3 (9.990e-11)
ENSG00000105664	COMP PPI subnetwork	MP:0010029	abnormal basicranium morphology	1.70E-07	<0.01	ACAN (3.868e-71)	PADI2 (1.559e-23)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	COL11A1 (1.646e-10)	FRZB (4.484e-10)	DKK3 (8.789e-09)
ECM RECEPTOR INTER/	KEGG_ECM_RECEPTOR_INTERACTION	GO:0031012	extracellular matrix	1.90E-07	<0.01	ACAN (3.868e-71)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	COL7A1 (8.882e-15)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	LAMB2 (2.200e-13)
GO:0005520	insulin-like growth factor binding	ENSG00000092969	TGFB2 PPI subnetwork	2.15E-07	<0.01	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	LRP5 (1.354e-14)	MFGE8 (1.226e-13)	LAMC1 (1.456e-13)	LAMB2 (2.200e-13)	PAPPA (1.177e-10)	PDLIM4 (1.237e-10)	SFRP4 (1.517e-09)	GLT8D2 (2.621e-09)
GO:0060351	evelopment involved in endochondral bone mor	GO:0060350	endochondral bone morphogenesis	2.15E-07	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	LOXL4 (1.426e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)	SFRP4 (1.517e-09)
MP:0005503	abnormal tendon morphology	MP:0008438	abnormal cutaneous collagen fibril morphology	2.32E-07	<0.01	ACAN (3.868e-71)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)
MP:0008272	abnormal endochondral bone ossification	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	3.08E-07	<0.01	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	PLEKHG4 (4.774e-15)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	IL11RA (5.211e-13)	SEMA4G (1.454e-12)
ENSG00000157227	MMP14 PPI subnetwork	ENSG00000149968	MMP3 PPI subnetwork	3.63E-07	<0.01	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	DKK3 (8.789e-09)	ECM2 (2.406e-08)
GO:0060349	bone morphogenesis	GO:0060350	endochondral bone morphogenesis	3.75E-07	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	IL11RA (5.211e-13)	ADAMTS10 (1.248e-11)	COL11A1 (1.646e-10)
MP:0006397	disorganized long bone epiphyseal plate	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	4.12E-07	<0.01	ACAN (3.868e-71)	MATN3 (2.666e-23)	KCNJ15 (9.461e-20)	DUSP1 (5.151e-14)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	LOXL4 (1.426e-11)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)	SLC35E3 (1.128e-09)
MP:0003109	short femur	MP:0000130	abnormal trabecular bone morphology	4.75E-07	<0.01	ACAN (3.868e-71)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	KCNJ15 (9.461e-20)	CYTL1 (4.018e-17)	GHR (3.331e-16)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	LOXL4 (1.426e-11)	SLC8A3 (9.990e-11)
ENSG00000136999	NOV PPI subnetwork	GO:0031012	extracellular matrix	4.79E-07	<0.01	MATN3 (2.666e-23)	COL7A1 (8.882e-15)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	LATS2 (6.856e-12)	CRISPLD2 (4.572e-11)	CCDC8 (3.518e-09)	DKK3 (8.789e-09)	SERPINF1 (6.272e-08)
GO:0001503	ossification	GO:0045667	regulation of osteoblast differentiation	4.83E-07	<0.01	ADAMTS17 (2.835e-129	ACAN (3.868e-71)	PTCH1 (3.154e-47)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)	SFRP4 (1.517e-09)	LTBP3 (1.192e-08)
MP:0002115	abnormal limb bone morphology	MP:0005306	abnormal phalanx morphology	5.01E-07	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)
ENSG00000116962	NID1 PPI subnetwork	GO:0005604	basement membrane	5.24E-07	<0.01	MTMR11 (5.149e-81)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	LRP5 (1.354e-14)	SSC5D (1.610e-14)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	LAMB2 (2.200e-13)	CRISPLD2 (4.572e-11)
ENSG00000101680	LAMA1 PPI subnetwork	GO:0005604	basement membrane	6.83E-07	<0.01	MTMR11 (5.149e-81)	GPR126 (2.783e-34)	LOXL2 (3.110e-19)	AMOTL1 (1.776e-15)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	LAMB2 (2.200e-13)	KANK2 (3.725e-12)	LTBP3 (1.192e-08)
MP:0005543	corneal thinning	GO:0031012	extracellular matrix	7.67E-07	<0.01	ADAMTSL3 (1.781e-78)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	SSC5D (1.610e-14)	IL11RA (5.211e-13)	COL11A1 (1.646e-10)	FRZB (4.484e-10)	ROR2 (8.806e-10)
MP:0002657	chondrodystrophy	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	7.74E-07	<0.01	HMGA2 (4.991e-98)	ACAN (3.868e-71)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	MFGE8 (1.226e-13)	SNAI1 (1.391e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)
MP:0000130	abnormal trabecular bone morphology	MP:0000130	abnormal trabecular bone morphology	7.96E-07	<0.01	ACAN (3.868e-71)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	LOXL4 (1.426e-11)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)	SFRP4 (1.517e-09)	GLT8D2 (2.621e-09)
MP:0002116	abnormal craniofacial bone morphology	MP:0000088	short mandible	8.33E-07	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	COL11A1 (1.646e-10)	TTC28 (3.793e-10)
ENSG00000183691	NOG PPI subnetwork	ENSG00000183691	NOG PPI subnetwork	9.38E-07	<0.01	ADAMTS17 (2.835e-129	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	AXIN2 (1.070e-11)
MP:0000065	abnormal bone marrow cavity morphology	MP:0000130	abnormal trabecular bone morphology	1.01E-06	<0.01	ACAN (3.868e-71)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	SSC5D (1.610e-14)	DUSP1 (5.151e-14)	COL9A2 (5.762e-14)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)
GO:0000228	nuclear chromosome	GO:0044427	chromosomal part	1.13E-06	<0.01	NCAPG (3.734e-39)	CSE1L (5.476e-35)	FANCE (2.452e-29)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)
ENSG00000105695	MAG PPI subnetwork	GO:0048407	platelet-derived growth factor binding	1.17E-06	<0.01	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)
GO:0001501	skeletal system development	GO:0048704	embryonic skeletal system morphogenesis	1.21E-06	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	LOXL4 (1.426e-11)	COL11A1 (1.646e-10)	ROR2 (8.806e-10)	GLT8D2 (2.621e-09)
MP:0009780	abnormal chondrocyte physiology	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	1.22E-06	<0.01	ACAN (3.868e-71)	MATN3 (2.666e-23)	CREB3L2 (5.230e-17)	COL9A2 (5.762e-14)	LATS2 (6.856e-12)	LOXL4 (1.426e-11)	SNAP47 (1.473e-11)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)	COL10A1 (5.366e-08)
MP:0004355	short radius	MP:0004359	short ulna	1.36E-06	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	C3orf18 (1.044e-14)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	COL11A1 (1.646e-10)	SFRP4 (1.517e-09)
MP:0004608	abnormal cervical axis morphology	MP:0003048	abnormal cervical vertebrae morphology	1.45E-06	<0.01	HMGA2 (4.991e-98)	ACAN (3.868e-71)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL11A1 (1.646e-10)	TTC28 (3.793e-10)	ROR2 (8.806e-10)	SNED1 (2.001e-06)
MP:0005269	abnormal occipital bone morphology	MP:0010029	abnormal basicranium morphology	1.45E-06	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	ID4 (1.034e-25)	TBX15 (3.226e-24)	COL9A2 (5.762e-14)	IL11RA (5.211e-13)	FRZB (4.484e-10)	SUSD5 (6.052e-07)	SNED1 (2.001e-06)
MP:0000550	abnormal forelimb morphology	GO:0035108	limb morphogenesis	1.46E-06	<0.01	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	ID4 (1.034e-25)	PTPN13 (1.744e-18)	AXIN2 (1.070e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)	ROR2 (8.806e-10)	DKK3 (8.789e-09)
MP:0006395	abnormal epiphyseal plate morphology	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	1.48E-06	<0.01	ACAN (3.868e-71)	PADI2 (1.559e-23)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	LOXL4 (1.426e-11)	COL11A1 (1.646e-10)	TPCN2 (3.656e-10)	SFRP4 (1.517e-09)	COL10A1 (5.366e-08)
ENSG00000166147	FBN1 PPI subnetwork	GO:0031012	extracellular matrix	1.58E-06	<0.01	ADAMTSL3 (1.781e-78)	FNDC3B (2.855e-67)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	SSC5D (1.610e-14)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	CRISPLD2 (4.572e-11)	PAPPA (1.177e-10)
MP:0002764	short tibia	MP:0004359	short ulna	1.61E-06	<0.01	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)
ENSG00000182492	BGN PPI subnetwork	GO:0031012	extracellular matrix	1.63E-06	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	CLPS (1.269e-21)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	ADAMTS10 (1.248e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)
MP:0001533	abnormal skeleton physiology	MP:0000130	abnormal trabecular bone morphology	1.85E-06	<0.01	ACAN (3.868e-71)	MATN3 (2.666e-23)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	LOXL4 (1.426e-11)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)	SFRP4 (1.517e-09)	GLT8D2 (2.621e-09)	VGLL4 (4.089e-09)
MP:0002544	brachydactyly	MP:0005306	abnormal phalanx morphology	1.86E-06	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	FBN2 (2.465e-32)	ID4 (1.034e-25)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	COL11A1 (1.646e-10)	TTC28 (3.793e-10)
MP:0003795	abnormal bone structure	MP:0000130	abnormal trabecular bone morphology	2.19E-06	<0.01	ACAN (3.868e-71)	KCNJ15 (9.461e-20)	DPEP1 (4.885e-15)	COL15A1 (1.245e-13)	LOXL4 (1.426e-11)	COL11A1 (1.646e-10)	SFRP4 (1.517e-09)	LTBP3 (1.192e-08)	ECM2 (2.406e-08)	ADAMTS2 (3.966e-08)
ENSG00000163520	FBLN2 PPI subnetwork	GO:0005604	basement membrane	2.22E-06	<0.01	FNDC3B (2.855e-67)	LOXL2 (3.110e-19)	NCOR2 (2.928e-18)	SSC5D (1.610e-14)	PKD1 (3.930e-14)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	LAMB2 (2.200e-13)	FRZB (4.484e-10)
MP:0005006	abnormal osteoblast physiology	MP:0000130	abnormal trabecular bone morphology	2.35E-06	<0.01	ACAN (3.868e-71)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	COL9A2 (5.762e-14)	SNAI1 (1.391e-11)	LOXL4 (1.426e-11)	SLC8A3 (9.990e-11)	PAPPA (1.177e-10)	COL11A1 (1.646e-10)	SFRP4 (1.517e-09)
MP:0000063	decreased bone mineral density	MP:0000130	abnormal trabecular bone morphology	2.43E-06	<0.01	ACAN (3.868e-71)	CLPS (1.269e-21)	KCNJ15 (9.461e-20)	LOXL2 (3.110e-19)	SLC17A1 (9.858e-17)	GHR (3.331e-16)	COL9A2 (5.762e-14)	SNAI1 (1.391e-11)	LOXL4 (1.426e-11)	PAPPA (1.177e-10)
MP:0000029	abnormal malleus morphology	MP:0005106	abnormal incus morphology	2.48E-06	<0.01	HMGA2 (4.991e-98)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	ID4 (1.034e-25)	TBX15 (3.226e-24)	CYTL1 (4.018e-17)	SNAI1 (1.391e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)
MP:0002114	abnormal axial skeleton morphology	MP:0000150	abnormal rib morphology	2.77E-06	<0.01	HMGA2 (4.991e-98)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	ID4 (1.034e-25)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	COL9A2 (5.762e-14)	SLC8A3 (9.990e-11)	ROR2 (8.806e-10)
ENSG00000147536	GINS4 PPI subnetwork	ENSG00000135336	ORC3 PPI subnetwork	2.91E-06	<0.01	NCAPG (3.734e-39)	FANCE (2.452e-29)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	RIBC2 (2.631e-12)
'OME NCAM1 INTERAC	REACTOME_NCAM1_INTERACTIONS	GO:0048407	platelet-derived growth factor binding	2.94E-06	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	FBN2 (2.465e-32)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	COL7A1 (8.882e-15)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)
MP:0000042	abnormal organ of Corti morphology	MP:0004404	cochlear outer hair cell degeneration	3.25E-06	<0.01	ADAMTSL3 (1.781e-78)	FGFR4 (7.881e-64)	IGF2 (7.130e-19)	CYTL1 (4.018e-17)	GHR (3.331e-16)	COL9A2 (5.762e-14)	LATS2 (6.856e-12)	COL10A1 (5.366e-08)	BMP3 (2.632e-07)	ADAMTS5 (1.159e-06)
MP:0004704	short vertebral column	MP:0010029	abnormal basicranium morphology	3.31E-06	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	LOXL4 (1.426e-11)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)	FADS1 (1.804e-08)
GO:0060348	bone development	GO:0060350	endochondral bone morphogenesis	3.64E-06	<0.01	ACAN (3.868e-71)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	SSC5D (1.610e-14)	COL9A2 (5.762e-14)	IL11RA (5.211e-13)	ADAMTS10 (1.248e-11)	COL11A1 (1.646e-10)	SFRP4 (1.517e-09)	GLT8D2 (2.621e-09)
ENSG00000187498	COL4A1 PPI subnetwork	GO:0005604	basement membrane	3.83E-06	<0.01	FBN2 (2.465e-32)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)	PLXND1 (2.498e-09)	DKK3 (8.789e-09)
GO:0005604	basement membrane	GO:0005604	basement membrane	3.84E-06	<0.01	MTMR11 (5.149e-81)	FBN2 (2.465e-32)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	COL7A1 (8.882e-15)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	LAMB2 (2.200e-13)	CRISPLD2 (4.572e-11)
ENSG00000101003	GINS1 PPI subnetwork	ENSG00000135336	ORC3 PPI subnetwork	3.95E-06	<0.01	NCAPG (3.734e-39)	FANCE (2.452e-29)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	RIBC2 (2.631e-12)
ENSG00000188064	WNT7B PPI subnetwork	ENSG00000085741	WNT11 PPI subnetwork	4.06E-06	<0.01	ADAMTSL3 (1.781e-78)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	ID4 (1.034e-25)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	TET1 (1.732e-14)	FRZB (4.484e-10)	ROR2 (8.806e-10)	SFRP4 (1.517e-09)
GO:0048407	platelet-derived growth factor binding	GO:0048407	platelet-derived growth factor binding	4.14E-06	<0.01	ACAN (3.868e-71)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	COL7A1 (8.882e-15)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)
GO:0010463	mesenchymal cell proliferation	GO:0010464	regulation of mesenchymal cell proliferation	4.22E-06	<0.01	ADAMTS17 (2.835e-129	ADAMTSL3 (1.781e-78)	TBX15 (3.226e-24)	CCDC108 (5.440e-15)	TBX4 (1.743e-13)	VGLL4 (4.089e-09)	RAB23 (5.586e-07)	DNMBP (1.177e-06)	B4GALNT3 (5.199e-05)	EYA4 (8.932e-05)
ENSG00000140285	FGF7 PPI subnetwork	ENSG00000158815	FGF17 PPI subnetwork	4.26E-06	<0.01	ACAN (3.868e-71)	FBN2 (2.465e-32)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	COL9A2 (5.762e-14)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	TBX4 (1.743e-13)	DLC1 (5.507e-09)	DENND2A (2.394e-08)
MP:0002187	abnormal fibula morphology	MP:0004359	short ulna	4.29E-06	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	COL11A1 (1.646e-10)	ADAMTS2 (3.966e-08)	COL10A1 (5.366e-08)
ENSG00000035928	RFC1 PPI subnetwork	E LAGGING STRAND	REACTOME_LAGGING_STRAND_SYNTHESIS	4.47E-06	<0.01	NCAPG (3.734e-39)	PML (2.204e-37)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	TACC3 (4.007e-11)
MP:0004672	short ribs	MP:0000150	abnormal rib morphology	4.75E-06	<0.01	ACAN (3.868e-71)	FGFR4 (7.881e-64)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	IP6K3 (7.105e-15)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	PDLIM4 (1.237e-10)	COL11A1 (1.646e-10)
GO:0090189	ion of branching involved in ureteric bud morph	GO:0001658	branching involved in ureteric bud morphogenesis	5.20E-06	<0.01	GDF5 (1.769e-166)	HMGA2 (4.991e-98)	ADAMTSL3 (1.781e-78)	FGFR4 (7.881e-64)	ZNF19 (5.466e-08)	DNAH10 (8.391e-07)	KIAA1614 (5.611e-06)	FGFRL1 (2.303e-05)	WNK4 (3.343e-05)	B4GALNT3 (5.199e-05)
MP:0004734	small thoracic cavity	GO:0060350	endochondral bone morphogenesis	5.39E-06	<0.01	GDF5 (1.769e-166)	CCDC91 (4.005e-33)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	COL11A1 (1.646e-10)	FRZB (4.484e-10)	COL10A1 (5.366e-08)	SUSD5 (6.052e-07)
MP:0008438	abnormal cutaneous collagen fibril morphology	MP:0008438	abnormal cutaneous collagen fibril morphology	6.01E-06	<0.01	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	SFRP4 (1.517e-09)	GLT8D2 (2.621e-09)	LTBP3 (1.192e-08)	ECM2 (2.406e-08)
MP:0000116	abnormal tooth development	MP:0005358	abnormal incisor morphology	6.30E-06	<0.01	FBN2 (2.465e-32)	MATN3 (2.666e-23)	ZBTB7B (7.298e-17)	AMOTL1 (1.776e-15)	COL9A2 (5.762e-14)	PDLIM4 (1.237e-10)	COL11A1 (1.646e-10)	ROR2 (8.806e-10)	SFRP4 (1.517e-09)	GLT8D2 (2.621e-09)
KEGG FOCAL ADHESIOI	KEGG_FOCAL_ADHESION	ENSG00000150093	ITGB1 PPI subnetwork	6.52E-06	<0.01	LOXL2 (3.110e-19)	COL7A1 (8.882e-15)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	LAMB2 (2.200e-13)	KANK2 (3.725e-12)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	PLEC (3.446e-10)
MP:0000111	cleft palate	MP:0009890	cleft secondary palate	6.52E-06	<0.01	HMGA2 (4.991e-98)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	IGF2 (7.130e-19)	LRP5 (1.354e-14)	COL11A1 (1.646e-10)	FRZB (4.484e-10)	ROR2 (8.806e-10)
MP:0004462	small basisphenoid bone	MP:0000088	short mandible	6.87E-06	<0.01	GDF5 (1.769e-166)	ADAMTS17 (2.835e-129	HMGA2 (4.991e-98)	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	FBN2 (2.465e-32)	ROR2 (8.806e-10)	COL10A1 (5.366e-08)	SUSD5 (6.052e-07)	SNED1 (2.001e-06)
MP:0000159	abnormal xiphoid process morphology	MP:0000088	short mandible	6.95E-06	<0.01	FBN2 (2.465e-32)	C14orf39 (4.983e-31)	ID4 (1.034e-25)	TBX15 (3.226e-24)	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	CYTL1 (4.018e-17)	ZNF354C (6.439e-15)	ROR2 (8.806e-10)	CCDC8 (3.518e-09)
MP:0000554	abnormal carpal bone morphology	MP:0005306	abnormal phalanx morphology	7.32E-06	<0.01	GDF5 (1.769e-166)	HMGA2 (4.991e-98)	ADAMTSL3 (1.781e-78)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	TBX4 (1.743e-13)	CCDC8 (3.518e-09)	LTBP1 (2.929e-06)	SULF2 (1.170e-05)	MECOM (4.955e-05)
ENSG00000142156	COL6A1 PPI subnetwork	GO:0048407	platelet-derived growth factor binding	7.88E-06	<0.01	ACAN (3.868e-71)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	COL9A2 (5.762e-14)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	PAPPA (1.177e-10)	COL11A1 (1.646e-10)	DLC1 (5.507e-09)
ENSG00000011465	DCN PPI subnetwork	GO:0031012	extracellular matrix	8.10E-06	<0.01	LOXL2 (3.110e-19)	COL7A1 (8.882e-15)	SSC5D (1.610e-14)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	ADAMTS10 (1.248e-11)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	GLT8D2 (2.621e-09)	DKK3 (8.789e-09)
ENSG00000164754	RAD21 PPI subnetwork	ENSG00000164754	RAD21 PPI subnetwork	8.31E-06	<0.01	NCAPG (3.734e-39)	ZNF638 (1.506e-26)	CCDC66 (4.241e-22)	FAM208A (7.755e-20)	PKN2 (8.562e-18)	ATAD5 (4.441e-16)	DNMT1 (1.199e-13)	TACC3 (4.007e-11)	TOP2A (1.673e-10)	SETD2 (4.492e-08)
MP:0000440	domed cranium	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	8.42E-06	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	MATN3 (2.666e-23)	COL9A2 (5.762e-14)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)	MEGF8 (4.174e-10)	DISP1 (4.454e-09)	SLC39A13 (3.673e-07)	SUSD5 (6.052e-07)
ENSG00000087303	NID2 PPI subnetwork	GO:0031012	extracellular matrix	8.91E-06	<0.01	LOXL2 (3.110e-19)	LRP5 (1.354e-14)	SSC5D (1.610e-14)	PKD1 (3.930e-14)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	ADAMTS10 (1.248e-11)	MYH7B (4.453e-10)	PLXND1 (2.498e-09)	LTBP3 (1.192e-08)
ENSG00000146674	IGFBP3 PPI subnetwork	)R IGF ACTIVITY BY	GROWTH FACTOR IGF ACTIVITY BY INSULIN:LIKE GF	9.49E-06	<0.01	IL11 (2.040e-57)	FBN2 (2.465e-32)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	COL7A1 (8.882e-15)	COL15A1 (1.245e-13)	PAPPA (1.177e-10)	GCKR (1.678e-10)	ADAMTS2 (3.966e-08)	SERPINF1 (6.272e-08)
ENSG00000113140	SPARC PPI subnetwork	GO:0048407	platelet-derived growth factor binding	1.05E-05	<0.01	ACAN (3.868e-71)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	COL15A1 (1.245e-13)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	PLXND1 (2.498e-09)	DLC1 (5.507e-09)	MMP14 (3.438e-08)	ADAMTS2 (3.966e-08)
)ME CELL CYCLE CHECI	REACTOME_CELL_CYCLE_CHECKPOINTS	TOME SYNTHESIS OI	REACTOME_SYNTHESIS_OF_DNA	1.08E-05	<0.01	PSMC5 (1.440e-40)	NCAPG (3.734e-39)	CSE1L (5.476e-35)	SLBP (1.576e-25)	RMI1 (2.377e-21)	MTCH2 (1.750e-17)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)
GO:0043394	proteoglycan binding	GO:0043394	proteoglycan binding	1.11E-05	<0.01	ADAMTSL3 (1.781e-78)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	SFRP4 (1.517e-09)	CCDC8 (3.518e-09)	ECM2 (2.406e-08)	ADAMTS2 (3.966e-08)
MP:0005352	small cranium	MP:0004359	short ulna	1.17E-05	<0.01	ACAN (3.868e-71)	FBN2 (2.465e-32)	LOXL2 (3.110e-19)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	LOXL4 (1.426e-11)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)	DLC1 (5.507e-09)	SERPINF1 (6.272e-08)
MP:0008395	abnormal osteoblast differentiation	MP:0000130	abnormal trabecular bone morphology	1.21E-05	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	IL11 (2.040e-57)	FBN2 (2.465e-32)	IL11RA (5.211e-13)	PAPPA (1.177e-10)	GLT8D2 (2.621e-09)	SERPINF1 (6.272e-08)	CD248 (2.235e-07)	CYP1B1 (4.225e-07)
MP:0000154	rib fusion	MP:0000150	abnormal rib morphology	1.24E-05	<0.01	HMGA2 (4.991e-98)	FBN2 (2.465e-32)	TBX15 (3.226e-24)	IGF2 (7.130e-19)	AXIN2 (1.070e-11)	SNAI1 (1.391e-11)	RARA (1.673e-10)	ROR2 (8.806e-10)	GLT8D2 (2.621e-09)	STRA6 (4.215e-08)
MP:0000556	abnormal hindlimb morphology	MP:0000088	short mandible	1.25E-05	<0.01	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	PLAG1 (2.977e-23)	CYTL1 (4.018e-17)	TBX4 (1.743e-13)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)	ROR2 (8.806e-10)
ENSG00000125378	BMP4 PPI subnetwork	ENSG00000153162	BMP6 PPI subnetwork	1.29E-05	<0.01	ADAMTS17 (2.835e-129	PTCH1 (3.154e-47)	ID4 (1.034e-25)	MATN3 (2.666e-23)	IL11RA (5.211e-13)	CRISPLD2 (4.572e-11)	PAPPA (1.177e-10)	RAB23 (5.586e-07)	MOS (1.217e-06)	COMP (2.568e-06)
MP:0004986	abnormal osteoblast morphology	MP:0000130	abnormal trabecular bone morphology	1.31E-05	<0.01	ACAN (3.868e-71)	KCNJ15 (9.461e-20)	LOXL2 (3.110e-19)	COL15A1 (1.245e-13)	COL11A1 (1.646e-10)	SFRP4 (1.517e-09)	GLT8D2 (2.621e-09)	DKK3 (8.789e-09)	ECM2 (2.406e-08)	ADAMTS2 (3.966e-08)
ENSG00000136982	DSCC1 PPI subnetwork	'OME CELL CYCLE M	REACTOME_CELL_CYCLE_MITOTIC	1.32E-05	<0.01	NCAPG (3.734e-39)	CSE1L (5.476e-35)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	TACC3 (4.007e-11)
ENSG00000116062	MSH6 PPI subnetwork	ENSG00000132383	RPA1 PPI subnetwork	1.34E-05	<0.01	NCAPG (3.734e-39)	CSE1L (5.476e-35)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	ANAPC4 (3.197e-13)
1E G1S:SPECIFIC TRAN!	REACTOME_G1S:SPECIFIC_TRANSCRIPTION	ENSG00000135336	ORC3 PPI subnetwork	1.36E-05	<0.01	NCAPG (3.734e-39)	SLBP (1.576e-25)	RMI1 (2.377e-21)	CCND3 (5.507e-17)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	RIBC2 (2.631e-12)	TACC3 (4.007e-11)
3G PATHWAYS IN CAN	KEGG_PATHWAYS_IN_CANCER	HRONIC MYELOID LI	KEGG_CHRONIC_MYELOID_LEUKEMIA	1.41E-05	<0.01	FNDC3B (2.855e-67)	IL11 (2.040e-57)	PTCH1 (3.154e-47)	COL7A1 (8.882e-15)	LAMC1 (1.456e-13)	AXIN2 (1.070e-11)	MAP3K1 (1.847e-10)	MMP14 (3.438e-08)	STRA6 (4.215e-08)	PDE7A (3.420e-05)
ENSG00000020922	MRE11A PPI subnetwork	ENSG00000132383	RPA1 PPI subnetwork	1.47E-05	<0.01	CSE1L (5.476e-35)	ZNF638 (1.506e-26)	POLR2A (6.186e-19)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	KNTC1 (2.992e-10)	THADA (4.668e-10)
ENSG00000104320	NBN PPI subnetwork	IOLOGOUS RECOME	REACTOME HOMOLOGOUS RECOMBINATION REPAII	1.50E-05	<0.01	NCAPG (3.734e-39)	CSE1L (5.476e-35)	SLBP (1.576e-25)	FAM208A (7.755e-20)	ATAD5 (4.441e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	KNTC1 (2.992e-10)	THADA (4.668e-10)	FANCI (9.308e-09)
MP:0002427	disproportionate dwarf	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	1.51E-05	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	MFGE8 (1.226e-13)	LOXL4 (1.426e-11)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)
MP:0000165	ıormal long bone hypertrophic chondrocyte zo	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	1.58E-05	<0.01	ACAN (3.868e-71)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	GHR (3.331e-16)	COL9A2 (5.762e-14)	LOXL4 (1.426e-11)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)	ROR2 (8.806e-10)
ENSG00000111602	TIMELESS PPI subnetwork	ENSG00000135336	ORC3 PPI subnetwork	1.62E-05	<0.01	NCAPG (3.734e-39)	SLBP (1.576e-25)	RMI1 (2.377e-21)	PHF20 (1.518e-18)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	RIBC2 (2.631e-12)
MP:0003209	abnormal pulmonary elastic fiber morphology	MP:0003209	abnormal pulmonary elastic fiber morphology	1.66E-05	<0.01	KCNJ15 (9.461e-20)	TBX4 (1.743e-13)	KANK2 (3.725e-12)	SLC39A8 (3.920e-12)	VEPH1 (4.371e-09)	DLC1 (5.507e-09)	DKK3 (8.789e-09)	LTBP3 (1.192e-08)	ARHGEF25 (1.417e-08)	DENND2A (2.394e-08)
ENSG00000106399	RPA3 PPI subnetwork	ENSG00000132383	RPA1 PPI subnetwork	1.75E-05	<0.01	NCAPG (3.734e-39)	FANCE (2.452e-29)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	ANAPC4 (3.197e-13)
ENSG00000113522	RAD50 PPI subnetwork	ENSG00000132383	RPA1 PPI subnetwork	1.84E-05	<0.01	NCAPG (3.734e-39)	CSE1L (5.476e-35)	SLBP (1.576e-25)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	SMC1B (4.877e-13)	TACC3 (4.007e-11)
ENSG00000168496	FEN1 PPI subnetwork	E LAGGING STRAND	REACTOME_LAGGING_STRAND_SYNTHESIS	1.85E-05	<0.01	NCAPG (3.734e-39)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	TACC3 (4.007e-11)	TOP2A (1.673e-10)
ENSG00000150093	ITGB1 PPI subnetwork	ENSG00000150093	ITGB1 PPI subnetwork	1.87E-05	<0.01	FNDC3B (2.855e-67)	LOXL2 (3.110e-19)	CYTL1 (4.018e-17)	COL7A1 (8.882e-15)	MFGE8 (1.226e-13)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	LAMB2 (2.200e-13)	KANK2 (3.725e-12)	CRISPLD2 (4.572e-11)
ENSG00000149311	ATM PPI subnetwork	ENSG00000132383	RPA1 PPI subnetwork	1.88E-05	<0.01	CSE1L (5.476e-35)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	CEP120 (2.456e-10)	KNTC1 (2.992e-10)	THADA (4.668e-10)
ACTOME G1S TRANSIT	REACTOME_G1S_TRANSITION	TOME SYNTHESIS OI	REACTOME_SYNTHESIS_OF_DNA	1.97E-05	<0.01	PSMC5 (1.440e-40)	NCAPG (3.734e-39)	CSE1L (5.476e-35)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	PSMD2 (2.019e-11)
MP:0010418	perimembraneous ventricular septal defect	MP:0000284	double outlet heart right ventricle	2.00E-05	<0.01	ADAMTSL3 (1.781e-78)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	IGF2 (7.130e-19)	TBX4 (1.743e-13)	AXIN2 (1.070e-11)	PAPPA (1.177e-10)	TTC28 (3.793e-10)	REST (4.717e-10)	ROR2 (8.806e-10)
GO:0004386	helicase activity	GO:0004386	helicase activity	2.06E-05	<0.01	CSE1L (5.476e-35)	ZNF638 (1.506e-26)	CCDC66 (4.241e-22)	ATAD5 (4.441e-16)	DNMT1 (1.199e-13)	ANAPC4 (3.197e-13)	METTL13 (1.169e-11)	R3HCC1L (1.518e-10)	THADA (4.668e-10)	DROSHA (3.262e-09)
GO:0072498	embryonic skeletal joint development	GO:0048704	embryonic skeletal system morphogenesis	2.07E-05	<0.01	GDF5 (1.769e-166)	ADAMTS17 (2.835e-129	ACAN (3.868e-71)	COL9A2 (5.762e-14)	LOXL4 (1.426e-11)	DNAH10 (8.391e-07)	DNMBP (1.177e-06)	KIAA1586 (2.184e-06)	LECT1 (3.167e-06)	OMD (3.722e-05)
GO:0060350	endochondral bone morphogenesis	GO:0060350	endochondral bone morphogenesis	2.07E-05	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	ADAMTS10 (1.248e-11)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)	FRZB (4.484e-10)	COL10A1 (5.366e-08)
ENSG00000127586	CHTF18 PPI subnetwork	'OME CELL CYCLE M	REACTOME_CELL_CYCLE_MITOTIC	2.09E-05	<0.01	NCAPG (3.734e-39)	CSE1L (5.476e-35)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	TACC3 (4.007e-11)
ENSG00000171992	SYNPO PPI subnetwork	ENSG00000134184	GSTM1 PPI subnetwork	2.10E-05	<0.01	MTMR11 (5.149e-81)	MICAL1 (3.255e-20)	LAMC1 (1.456e-13)	PLEC (3.446e-10)	NQO1 (1.440e-09)	MMP14 (3.438e-08)	STARD13 (1.165e-07)	AAGAB (2.718e-07)	MAP4 (2.422e-06)	FLNB (1.945e-05)
ENSG00000100297	MCM5 PPI subnetwork	ENSG00000135336	ORC3 PPI subnetwork	2.20E-05	<0.01	NCAPG (3.734e-39)	CSE1L (5.476e-35)	FANCE (2.452e-29)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)
MP:0002835	abnormal cranial suture morphology	MP:0005358	abnormal incisor morphology	2.30E-05	<0.01	ADAMTS17 (2.835e-129	ACAN (3.868e-71)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	TBX4 (1.743e-13)	PIGC (6.716e-12)	COL11A1 (1.646e-10)	SFRP4 (1.517e-09)	MMP14 (3.438e-08)	ADAMTS2 (3.966e-08)
GO:0000793	condensed chromosome	ENSG00000134690	CDCA8 PPI subnetwork	2.35E-05	<0.01	NCAPG (3.734e-39)	CSE1L (5.476e-35)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	SMC1B (4.877e-13)	TACC3 (4.007e-11)	TOP2A (1.673e-10)
ENSG00000105011	ASF1B PPI subnetwork	GO:0044427	chromosomal part	2.35E-05	<0.01	NCAPG (3.734e-39)	HIST1H1T (4.497e-37)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	TACC3 (4.007e-11)
ENSG00000002745	WNT16 PPI subnetwork	ENSG00000180855	ZNF443 PPI subnetwork	2.53E-05	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	PTCH1 (3.154e-47)	CHSY1 (1.007e-34)	FRZB (4.484e-10)	GLTSCR1 (2.010e-07)	YEATS2 (3.166e-06)	LECT1 (3.167e-06)	SLC38A2 (3.860e-05)	ZNF608 (2.923e-04)
DIATED REGULATION C	ME E2F MEDIATED REGULATION OF DNA REP	ENSG00000135336	ORC3 PPI subnetwork	2.55E-05	<0.01	NCAPG (3.734e-39)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	RIBC2 (2.631e-12)	TACC3 (4.007e-11)	TOP2A (1.673e-10)
ENSG00000120708	TGFBI PPI subnetwork	GO:0048407	platelet-derived growth factor binding	2.55E-05	<0.01	ACAN (3.868e-71)	LOXL2 (3.110e-19)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	COL11A1 (1.646e-10)	FRZB (4.484e-10)	MMP14 (3.438e-08)	ADAMTS2 (3.966e-08)	SERPINF1 (6.272e-08)
MP:0004200	decreased fetal size	MP:0011087	complete neonatal lethality	2.60E-05	<0.01	GDF5 (1.769e-166)	FNDC3B (2.855e-67)	PTCH1 (3.154e-47)	FBN2 (2.465e-32)	IGF2 (7.130e-19)	LRP5 (1.354e-14)	SNAI1 (1.391e-11)	DISP1 (4.454e-09)	COL27A1 (7.444e-07)	NPR3 (9.385e-06)
SIGNALING FOR NEU	OME NCAM SIGNALING FOR NEURITE OUT:GI	CTOME AXON GUID/	REACTOME_AXON_GUIDANCE	2.84E-05	<0.01	ACAN (3.868e-71)	FBN2 (2.465e-32)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	TET1 (1.732e-14)	COL9A2 (5.762e-14)	COL15A1 (1.245e-13)	COL11A1 (1.646e-10)	ADAMTS2 (3.966e-08)	CD248 (2.235e-07)
CTOME G0 AND EARL'	REACTOME_G0_AND_EARLY_G1	KEGG_CELL_CYCLE	KEGG_CELL_CYCLE	2.85E-05	<0.01	NCAPG (3.734e-39)	SLBP (1.576e-25)	RMI1 (2.377e-21)	CCND3 (5.507e-17)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	PRIM1 (8.882e-16)	TACC3 (4.007e-11)	TOP2A (1.673e-10)	KNTC1 (2.992e-10)
GO:0044454	nuclear chromosome part	GO:0044427	chromosomal part	2.88E-05	<0.01	NCAPG (3.734e-39)	FANCE (2.452e-29)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	SMC1B (4.877e-13)
GO:0001502	cartilage condensation	MP:0010029	abnormal basicranium morphology	2.91E-05	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	COL11A1 (1.646e-10)	FRZB (4.484e-10)	FAM198A (8.935e-10)	COL10A1 (5.366e-08)	SUSD5 (6.052e-07)
ENSG00000014138	POLA2 PPI subnetwork	E LAGGING STRAND	REACTOME_LAGGING_STRAND_SYNTHESIS	2.99E-05	<0.01	NCAPG (3.734e-39)	CSE1L (5.476e-35)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	TACC3 (4.007e-11)
ENSG00000126351	THRA PPI subnetwork	ENSG00000182093	WRB PPI subnetwork	3.01E-05	<0.01	HMGA2 (4.991e-98)	ZNFX1 (3.160e-39)	TET2 (7.234e-24)	PKN2 (8.562e-18)	CNOT4 (1.110e-16)	RARA (1.673e-10)	ATF7IP (1.440e-09)	TNRC6A (5.394e-09)	SAMD9 (3.297e-05)	PTPN12 (4.382e-05)
MP:0008151	increased diameter of long bones	MP:0000130	abnormal trabecular bone morphology	3.12E-05	<0.01	ACAN (3.868e-71)	FBN2 (2.465e-32)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	COL9A2 (5.762e-14)	LOXL4 (1.426e-11)	SLC8A3 (9.990e-11)	PDLIM4 (1.237e-10)	SFRP4 (1.517e-09)	DKK3 (8.789e-09)
ENSG00000049540	ELN PPI subnetwork	GO:0031012	extracellular matrix	3.22E-05	<0.01	MTMR11 (5.149e-81)	SLC22A4 (8.752e-31)	LOXL2 (3.110e-19)	COL15A1 (1.245e-13)	VILL (6.099e-12)	CRISPLD2 (4.572e-11)	COL11A1 (1.646e-10)	GLT8D2 (2.621e-09)	MMP14 (3.438e-08)	ADAMTS2 (3.966e-08)
GO:0010464	regulation of mesenchymal cell proliferation	GO:0010464	regulation of mesenchymal cell proliferation	3.36E-05	<0.01	ADAMTS17 (2.835e-129	ADAMTSL3 (1.781e-78)	TBX15 (3.226e-24)	TBX4 (1.743e-13)	VGLL4 (4.089e-09)	DNMBP (1.177e-06)	EYA4 (8.932e-05)	RSPO2 (9.382e-05)	DDR2 (2.242e-04)	RNF43 (9.141e-04)
ENSG00000133119	RFC3 PPI subnetwork	E LAGGING STRAND	REACTOME_LAGGING_STRAND_SYNTHESIS	3.36E-05	<0.01	NCAPG (3.734e-39)	CSE1L (5.476e-35)	FANCE (2.452e-29)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	TACC3 (4.007e-11)
MP:0000166	abnormal chondrocyte morphology	MP:0003662	abnormal long bone epiphyseal plate proliferative zon	3.37E-05	<0.01	GDF5 (1.769e-166)	ACAN (3.868e-71)	MATN3 (2.666e-23)	CYTL1 (4.018e-17)	GHR (3.331e-16)	COL9A2 (5.762e-14)	TBX4 (1.743e-13)	LOXL4 (1.426e-11)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)
'OR IGF ACTIVITY BY I	OWTH FACTOR IGF ACTIVITY BY INSULIN:LIKE	)R IGF ACTIVITY BY	GROWTH FACTOR IGF ACTIVITY BY INSULIN:LIKE GF	3.50E-05	<0.01	FBN2 (2.465e-32)	LOXL2 (3.110e-19)	IGF2 (7.130e-19)	SSC5D (1.610e-14)	COL15A1 (1.245e-13)	CRISPLD2 (4.572e-11)	PAPPA (1.177e-10)	PDLIM4 (1.237e-10)	GCKR (1.678e-10)	STRA6 (4.215e-08)
ENSG00000109072	SEBOX PPI subnetwork	GO:0031093	platelet alpha granule lumen	3.50E-05	<0.01	IL11 (2.040e-57)	SERPINA1 (6.951e-45)	LOXL2 (3.110e-19)	LCAT (2.665e-13)	PAPPA (1.177e-10)	GCKR (1.678e-10)	FRZB (4.484e-10)	DKK3 (8.789e-09)	COL5A2 (5.320e-06)	NGF (1.472e-05)
ENSG00000071909	MYO3B PPI subnetwork	ENSG00000134184	GSTM1 PPI subnetwork	3.64E-05	<0.01	MTMR11 (5.149e-81)	MICAL1 (3.255e-20)	LAMC1 (1.456e-13)	LATS2 (6.856e-12)	NQO1 (1.440e-09)	AAGAB (2.718e-07)	NOSTRIN (8.954e-07)	MAP4 (2.422e-06)	CYP1A1 (8.681e-06)	FLNB (1.945e-05)
GO:0043395	heparan sulfate proteoglycan binding	GO:0043394	proteoglycan binding	3.66E-05	<0.01	ADAMTSL3 (1.781e-78)	ACAN (3.868e-71)	MATN3 (2.666e-23)	IGF2 (7.130e-19)	GHR (3.331e-16)	COL11A1 (1.646e-10)	SFRP4 (1.517e-09)	COL10A1 (5.366e-08)	FBP1 (9.470e-08)	ITIH1 (5.558e-07)
MP:0000160	kyphosis	MP:0000150	abnormal rib morphology	3.78E-05	<0.01	TBX15 (3.226e-24)	LOXL2 (3.110e-19)	MYPN (4.441e-16)	IP6K3 (7.105e-15)	COL9A2 (5.762e-14)	SCN4A (4.217e-13)	SLC8A3 (9.990e-11)	COL11A1 (1.646e-10)	MEGF8 (4.174e-10)	SFRP4 (1.517e-09)
)ME MITOTIC G1:G1S	REACTOME_MITOTIC_G1:G1S_PHASES	TOME SYNTHESIS OI	REACTOME_SYNTHESIS_OF_DNA	3.86E-05	<0.01	PSMC5 (1.440e-40)	NCAPG (3.734e-39)	CSE1L (5.476e-35)	SLBP (1.576e-25)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	TACC3 (4.007e-11)	TOP2A (1.673e-10)
GO:0071229	cellular response to acid	GO:0071418	cellular response to amine stimulus	3.87E-05	<0.01	COL7A1 (8.882e-15)	COL15A1 (1.245e-13)	PIGC (6.716e-12)	CRISPLD2 (4.572e-11)	GLT8D2 (2.621e-09)	ADAMTS2 (3.966e-08)	SERPINF1 (6.272e-08)	DOPEY1 (1.078e-07)	CD248 (2.235e-07)	ADAMTS5 (1.159e-06)
TOME UNWINDING OI	REACTOME_UNWINDING_OF_DNA	ENSG00000135336	ORC3 PPI subnetwork	3.94E-05	<0.01	NCAPG (3.734e-39)	FANCE (2.452e-29)	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	RIBC2 (2.631e-12)
ENSG00000125686	MED1 PPI subnetwork	ENSG00000164758	MED30 PPI subnetwork	4.01E-05	<0.01	RREB1 (8.917e-36)	POLR2A (6.186e-19)	NCOR2 (2.928e-18)	ZNF142 (1.443e-15)	SEC16A (6.125e-13)	RARA (1.673e-10)	BRPF3 (1.048e-08)	GAB1 (2.089e-08)	SPTY2D1 (2.038e-06)	BOD1L1 (2.821e-06)
ENSG00000174371	EXO1 PPI subnetwork	ENSG00000132383	RPA1 PPI subnetwork	4.09E-05	<0.01	SLBP (1.576e-25)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	WDR90 (6.661e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	SMC1B (4.877e-13)	RIBC2 (2.631e-12)	KNTC1 (2.992e-10)
MP:0009866	abnormal aorta wall morphology	MP:0008438	abnormal cutaneous collagen fibril morphology	4.29E-05	<0.01	LOXL2 (3.110e-19)	PKD1 (3.930e-14)	COL15A1 (1.245e-13)	LAMC1 (1.456e-13)	IL11RA (5.211e-13)	GLT8D2 (2.621e-09)	LTBP3 (1.192e-08)	MMP14 (3.438e-08)	ADAMTS2 (3.966e-08)	SERPINF1 (6.272e-08)
ENSG00000126215	XRCC3 PPI subnetwork	IOLOGOUS RECOME	REACTOME HOMOLOGOUS RECOMBINATION REPAII	4.33E-05	<0.01	CCDC91 (4.005e-33)	RMI1 (2.377e-21)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	PRIM1 (8.882e-16)	KNTC1 (2.992e-10)	ZDHHC24 (7.677e-10)	NQO1 (1.440e-09)	FANCI (9.308e-09)	ZRANB3 (2.057e-08)

MP:0010876	decreased bone volume	MP:0010869	decreased bone trabecula number	2.70E-03	<0.05	ACAN (3.868e-71)	IGF2 (7.130e-19)	COL15A1 (1.245e-13)	CRISPLD2 (4.572e-11)	DLG5 (1.637e-10)	B3GNT7 (2.285e-09)	GLT8D2 (2.621e-09)	LTBP3 (1.192e-08)	OLFML2A (2.517e-05)	OSMR (3.242e-04)			
ENSG00000145423	SFBP2 PPI subnetwork	ENSG00000104332	SFRP1 PPI subnetwork	2.71E-03	<0.05	LOXL2 (3.110e-19)	AMOTL1 (1.770e-15)	COL7A1 (8.882e-15)	AXIN2 (1.070e-11)	RORZ (8.806e-10)	GLT8D2 (2.621e-09)	ADAMTS2 (3.966e-08)	STRA6 (4.215e-08)	BCAM (8.975e-06)	OLFML2A (2.517e-05)			
ENSG00000134690	CDCA8 PPI subnetwork	ENSG00000134690	CDCA8 PPI subnetwork	2.71E-03	<0.05	NCAPG (3.734e-39)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	TACC3 (4.007e-11)	TOP2A (1.673e-10)	KNTC1 (2.992e-10)	FANCI (9.308e-09)	ZRANB3 (2.057e-08)			
/ATION OF CHAPERON TOME	ACTIVATION OF CHAPERONES BY IRE1	UNFOLDED PROTEI	REACTOME_UNFOLDED_PROTEIN_RESPONSE	2.73E-03	<0.05	FNDC3B (2.855e-67)	EIF2AK3 (8.237e-24)	CREB3L2 (5.230e-17)	SSR1 (3.131e-14)	SEC16A (6.125e-13)	RPN2 (1.137e-12)	NUCB2 (7.502e-12)	HDLBP (6.709e-09)	EDEM2 (2.328e-08)	OS9 (6.003e-08)			
IBITION OF PRE-REPLICABILED	INHIBITION OF PRE-REPLICATION COM	ENSG00000215536	CRC3 PPI subnetwork	2.74E-03	<0.05	NCAPG (3.734e-39)	RNR1 (2.377e-21)	ATAD5 (4.441e-16)	PRIM1 (8.882e-16)	TACC3 (4.007e-11)	TOP2A (1.673e-10)	KNTC1 (2.992e-10)	FANCI (9.308e-09)	ZRANB3 (2.057e-08)	CENPO (3.148e-08)			
MP:0002724	enhanced wound healing	MP:0005554	decreased circulating creatinine level	2.75E-03	<0.05	LOXL2 (3.110e-19)	LATS2 (6.856e-12)	PAPPA (1.177e-10)	ADAMTS2 (3.966e-08)	SERPINF1 (6.272e-08)	TNS4 (4.110e-07)	CLDN20 (3.509e-06)	H6PD (4.026e-06)	DSE (1.650e-05)	COL1A1 (3.366e-05)			
MP:0004395	increased cochlear inner hair cell number	MP:0005106	abnormal incus morphology	2.76E-03	<0.05	HMGA2 (4.991e-08)	FBN2 (2.465e-32)	ID4 (1.034e-25)	TBX15 (3.226e-24)	BCAM (8.975e-06)	GLI3 (7.099e-05)	EYA4 (8.932e-05)	ZNF423 (1.133e-04)	LRP4 (1.729e-04)	ZFHX4 (3.783e-04)			
ENSG00000161283	ALPP PPI subnetwork	ENSG00000130803	ZNF317 PPI subnetwork	2.76E-03	<0.05	NGDS (5.584e-26)	COASY (1.635e-09)	TADK2 (2.610e-09)	ZNF646 (4.169e-09)	TNRC6A (5.394e-09)	DOPEY1 (1.078e-07)	AP5B1 (1.787e-07)	HERC1 (1.637e-06)	XPC (1.497e-05)	AKAP9 (2.908e-05)			
ENSG00000163539	CLASP2 PPI subnetwork	ENSG00000134690	CDCA8 PPI subnetwork	2.77E-03	<0.05	NCAPG (3.734e-39)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	PRIM1 (8.882e-16)	TACC3 (4.007e-11)	TOP2A (1.673e-10)	KNTC1 (2.992e-10)	FANCI (9.308e-09)	ZRANB3 (2.057e-08)	CENPO (3.148e-08)			
ENSG00000083642	PDS5B PPI subnetwork	ENSG00000164754	RAD21 PPI subnetwork	2.77E-03	<0.05	ZNF638 (1.506e-26)	PRKG2 (8.562e-18)	PDHX1L (2.222e-16)	MYH7B (4.453e-10)	SETD2 (4.492e-08)	TAF2 (3.822e-07)	SMCHD1 (1.905e-06)	PBRM1 (2.600e-06)	ARIDAA (1.000e-04)	JMJD1C (1.255e-04)			
ENSG00000104332	SFRP1 PPI subnetwork	ENSG00000104332	SFRP1 PPI subnetwork	2.77E-03	<0.05	PTPN13 (1.744e-18)	AMOTL1 (1.770e-15)	COL7A1 (8.882e-15)	AXIN2 (1.070e-11)	PPL (2.679e-11)	RORZ (8.806e-10)	GLT8D2 (2.621e-09)	ADAMTS2 (3.966e-08)	STRA6 (4.215e-08)	GPR98 (1.569e-07)			
ENSG00000106483	SFRP4 PPI subnetwork	ENSG00000104332	SFRP1 PPI subnetwork	2.77E-03	<0.05	PTPN13 (1.744e-18)	AMOTL1 (1.770e-15)	COL7A1 (8.882e-15)	AXIN2 (1.070e-11)	PPL (2.679e-11)	RORZ (8.806e-10)	GLT8D2 (2.621e-09)	ADAMTS2 (3.966e-08)	STRA6 (4.215e-08)	GPR98 (1.569e-07)			
ENSG00000120057	SFRP5 PPI subnetwork	ENSG00000104332	SFRP1 PPI subnetwork	2.77E-03	<0.05	PTPN13 (1.744e-18)	AMOTL1 (1.770e-15)	COL7A1 (8.882e-15)	AXIN2 (1.070e-11)	PPL (2.679e-11)	RORZ (8.806e-10)	GLT8D2 (2.621e-09)	ADAMTS2 (3.966e-08)	STRA6 (4.215e-08)	GPR98 (1.569e-07)			
ENSG00000124571	XPO5 PPI subnetwork	ENSG00000013275	PSMC4 PPI subnetwork	2.81E-03	<0.05	CPNE1 (1.173e-40)	CSE1L (5.476e-35)	ANAPC4 (3.197e-13)	METTL13 (1.169e-11)	PSMD2 (2.019e-11)	DPP3 (4.758e-10)	EIF4G1 (2.275e-06)	IGHMBP2 (3.517e-05)	FUI (5.439e-05)	EFTUD2 (8.621e-05)			
GO:0004065	arylsulfatase activity	GO:0008484	sulfuric ester hydrolase activity	2.81E-03	<0.05	MATN3 (2.666e-23)	LOXL2 (3.110e-19)	SSC5D (1.610e-14)	COL11A1 (1.646e-10)	COL10A1 (5.366e-08)	COMP (2.568e-06)	COL14A1 (1.470e-05)	THBS3 (2.786e-05)	THBS2 (4.623e-04)	MANBA (6.319e-04)			
ENSG00000148835	TAF5 PPI subnetwork	ENSG00000085231	TAF9 PPI subnetwork	2.81E-03	<0.05	HIST1H1T (4.497e-37)	SNRPC (9.208e-33)	AP4E1 (1.312e-13)	MRPL43 (1.543e-12)	HIST1H1C (1.187e-09)	SUGP1 (8.619e-08)	TAF2 (3.822e-07)	HIST1H1B (1.957e-05)	HIST1H2BI (2.364e-05)	TAF11 (5.462e-05)			
ENSG00000031691	CENPQ PPI subnetwork	ENSG00000134690	CDCA8 PPI subnetwork	2.83E-03	<0.05	NCAPG (3.734e-39)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	TACC3 (4.007e-11)	TOP2A (1.673e-10)	KNTC1 (2.992e-10)	FANCI (9.308e-09)	ZRANB3 (2.057e-08)			
ENSG00000123219	CENPK PPI subnetwork	ENSG00000134690	CDCA8 PPI subnetwork	2.85E-03	<0.05	NCAPG (3.734e-39)	ATAD5 (4.441e-16)	E2F1 (4.441e-16)	PRIM1 (8.882e-16)	DNMT1 (1.199e-13)	TACC3 (4.007e-11)	TOP2A (1.673e-10)	KNTC1 (2.992e-10)	FANCI (9.308e-09)	ZRANB3 (2.057e-08)			
MP:0009113	decreased white fat cell size	MP:0008034	enhanced lipolysis	2.85E-03	<0.05	ZBTB4 (2.293e-31)	FANCE (2.452e-29)	NSD1 (5.584e-26)	ABHD15 (7.448e-23)	GHR (3.331e-16)	AP4E1 (1.312e-13)	GPAM (2.024e-06)	PEMT (2.286e-06)	MLXIPL (2.456e-04)	CIDEC (5.087e-04)			
ENSG00000198824	CHAMP1 PPI subnetwork	ENSG00000149016	TUT1 PPI subnetwork	2.88E-03	<0.05	UBE2Z (2.196e-24)	POLR2A (6.186e-19)	USP36 (5.218e-11)	NUP153 (4.232e-08)	PCNXL3 (1.092e-07)	THUMPD1 (1.828e-07)	COPG1 (6.597e-07)	PBRM1 (2.600e-06)	WDR6 (7.596e-06)	HECTD1 (3.562e-05)			
ENSG00000127337	YEATS4 PPI subnetwork	ENSG00000080603	SRCAP PPI subnetwork	2.90E-03	<0.05	HIST1H1T (4.497e-37)	POLR2A (6.186e-19)	HIST1H1C (1.187e-09)	MTERFD2 (1.884e-06)	HIST1H1B (1.957e-05)	HIST1H2BI (2.364e-05)	CSPP1 (1.642e-04)	HIST1H1E (1.290e-03)	HINFP (7.850e-03)	CCDC12 (3.500e-02)			

Supplementary Table 22. GWAS PASCAL results for height

Full pathway membership data can be accessed at: http://www.broadinstitute.org/mpg/depict/depict_download/reconstituted_genesets/GPL570-GPL96-GPL1261-GPL1355TermGeneZScores-MGI_MF_CC_RT_IW_BP_KEGG_z_z.txt.gz

Only results with FDR <0.05 are presented. Pascal genescore top corresponds to the 10 genes most strongly associated with height in a given gene set.

Original gene set ID	Original gene set description	Meta-gene set	Meta-gene set description	Nominal P value	False discovery rate	Pascal genescore top 1	Pascal genescore top 2	Pascal genescore top 3	Pascal genescore top 4	Pascal genescore top 5	Pascal genescore top 6	Pascal genescore top 7	Pascal genescore top 8	Pascal genescore top 9	Pascal genescore top 10
ENSG00000169045	HNRNPH1 PPI subnetwork	ENSG00000153187	HNRNPU PPI subnetwork	2.58E-08	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	RBM12 (6.00e-52)	RBM39 (9.20e-51)	DDX42 (1.47e-38)	FTSJ3 (6.30e-32)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)
GO:0002062	chondrocyte differentiation	GO:0032330	regulation of chondrocyte differentiation	1.15E-07	<0.01	GDF5 (1.400e-59)	COLGALT2 (2.880e-50)	PRKG2 (5.810e-47)	SCUBE3 (2.960e-28)	ADAMTS3 (1.040e-20)	ACAN (1.200e-19)	OMD (4.441e-16)	CRISPLD1 (3.308e-14)	FAM101A (1.259e-12)	PITX1 (4.189e-11)
ENSG00000169813	HNRNPF PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.16E-07	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)
ENSG00000181222	POLR2A PPI subnetwork	ENSG00000005075	POLR2J PPI subnetwork	1.25E-07	<0.01	RBM12 (6.00e-52)	RBM39 (9.20e-51)	SF3B4 (8.80e-50)	DDX42 (1.47e-38)	FUBP3 (6.32e-25)	DDX27 (4.40e-24)	TRA2A (5.52e-24)	NCL (1.35e-18)	FNBP4 (2.88e-17)	SLBP (6.00e-17)
ENSG00000108883	EFTUD2 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.57E-07	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	CSE1L (2.220e-15)
ENSG00000125944	HNRNPR PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.72E-07	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	RBM12 (6.00e-52)	RBM39 (9.20e-51)	DDX42 (1.47e-38)	FTSJ3 (6.30e-32)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)
ENSG00000065978	YBX1 PPI subnetwork	ENSG00000153187	HNRNPU PPI subnetwork	2.52E-07	<0.01	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	RBM12 (6.00e-52)	RBM39 (9.20e-51)	DDX42 (1.47e-38)	HIST1H2BD (2.17e-28)	HIST1H2AC (2.61e-26)	HEXIM1 (4.56e-26)	TRA2A (5.52e-24)	HIST2H2BE (4.80e-22)
ENSG00000162231	NXF1 PPI subnetwork	GO:0050658	RNA transport	5.42E-07	<0.01	RBM12 (6.000e-52)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	OTUD4 (2.400e-20)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)	SUPT16H (3.182e-12)
MP:0002657	chondrodystrophy	MP:0003662	abnormal long bone epiphyseal plate proliferative zone	5.60E-07	<0.01	PRKG2 (5.810e-47)	BMP6 (2.700e-38)	SCUBE3 (2.960e-28)	ACAN (1.200e-19)	FBLN5 (3.220e-19)	OMD (4.441e-16)	CRISPLD1 (3.308e-14)	SLC39A13 (5.951e-14)	FAM101A (1.259e-12)	FLNB (1.568e-12)
ENSG00000144028	SNRNP200 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	6.53E-07	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	FTSJ3 (6.300e-32)	FUBP3 (6.320e-25)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)
GO:0051216	cartilage development	GO:0060350	endochondral bone morphogenesis	7.46E-07	<0.01	GDF5 (1.400e-59)	COLGALT2 (2.880e-50)	PRKG2 (5.810e-47)	SCUBE3 (2.960e-28)	NFATC4 (1.920e-21)	IHH (1.600e-20)	ACAN (1.200e-19)	OMD (4.441e-16)	CRISPLD1 (3.308e-14)	OGN (7.494e-14)
ENSG00000132475	H3F3B PPI subnetwork	ENSG00000196226	HIST1H2BB PPI subnetwork	1.03E-06	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000163041	H3F3A PPI subnetwork	ENSG00000196226	HIST1H2BB PPI subnetwork	1.03E-06	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000196285	ENSG00000196285 PPI subnetwork	ENSG00000196226	HIST1H2BB PPI subnetwork	1.03E-06	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000135486	HNRNPA1 PPI subnetwork	ENSG00000153187	HNRNPU PPI subnetwork	1.12E-06	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	HEXIM1 (4.560e-26)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	POLR2A (7.661e-15)
ENSG00000177733	HNRNPA0 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.55E-06	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	CSE1L (2.220e-15)
MP:0003419	delayed endochondral bone ossification	MP:0005306	abnormal phalanx morphology	2.49E-06	<0.01	GDF5 (1.400e-59)	ADAMTSL3 (9.600e-29)	IHH (1.600e-20)	ACAN (1.200e-19)	ID4 (3.331e-16)	OMD (4.441e-16)	ASPN (4.441e-16)	ECM2 (1.332e-15)	CRISPLD1 (3.308e-14)	OGN (7.494e-14)
ENSG00000104852	SNRNP70 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	2.82E-06	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	STAG1 (1.998e-15)
ENSG00000128908	INO80 PPI subnetwork	ENSG00000196226	HIST1H2BB PPI subnetwork	3.12E-06	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
MP:0003120	abnormal tracheal cartilage morphology	MP:0000088	short mandible	3.20E-06	<0.01	HHIP (1.960e-66)	GDF5 (1.400e-59)	ADAMTSL3 (9.600e-29)	SCUBE3 (2.960e-28)	LOXL1 (1.020e-19)	ACAN (1.200e-19)	NPR3 (1.800e-17)	OMD (4.441e-16)	ASPN (4.441e-16)	GPR126 (1.332e-15)
MP:0004351	short humerus	MP:0004359	short ulna	3.41E-06	<0.01	HHIP (1.960e-66)	SCUBE3 (2.960e-28)	NFATC4 (1.920e-21)	ADAMTS3 (1.040e-20)	IHH (1.600e-20)	ACAN (1.200e-19)	NPR3 (1.800e-17)	OMD (4.441e-16)	ISLR (9.437e-15)	CRISPLD1 (3.308e-14)
ENSG00000092969	TGFB2 PPI subnetwork	ENSG00000092969	TGFB2 PPI subnetwork	3.50E-06	<0.01	BMP6 (2.700e-38)	CABLES1 (7.600e-21)	LOXL1 (1.020e-19)	ACAN (1.200e-19)	FBLN5 (3.220e-19)	IGFBP4 (1.650e-16)	OMD (4.441e-16)	ASPN (4.441e-16)	FBLN2 (9.992e-16)	LTBP3 (1.221e-15)
ENSG00000163875	MEAF6 PPI subnetwork	ENSG00000080603	SRCAP PPI subnetwork	4.11E-06	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)	HIST2H2BE (4.80e-22)
MP:0003560	osteoarthritis	MP:0003662	abnormal long bone epiphyseal plate proliferative zone	4.26E-06	<0.01	GDF5 (1.400e-59)	PRKG2 (5.810e-47)	ADAMTSL3 (9.600e-29)	SCUBE3 (2.960e-28)	LOXL1 (1.020e-19)	ACAN (1.200e-19)	OMD (4.441e-16)	ASPN (4.441e-16)	FBLN2 (9.992e-16)	GPR126 (1.332e-15)
ENSG00000087365	SF3B2 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	4.27E-06	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	FUBP3 (6.320e-25)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)
ENSG00000047315	POLR2B PPI subnetwork	ENSG00000005075	POLR2J PPI subnetwork	4.42E-06	<0.01	RBM12 (6.00e-52)	SF3B4 (8.80e-50)	FTSJ3 (6.30e-32)	AAR2 (2.25e-26)	FUBP3 (6.32e-25)	DDX27 (4.40e-24)	TRA2A (5.52e-24)	NCL (1.35e-18)	NUP160 (2.43e-17)	FNBP4 (2.88e-17)
ENSG00000131747	TOP2A PPI subnetwork	GO:0044427	chromosomal part	4.56E-06	<0.01	HIST1H2AE (4.140e-73)	HIST1H1D (4.410e-66)	ZNF367 (8.000e-33)	HIST1H1E (2.170e-28)	USP37 (8.600e-21)	E2F1 (3.300e-20)	NUP160 (2.430e-17)	TOP2A (1.110e-16)	HIST1H2BB (3.331e-16)	POLR2B (9.992e-16)
ENSG00000060339	CCAR1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	4.72E-06	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)
ENSG00000114166	KAT2B PPI subnetwork	ENSG00000196226	HIST1H2BB PPI subnetwork	5.02E-06	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HEXIM1 (4.56e-26)
ENSG00000094916	CBX5 PPI subnetwork	GO:0044427	chromosomal part	5.04E-06	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	NCAPG (1.17e-57)	CENPW (4.80e-40)	ZNF367 (8.00e-33)	CENPO (1.26e-30)	HIST1H1E (2.17e-28)
GO:0000785	chromatin	GO:0044427	chromosomal part	5.51E-06	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HEXIM1 (4.56e-26)
GO:0001871	pattern binding	GO:0005539	glycosaminoglycan binding	5.55E-06	<0.01	HHIP (1.960e-66)	COLGALT2 (2.880e-50)	ADAMTSL3 (9.600e-29)	SCUBE3 (2.960e-28)	LOXL1 (1.020e-19)	ACAN (1.200e-19)	FBLN5 (3.220e-19)	IGFBP4 (1.650e-16)	HK3 (2.220e-16)	OMD (4.441e-16)
GO:0030247	polysaccharide binding	GO:0005539	glycosaminoglycan binding	5.55E-06	<0.01	HHIP (1.960e-66)	COLGALT2 (2.880e-50)	ADAMTSL3 (9.600e-29)	SCUBE3 (2.960e-28)	LOXL1 (1.020e-19)	ACAN (1.200e-19)	FBLN5 (3.220e-19)	IGFBP4 (1.650e-16)	HK3 (2.220e-16)	OMD (4.441e-16)
ENSG00000165119	HNRNPK PPI subnetwork	ENSG00000153187	HNRNPU PPI subnetwork	6.25E-06	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	RBM12 (6.00e-52)	RBM39 (9.20e-51)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)
ENSG00000115128	ENSG00000115128 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	6.31E-06	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FUBP3 (6.320e-25)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)
ENSG00000162385	MAGOH PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	6.71E-06	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	POLR2A (7.661e-15)
ENSG00000100410	PHF5A PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	6.83E-06	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	POLR2A (7.661e-15)
ENSG00000122566	HNRNPA2B1 PPI subnetwork	ENSG00000153187	HNRNPU PPI subnetwork	6.98E-06	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	DDX42 (1.470e-38)	HEXIM1 (4.560e-26)	FUBP3 (6.320e-25)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	POLR2A (7.661e-15)
ENSG00000100836	PABPN1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	7.03E-06	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
ENSG00000063244	U2AF2 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	7.15E-06	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FUBP3 (6.320e-25)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	PAN2 (6.217e-15)
ENSG00000119699	TGFB3 PPI subnetwork	ENSG00000092969	TGFB2 PPI subnetwork	7.51E-06	<0.01	BMP6 (2.700e-38)	CABLES1 (7.600e-21)	LOXL1 (1.020e-19)	ACAN (1.200e-19)	FBLN5 (3.220e-19)	IGFBP4 (1.650e-16)	OMD (4.441e-16)	ASPN (4.441e-16)	FBLN2 (9.992e-16)	LTBP3 (1.221e-15)
GO:0000228	nuclear chromosome	GO:0044427	chromosomal part	7.67E-06	<0.01	CEP250 (5.50e-121)	NCAPG (1.17e-57)	CENPW (4.80e-40)	ZNF367 (8.00e-33)	FANCE (2.64e-25)	H1FX (3.08e-24)	USP37 (8.60e-21)	E2F1 (3.30e-20)	SLBP (6.00e-17)	TOP2A (1.11e-16)
ENSG00000127616	SMARCA4 PPI subnetwork	ENSG00000196226	HIST1H2BB PPI subnetwork	7.77E-06	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000137259	HIST1H2AB PPI subnetwork	ENSG00000196787	HIST1H2AG PPI subnetwork	8.98E-06	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000168274	HIST1H2AE PPI subnetwork	ENSG00000196787	HIST1H2AG PPI subnetwork	8.98E-06	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000183684	ALYREF PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	9.01E-06	<0.01	RBM12 (6.000e-52)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	UTP6 (1.665e-15)
ENSG00000115524	SF3B1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	9.12E-06	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)
S OF CAPPED INTRON:	EACTOME PROCESSING OF CAPPED INTRON:CONTAINING PRE:MRN	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	9.25E-06	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	NUP160 (2.430e-17)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	CSE1L (2.220e-15)
ENSG00000153187	HNRNPU PPI subnetwork	ENSG00000153187	HNRNPU PPI subnetwork	9.63E-06	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	DDX42 (1.470e-38)	HEXIM1 (4.560e-26)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)
ENSG00000176102	CSTF3 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	9.67E-06	<0.01	HIST1H2BG (2.200e-67)	HIST1H1D (4.410e-66)	RBM12 (6.000e-52)	RBM39 (9.200e-51)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	HIST1H2BB (3.331e-16)	POLR2B (9.992e-16)
ENSG00000168438	CDC40 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	9.88E-06	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)
ENSG00000165494	PCF11 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.06E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	POLR2A (7.661e-15)
ENSG00000127337	YEATS4 PPI subnetwork	ENSG00000080603	SRCAP PPI subnetwork	1.07E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000147133	TAF1 PPI subnetwork	ENSG00000085231	TAF9 PPI subnetwork	1.10E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	SNRPC (6.80e-40)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)
ENSG00000112526	ENSG00000112526 PPI subnetwork	ENSG00000215077	BRD2 PPI subnetwork	1.10E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000204256	BRD2 PPI subnetwork	ENSG00000215077	BRD2 PPI subnetwork	1.10E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000215077	BRD2 PPI subnetwork	ENSG00000215077	BRD2 PPI subnetwork	1.10E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000165934	CPSF2 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.13E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	DDX42 (1.470e-38)	FUBP3 (6.320e-25)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)
ENSG00000099995	SF3A1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.20E-05	<0.01	RBM12 (6.00e-52)	RBM39 (9.20e-51)	SF3B4 (8.80e-50)	DDX42 (1.47e-38)	FTSJ3 (6.30e-32)	FUBP3 (6.32e-25)	DDX27 (4.40e-24)	TRA2A (5.52e-24)	NCL (1.35e-18)	FNBP4 (2.88e-17)
ENSG00000077097	TOP2B PPI subnetwork	GO:0071564	npBAF complex	1.21E-05	<0.01	LIMD2 (3.500e-38)	H1FX (3.080e-24)	RQCD1 (7.800e-21)	USP37 (8.600e-21)	KDM1A (5.329e-15)	CS (3.697e-14)	SUZ12 (5.340e-14)	NASP (1.781e-12)	SUPT16H (3.182e-12)	PBRM1 (1.001e-11)
ENSG00000197111	PCBP2 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.23E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	FUBP3 (6.320e-25)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
ENSG00000174231	PRPF8 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.31E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)
ENSG00000169564	PCBP1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.33E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	PAN2 (6.217e-15)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)
MRNA DERIVED FROM	NSPORT OF MATURE MRNA DERIVED FROM AN INTRON:CONTAINI	GO:0050658	RNA transport	1.33E-05	<0.01	RBM12 (6.000e-52)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	RQCD1 (7.800e-21)	NUP160 (2.430e-17)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	UTP6 (1.665e-15)	CSE1L (2.220e-15)	PAN2 (6.217e-15)
ENSG00000188486	H2AFX PPI subnetwork	ENSG00000196787	HIST1H2AG PPI subnetwork	1.38E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HIST2H2BE (4.80e-22)
ENSG00000092199	HNRNPC PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.39E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
ENSG00000169217	CD2BP2 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.43E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FUBP3 (6.320e-25)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	POLR2A (7.661e-15)
ENSG00000196890	HIST3H2BB PPI subnetwork	ENSG00000196226	HIST1H2BB PPI subnetwork	1.48E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000163159	VPS72 PPI subnetwork	ENSG00000080603	SRCAP PPI subnetwork	1.51E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	SCAND1 (4.20e-50)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)
ENSG00000149532	CPSF7 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.58E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FUBP3 (6.320e-25)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)
ENSG00000205937	RNPS1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.68E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)
ENSG00000100650	SRSF5 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.69E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)
ENSG00000090060	PAPOLA PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.73E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)
ENSG00000116062	MSH6 PPI subnetwork	ENSG00000132383	RPA1 PPI subnetwork	1.74E-05	<0.01	CEP250 (5.500e-121)	NCAPG (1.170e-57)	ZNF367 (8.000e-33)	PEX1 (2.040e-25)	MPHOSPH9 (6.000e-21)	USP37 (8.600e-21)	E2F1 (3.300e-20)	SLBP (6.000e-17)	CSE1L (2.220e-15)	PAN2 (6.217e-15)
MP:0000163	abnormal cartilage morphology	MP:0010029	abnormal basicranium morphology	1.79E-05	<0.01	HHIP (1.960e-66)	GDF5 (1.400e-59)	COLGALT2 (2.880e-50)	PRKG2 (5.810e-47)	SCUBE3 (2.960e-28)	IHH (1.600e-20)	ACAN (1.200e-19)	OMD (4.441e-16)	ASPN (4.441e-16)	CRISPLD1 (3.308e-14)
MP:0004359	short ulna	MP:0004359	short ulna	1.80E-05	<0.01	HHIP (1.960e-66)	GDF5 (1.400e-59)	NFATC4 (1.920e-21)	IHH (1.600e-20)	ACAN (1.200e-19)	OMD (4.441e-16)	ASPN (4.441e-16)	ISLR (9.437e-15)	CRISPLD1 (3.308e-14)	OGN (7.494e-14)
ENSG00000136937	NCBP1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.82E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	HEXIM1 (4.560e-26)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)
ENSG00000101189	C20orf20 PPI subnetwork	ENSG00000080603	SRCAP PPI subnetwork	1.83E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)	HIST2H2BE (4.80e-22)
ENSG00000148229	POLE3 PPI subnetwork	ENSG00000196226	HIST1H2BB PPI subnetwork	1.84E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	ZNF367 (8.00e-33)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)
ENSG00000197597	ENSG00000197597 PPI subnetwork	ENSG00000196226	HIST1H2BB PPI subnetwork	1.87E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000089280	FUS PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.91E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)
ENSG00000147274	RBMX PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.95E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
ENSG00000125351	UPF3B PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.97E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	DDX42 (1.470e-38)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	PAN2 (6.217e-15)
MP:0000559	abnormal femur morphology	MP:0000130	abnormal trabecular bone morphology	1.98E-05	<0.01	GDF5 (1.400e-59)	NFATC4 (1.920e-21)	ADAMTS3 (1.040e-20)	IHH (1.600e-20)	LOXL1 (1.020e-19)	ACAN (1.200e-19)	IGFBP4 (1.650e-16)	OMD (4.441e-16)	ASPN (4.441e-16)	ECM2 (1.332e-15)
ENSG00000131876	SNRPA1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	2.00E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)
ENSG00000170144	HNRNPA3 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	2.04E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FUBP3 (6.320e-25)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)
RT OF MATURE TRANS	REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	GO:0050658	RNA transport	2.05E-05	<0.01	RBM12 (6.000e-52)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	RQCD1 (7.800e-21)	NUP160 (2.430e-17)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	UTP6 (1.665e-15)	CSE1L (2.220e-15)	PAN2 (6.217e-15)
ENSG00000116001	TIA1 PPI subnetwork	ENSG00000164167	LSM6 PPI subnetwork	2.13E-05	<0.01	CEP250 (5.500e-121)	CPNE1 (6.000e-52)	FTSJ3 (6.300e-32)	AP3D1 (4.800e-27)	DDX27 (4.400e-24)	NCL (1.350e-18)	NUP160 (2.430e-17)	UTP6 (1.665e-15)	CSE1L (2.220e-15)	KDM1A (5.329e-15)
ENSG00000080603	SRCAP PPI subnetwork	ENSG00000080603	SRCAP PPI subnetwork	2.19E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000092201	SUPT16H PPI subnetwork	ENSG00000196787	HIST1H2AG PPI subnetwork	2.20E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HEXIM1 (4.56e-26)
ENSG00000133226	SRRM1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	2.33E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
ENSG00000101361	NOP56 PPI subnetwork	ENSG00000088205	DDX18 PPI subnetwork	2.37E-05	<0.01	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	EXOSC5 (8.500e-21)	NCL (1.350e-18)	SSSCA1 (9.992e-16)	NOL8 (1.221e-15)	UTP6 (1.665e-15)	CSE1L (2.220e-15)	TRMT61A (6.006e-14)	NPM1 (5.040e-12)
MP:0008271	abnormal bone ossification	MP:0000130	abnormal trabecular bone morphology	2.40E-05	<0.01	GDF5 (1.400e-59)	SCUBE3 (2.960e-28)	ACAN (1.200e-19)	IGF1R (8.400e-18)	OMD (4.441e-16)	ASPN (4.441e-16)	CRISPLD1 (3.308e-14)	OGN (7.494e-14)	FAM101A (1.259e-12)	DAB2 (2.161e-12)
MP:0010103	small thoracic cage	MP:0010029	abnormal basicranium morphology	2.44E-05	<0.01	GDF5 (1.400e-59)	PRKG2 (5.810e-47)	SCUBE3 (2.960e-28)	IHH (1.600e-20)	ACAN (1.200e-19)	ID4 (3.331e-16)	OMD (4.441e-16)	CRISPLD1 (3.308e-14)	TBX4 (3.690e-13)	FAM101A (1.259e-12)
ENSG00000120688	WBP4 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	2.47E-05	<0.01	RBM12 (6.000e-52)	SF3B4 (8.800e-50)	FTSJ3 (6.300e-32)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	SLBP (6.000e-17)	POLR2A (7.661e-15)	SUPT16H (3.182e-12)	ZNF574 (5.513e-12)
MP:0000131	abnormal long bone epiphysis morphology	MP:0010029	abnormal basicranium morphology	2.48E-05	<0.01	GDF5 (1.400e-59)	SCUBE3 (2.960e-28)	IHH (1.600e-20)	ACAN (1.200e-19)	NPR3 (1.800e-17)	OMD (4.441e-16)	CRISPLD1 (3.308e-14)	FAM101A (1.259e-12)	IGF2 (3.257e-12)	CYTL1 (1.636e-10)
ENSG00000124635	HIST1H2BJ PPI subnetwork	ENSG00000196226	HIST1H2BB PPI subnetwork	2.50E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
MP:0003055	abnormal long bone epiphyseal plate morphology	MP:0003662	abnormal long bone epiphyseal plate proliferative zone	2.57E-05	<0.01	GDF5 (1.400e-59)	COLGALT2 (2.880e-50)	PDLIM4 (9.100e-34)	SCUBE3 (2.960e-28)	IHH (1.600e-20)	ACAN (1.200e-19)	OMD (4.441e-16)	ASPN (4.441e-16)	ECM2 (1.332e-15)	ISLR (9.437e-15)
ENSG00000175221	MED16 PPI subnetwork	ENSG00000164758	MED30 PPI subnetwork	2.62E-05	<0.01	TEFM (9.000e-41)	TRIM13 (4.000e-25)	ANAPC10 (1.500e-24)	RBM48 (1.020e-21)	ZNF142 (2.640e-20)	IPPK (3.442e-13)	ISCA2 (6.800e-12)	SEC16A (2.103e-11)	VTA1 (3.622e-11)	MED20 (6.233e-10)
ENSG00000126698	DNAJC8 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	2.65E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
POLYMERASE I PROM	REACTOME_RNA_POLYMERASE_I_PROMOTER_OPENING	ENSG00000167491	GATAD2A PPI subnetwork	2.66E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HEXIM1 (4.56e-26)
ENSG00000125870	SNRPB2 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	2.66E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
ENSG00000126945	HNRNPH2 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	2.73E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	DDX42 (1.470e-38)	HEXIM1 (4.560e-26)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)
ENSG00000111786	SRSF9 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	2.74E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	POLR2A (7.661e-15)
CTOME MRNA PROCES	REACTOME_MRNA_PROCESSING	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	2.87E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	TRA2A (5.520e-24)	RQCD1 (7.800e-21)	NCL (1.350e-18)	NUP160 (2.430e-17)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	UTP6 (1.665e-15)
ENSG00000139219	COL2A1 PPI subnetwork	GO:0031012	extracellular matrix	2.94E-05	<0.01	GDF5 (1.400e-59)	COLGALT2 (2.880e-50)	SCUBE3 (2.960e-28)	LOXL1 (1.020e-19)	ACAN (1.200e-19)	OMD (4.441e-16)	ASPN (4.441e-16)	ECM2 (1.332e-15)	ISLR (9.437e-15)	CRISPLD1 (3.308e-14)
ENSG00000070770	CSNK2A2 PPI subnetwork	ENSG00000206300	ENSG00000206300 PPI subnetwork	2.95E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HMGA1 (6.00e-49)	DDX42 (1.47e-38)	FTSJ3 (6.30e-32)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)
ENSG00000105329	TGFB1 PPI subnetwork	ENSG00000092969	TGFB2 PPI subnetwork	2.99E-05	<0.01	BMP6 (2.700e-38)	ADAMTSL3 (9.600e-29)	LOXL1 (1.020e-19)	ACAN (1.200e-19)	FBLN5 (3.220e-19)	IGFBP4 (1.650e-16)	ID4 (3.331e-16)	OMD (4.441e-16)	ASPN (4.441e-16)	FBLN2 (9.992e-16)
GO:0004402	histone acetyltransferase activity	GO:0008080	N-acetyltransferase activity	3.02E-05	<0.01	NCOA6 (5.200e-25)	RBM48 (1.020e-21)	STAG1 (1.998e-15)	NSD1 (1.277e-14)	EZH1 (1.805e-12)	KLF11 (3.620e-12)	NCOA1 (1.290e-10)	GOSR1 (1.057e-09)	TLK1 (3.187e-09)	INTS7 (3.710e-09)
ENSG00000177565	TBL1XR1 PPI subnetwork	ENSG00000080603	SRCAP PPI subnetwork	3.12E-05	<0.01	HIST1H2AE (4.14e-73)	LCORL (2.45e-70)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)
ENSG00000138668	HNRNPD PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	3.16E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	DDX42 (1.470e-38)	FUBP3 (6.320e-25)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
ENSG00000169925	BRD3 PPI subnetwork	ENSG00000215077	BRD2 PPI subnetwork	3.25E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	CCDC91 (1.76e-29)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)
ENSG00000011304	PTBP1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	3.28E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)
ENSG00000135801	TAF5L PPI subnetwork	ENSG00000135801	TAF5L PPI subnetwork	3.34E-05	<0.01	CRLF3 (1.350e-40)	PEX1 (2.040e-25)	NCOA6 (5.200e-25)	ZNF142 (2.640e-20)	RPIA (4.300e-18)	NEK4 (1.110e-16)	FAM178A (3.098e-14)	SDCCAG3 (1.029e-13)	ZFYVE26 (1.582e-08)	SENP8 (1.924e-08)
GO:0005839	proteasome core complex	IATED PHOSPHORYLATION AND	CDK:MEDIATED PHOSPHORYLATION AND REMOVA	3.40E-05	<0.01	ROMO1 (5.400e-52)	SNRPC (6.800e-40)	PSMC5 (1.800e-38)	PIGU (1.170e-27)	DYNLRB1 (3.600e-24)	PSMC3 (4.950e-19)	SDHB (8.800e-18)	BTN3A2 (2.880e-17)	IRF1 (2.220e-16)	SNF8 (4.441e-16)
ENSG00000100028	SNRPD3 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	3.44E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)
ENSG00000104824	HNRNPL PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	3.47E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)	SUPT16H (3.182e-12)	SMARCA5 (1.013e-10)
ENSG00000196367	TRRAP PPI subnetwork	ENSG00000080603	SRCAP PPI subnetwork	3.47E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	NCOA6 (5.20e-25)
ENSG00000105968	H2AFV PPI subnetwork	ENSG00000080603	SRCAP PPI subnetwork	3.52E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	CCDC91 (1.76e-29)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)
ENSG00000012048	BRCA1 PPI subnetwork	GO:0044427	chromosomal part	3.53E-05	<0.01	NCAPG (1.170e-57)	CENPW (4.800e-40)	ZNF367 (8.000e-33)	CENPO (1.260e-30)	USP37 (8.600e-21)	E2F1 (3.300e-20)	TOP2A (1.110e-16)	TACC3 (1.110e-16)	STAG1 (1.998e-15)	CSE1L (2.220e-15)
ENSG00000183558	HIST2H2AA3 PPI subnetwork	ENSG00000196787	HIST1H2AG PPI subnetwork	3.53E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000203812	HIST2H2AA4 PPI subnetwork	ENSG00000196787	HIST1H2AG PPI subnetwork	3.53E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000077721	UBE2A PPI subnetwork	ENSG00000080603	SRCAP PPI subnetwork	3.55E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000105323	HNRNPUL1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	3.68E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
ENSG00000143621	ILF2 PPI subnetwork	ENSG00000153187	HNRNPU PPI subnetwork	3.69E-05	<0.01	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	CCDC47 (4.200e-39)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	UTP6 (1.665e-15)	HNRNPK (1.188e-14)
MP:0000164	abnormal cartilage development	MP:0010029	abnormal basicranium morphology	3.78E-05	<0.01	GDF5 (1.400e-59)	COLGALT2 (2.880e-50)	PRKG2 (5.810e-47)	ADAMTSL3 (9.600e-29)	SCUBE3 (2.960e-28)	ACAN (1.200e-19)	ID4 (3.331e-16)	OMD (4.441e-16)	ASPN (4.441e-16)	CRISPLD1 (3.308e-14)
ENSG00000153914	SREK1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	3.80E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	PAN2 (6.217e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
ENSG00000116350	SRSF4 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	3.86E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
ENSG00000153147	SMARCA5 PPI subnetwork	ENSG00000196226	HIST1H2BB PPI subnetwork	3.88E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ACTOME MRNA SPLICI	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	3.94E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
MRNA SPLICING : MAJ	REACTOME_MRNA_SPLICING_:_MAJOR_PATHWAY	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	3.94E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
ENSG00000184348	HIST1H2AK PPI subnetwork	ENSG00000196787	HIST1H2AG PPI subnetwork	3.99E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000196747	HIST1H2AI PPI subnetwork	ENSG00000196787	HIST1H2AG PPI subnetwork	3.99E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000196787	HIST1H2AG PPI subnetwork	ENSG00000196787	HIST1H2AG PPI subnetwork	3.99E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000196866	HIST1H2AD PPI subnetwork	ENSG00000196787	HIST1H2AG PPI subnetwork	3.99E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000198374	HIST1H2AL PPI subnetwork	ENSG00000196787	HIST1H2AG PPI subnetwork	3.99E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000060688	SNRNP40 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	4.11E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FUBP3 (6.320e-25)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	HNRNPK (1.188e-14)	NASP (1.781e-12)
GO:0031012	extracellular matrix	GO:0031012	extracellular matrix	4.14E-05	<0.01	ADAMTSL3 (9.600e-29)	SCUBE3 (2.960e-28)	LOXL1 (1.020e-19)	ACAN (1.200e-19)	FBLN5 (3.220e-19)	IGFBP4 (1.650e-16)	OMD (4.441e-16)	ASPN (4.441e-16)	FBLN2 (9.992e-16)	LTBP3 (1.221e-15)
ENSG00000104897	SF3A2 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	4.19E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)
MP:0002187	abnormal fibula morphology	MP:0004359	short ulna	4.21E-05	<0.01	HHIP (1.960e-66)	GDF5 (1.400e-59)	NFATC4 (1.920e-21)	ACAN (1.200e-19)	FKBP5 (5.329e-15)	OGN (7.494e-14)	TBX4 (3.690e-13)	FAM101A (1.259e-12)	IGF2 (3.257e-12)	PITX1 (4.189e-11)
ENSG00000086102	NFX1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	4.21E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
ENSG00000099783	HNRNPM PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	4.31E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
ENSG00000105705	SUGP1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	4.32E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)	SUPT16H (3.182e-12)
ENSG00000196331	HIST1H2BO PPI subnetwork	ENSG00000196226	HIST1H2BB PPI subnetwork	4.44E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000101138	CSTF1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	4.47E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)
ENSG00000141759	TXNL4A PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	4.49E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	FTSJ3 (6.300e-32)	FUBP3 (6.320e-25)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	HNRNPK (1.188e-14)
ENSG00000105202	FBL PPI subnetwork	ENSG00000088205	DDX18 PPI subnetwork	4.49E-05	<0.01	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	EXOSC5 (8.500e-21)	BCS1L (2.080e-20)	OTUD4 (2.400e-20)	NCL (1.350e-18)	SSSCA1 (9.992e-16)	NOL8 (1.221e-15)	UTP6 (1.665e-15)	TRMT61A (6.006e-14)
GO:0043021	ribonucleoprotein complex binding	GO:0008135	translation factor activity, nucleic acid binding	4.55E-05	<0.01	EDEM2 (7.000e-33)	CDK5RAP1 (1.200e-27)	AP3D1 (4.800e-27)	DDX27 (4.400e-24)	GSS (6.000e-19)	SSSCA1 (9.992e-16)	ANKRD52 (4.441e-15)	WDR24 (5.418e-14)	LMAN2 (2.379e-13)	HDLBP (7.119e-12)
ENSG00000007392	LUC7L PPI subnetwork	ENSG00000164167	LSM6 PPI subnetwork	4.60E-05	<0.01	CPNE1 (6.000e-52)	RBM12 (6.000e-52)	SF3B4 (8.800e-50)	FTSJ3 (6.300e-32)	AP3D1 (4.800e-27)	DDX27 (4.400e-24)	NCL (1.350e-18)	POLR2B (9.992e-16)	SUPT16H (3.182e-12)	SUGP1 (3.598e-11)
ENSG00000087303	NID2 PPI subnetwork	GO:0031012	extracellular matrix	4.69E-05	<0.01	HHIP (1.960e-66)	BMP6 (2.700e-38)	MYH7B (5.400e-36)	SCUBE3 (2.960e-28)	LOXL1 (1.020e-19)	FBLN5 (3.220e-19)	TBX2 (9.960e-17)	ASPN (4.441e-16)	FBLN2 (9.992e-16)	LTBP3 (1.221e-15)
ENSG00000100138	NHP2L1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	4.71E-05	<0.01	RBM12 (6.000e-52)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	NUP160 (2.430e-17)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)
ENSG00000196235	SUPT5H PPI subnetwork	ENSG00000088205	DDX18 PPI subnetwork	4.79E-05	<0.01	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	EXOSC5 (8.500e-21)	RNF25 (1.760e-20)	NCL (1.350e-18)	NUP160 (2.430e-17)	SSSCA1 (9.992e-16)	NOL8 (1.221e-15)	UTP6 (1.665e-15)
ENSG00000095564	BTAF1 PPI subnetwork	ENSG00000196226	HIST1H2BB PPI subnetwork	4.83E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
MP:0005269	abnormal occipital bone morphology	MP:0010029	abnormal basicranium morphology	4.87E-05	<0.01	GDF5 (1.400e-59)	BMP6 (2.700e-38)	SCUBE3 (2.960e-28)	NFATC4 (1.920e-21)	ACAN (1.200e-19)	ID4 (3.331e-16)	OMD (4.441e-16)	FAM101A (1.259e-12)	SHOX2 (1.036e-09)	SMAD6 (2.485e-09)
ENSG00000158373	HIST1H2BD PPI subnetwork	ENSG00000196226	HIST1H2BB PPI subnetwork	4.94E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
MP:0000443	abnormal snout morphology	MP:0010029	abnormal basicranium morphology	5.01E-05	<0.01	GDF5 (1.400e-59)	SCUBE3 (2.960e-28)	NFATC4 (1.920e-21)	IHH (1.600e-20)	ACAN (1.200e-19)	ID4 (3.331e-16)	OMD (4.441e-16)	CRISPLD1 (3.308e-14)	FAM101A (1.259e-12)	CYTL1 (1.636e-10)
ENSG00000129757	CDKN1C PPI subnetwork	KEGG_CELL_CYCLE	KEGG_CELL_CYCLE	5.09E-05	<0.01	CEP250 (5.500e-121)	NCAPG (1.170e-57)	CENPW (4.800e-40)	ZNF367 (8.000e-33)	E2F1 (3.300e-20)	RAPSN (1.320e-17)	SLBP (6.000e-17)	TOP2A (1.110e-16)	FAM178A (3.098e-14)	CENPP (6.839e-14)
ENSG00000203852	HIST2H3A PPI subnetwork	ENSG00000178458	ENSG00000178458 PPI subnetwork	5.14E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HEXIM1 (4.56e-26)
MP:0000440	domed cranium	MP:0003662	abnormal long bone epiphyseal plate proliferative zone	5.15E-05	<0.01	GDF5 (1.400e-59)	ACAN (1.200e-19)	NYNRIN (2.250e-18)	OMD (4.441e-16)	CRISPLD1 (3.308e-14)	SLC39A13 (5.951e-14)	OGN (7.494e-14)	FAM101A (1.259e-12)	IFT172 (5.205e-11)	SMAD6 (2.485e-09)
ENSG00000172409	CLP1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	5.26E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	POLR2A (7.661e-15)
GO:0005578	proteinaceous extracellular matrix	GO:0031012	extracellular matrix	5.47E-05	<0.01	ADAMTSL3 (9.600e-29)	SCUBE3 (2.960e-28)	LOXL1 (1.020e-19)	ACAN (1.200e-19)	FBLN5 (3.220e-19)	IGFBP4 (1.650e-16)	OMD (4.441e-16)	ASPN (4.441e-16)	FBLN2 (9.992e-16)	LTBP3 (1.221e-15)
ENSG00000115875	SRSF7 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	5.49E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)
MP:0002427	disproportionate dwarf	MP:0003662	abnormal long bone epiphyseal plate proliferative zone	5.53E-05	<0.01	GDF5 (1.400e-59)	COLGALT2 (2.880e-50)	PRKG2 (5.810e-47)	SCUBE3 (2.960e-28)	IHH (1.600e-20)	ACAN (1.200e-19)	OMD (4.441e-16)	ASPN (4.441e-16)	ECM2 (1.332e-15)	ISLR (9.437e-15)
MP:0004989	decreased osteoblast cell number	MP:0000130	abnormal trabecular bone morphology	5.60E-05	<0.01	GDF5 (1.400e-59)	ACAN (1.200e-19)	IGFBP4 (1.650e-16)	ID4 (3.331e-16)	OMD (4.441e-16)	ASPN (4.441e-16)	ECM2 (1.332e-15)	CRISPLD1 (3.308e-14)	OGN (7.494e-14)	FAM101A (1.259e-12)
ENSG00000160201	U2AF1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	5.61E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)
ENSG00000116560	SFPQ PPI subnetwork	ENSG00000153187	HNRNPU PPI subnetwork	5.80E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	CCDC47 (4.200e-39)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	UBE2Z (2.220e-16)	POLR2A (7.661e-15)
ENSG00000189091	SF3B3 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	5.86E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	FUBP3 (6.320e-25)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)
ENSG00000080503	SMARCA2 PPI subnetwork	ENSG00000196787	HIST1H2AG PPI subnetwork	6.00E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000196419	XRCC6 PPI subnetwork	ENSG00000197837	HIST4H4 PPI subnetwork	6.02E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HEXIM1 (4.56e-26)	HIST2H2BE (4.80e-22)
ENSG00000124795	DEK PPI subnetwork	ENSG00000185513	L3MBTL1 PPI subnetwork	6.02E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000100316	RPL3 PPI subnetwork	ENSG00000083845	RPS5 PPI subnetwork	6.36E-05	<0.01	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	RBM12 (6.00e-52)	FTSJ3 (6.30e-32)	HIST1H1E (2.17e-28)	AAR2 (2.25e-26)	FUBP3 (6.32e-25)	DDX27 (4.40e-24)	EXOSC5 (8.50e-21)	NCL (1.35e-18)
ENSG00000167088	SNRPD1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	6.36E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	UTP6 (1.665e-15)
ENSG00000131795	RBM8A PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	6.40E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	POLR2A (7.661e-15)
GO:0004298	threonine-type endopeptidase activity	IATED PHOSPHORYLATION AND	CDK:MEDIATED PHOSPHORYLATION AND REMOVA	6.48E-05	<0.01	ROMO1 (5.400e-52)	SNRPC (6.800e-40)	PSMC5 (1.800e-38)	DYNLRB1 (3.600e-24)	PSMC3 (4.950e-19)	SDHB (8.800e-18)	BTN3A2 (2.880e-17)	IRF1 (2.220e-16)	SNF8 (4.441e-16)	HINT1 (3.109e-15)
GO:0070003	threonine-type peptidase activity	IATED PHOSPHORYLATION AND	CDK:MEDIATED PHOSPHORYLATION AND REMOVA	6.48E-05	<0.01	ROMO1 (5.400e-52)	SNRPC (6.800e-40)	PSMC5 (1.800e-38)	DYNLRB1 (3.600e-24)	PSMC3 (4.950e-19)	SDHB (8.800e-18)	BTN3A2 (2.880e-17)	IRF1 (2.220e-16)	SNF8 (4.441e-16)	HINT1 (3.109e-15)
ENSG00000140829	DHX38 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	6.48E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
MP:0002089	abnormal postnatal growth/weight/body size	MP:0003662	abnormal long bone epiphyseal plate proliferative zone	6.56E-05	<0.01	HHIP (1.960e-66)	MAP1LC3A (2.100e-23)	ACAN (1.200e-19)	RAPSN (1.320e-17)	TRIM8 (3.331e-16)	OMD (4.441e-16)	FARP2 (1.555e-12)	C1orf105 (5.670e-11)	TGFB2 (2.945e-09)	COL9A2 (8.489e-09)
MP:0002113	abnormal skeleton development	MP:0003662	abnormal long bone epiphyseal plate proliferative zone	6.58E-05	<0.01	GDF5 (1.400e-59)	ACAN (1.200e-19)	CD164 (1.000e-16)	IGFBP4 (1.650e-16)	OMD (4.441e-16)	CRISPLD1 (3.308e-14)	OGN (7.494e-14)	FAM101A (1.259e-12)	DAB2 (2.161e-12)	IGF2 (3.257e-12)
OWING TRANSCRIPT I	OME CLEAVAGE OF GROWING TRANSCRIPT IN THE TERMINATION	POLYMERASE II TRANSCRIPTIC	OME RNA POLYMERASE II TRANSCRIPTION TERMIN	6.59E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	TRA2A (5.520e-24)	FNBP4 (2.880e-17)	PAN2 (6.217e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)	SUPT16H (3.182e-12)	GPBP1L1 (1.990e-11)	SF3B14 (5.084e-09)
NGATION PROCESSING	REACTOME_POST:ELONGATION_PROCESSING_OF_THE_TRANSCRIPT	POLYMERASE II TRANSCRIPTIC	OME RNA POLYMERASE II TRANSCRIPTION TERMIN	6.59E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	TRA2A (5.520e-24)	FNBP4 (2.880e-17)	PAN2 (6.217e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)	SUPT16H (3.182e-12)	GPBP1L1 (1.990e-11)	SF3B14 (5.084e-09)
YMERASE II TRANSCRI	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_TERMINATION	POLYMERASE II TRANSCRIPTIC	OME RNA POLYMERASE II TRANSCRIPTION TERMIN	6.59E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	TRA2A (5.520e-24)	FNBP4 (2.880e-17)	PAN2 (6.217e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)	SUPT16H (3.182e-12)	GPBP1L1 (1.990e-11)	SF3B14 (5.084e-09)
ENSG00000184270	HIST2H2AB PPI subnetwork	ENSG00000185513	L3MBTL1 PPI subnetwork	6.67E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	ACTL10 (1.02e-27)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)
ENSG00000196374	HIST1H2BM PPI subnetwork	ENSG00000196226	HIST1H2BB PPI subnetwork	6.71E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)
ENSG00000183207	RUVBL2 PPI subnetwork	ENSG00000198558	HIST1H4L PPI subnetwork	6.72E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	PSMC5 (1.80e-38)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)
ENSG00000130520	LSM4 PPI subnetwork	ENSG00000164167	LSM6 PPI subnetwork	6.81E-05	<0.01	CEP250 (5.500e-121)	SF3B4 (8.800e-50)	FTSJ3 (6.300e-32)	DYNLRB1 (3.600e-24)	DDX27 (4.400e-24)	POLR2B (9.992e-16)	SUGP1 (3.598e-11)	VTA1 (3.622e-11)	SMARCA5 (1.013e-10)	TSC2 (1.267e-10)
ENSG00000124529	HIST1H4B PPI subnetwork	ENSG00000124529	HIST1H4B PPI subnetwork	6.92E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HIST2H2BE (4.80e-22)
ENSG00000158406	HIST1H4H PPI subnetwork	ENSG00000158406	HIST1H4H PPI subnetwork	6.92E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HIST2H2BE (4.80e-22)
ENSG00000182217	HIST2H4B PPI subnetwork	ENSG00000182217	HIST2H4B PPI subnetwork	6.92E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HIST2H2BE (4.80e-22)
ENSG00000183941	HIST2H4A PPI subnetwork	ENSG00000183941	HIST2H4A PPI subnetwork	6.92E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HIST2H2BE (4.80e-22)
ENSG00000188987	HIST1H4D PPI subnetwork	ENSG00000188987	HIST1H4D PPI subnetwork	6.92E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HIST2H2BE (4.80e-22)
ENSG00000196176	HIST1H4A PPI subnetwork	ENSG00000196176	HIST1H4A PPI subnetwork	6.92E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HIST2H2BE (4.80e-22)
ENSG00000197061	HIST1H4C PPI subnetwork	ENSG00000197061	HIST1H4C PPI subnetwork	6.92E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HIST2H2BE (4.80e-22)
ENSG00000197238	HIST1H4J PPI subnetwork	ENSG00000197238	HIST1H4J PPI subnetwork	6.92E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HIST2H2BE (4.80e-22)
ENSG00000197837	HIST4H4 PPI subnetwork	ENSG00000197837	HIST4H4 PPI subnetwork	6.92E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HIST2H2BE (4.80e-22)
ENSG00000197914	HIST1H4K PPI subnetwork	ENSG00000197914	HIST1H4K PPI subnetwork	6.92E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HIST2H2BE (4.80e-22)
ENSG00000198327	HIST1H4F PPI subnetwork	ENSG00000198327	HIST1H4F PPI subnetwork	6.92E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HIST2H2BE (4.80e-22)
ENSG00000198339	HIST1H4I PPI subnetwork	ENSG00000198339	HIST1H4I PPI subnetwork	6.92E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HIST2H2BE (4.80e-22)
ENSG00000198518	HIST1H4E PPI subnetwork	ENSG00000158406	HIST1H4H PPI subnetwork	6.92E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HIST2H2BE (4.80e-22)
ENSG00000198558	HIST1H4L PPI subnetwork	ENSG00000198558	HIST1H4L PPI subnetwork	6.92E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HIST2H2BE (4.80e-22)
ENSG00000169976	SF3B5 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	6.94E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
ENSG00000162227	TAF6L PPI subnetwork	ENSG00000135801	TAF5L PPI subnetwork	7.00E-05	<0.01	PEX1 (2.040e-25)	NCOA6 (5.200e-25)	FAM208A (5.600e-21)	ZNF142 (2.640e-20)	RPIA (4.300e-18)	NEK4 (1.110e-16)	PAN2 (6.217e-15)	INPP5E (3.963e-12)	ZFYVE26 (1.582e-08)	RUNX2 (1.940e-08)
ENSG00000101811	CSTF2 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	7.08E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	POLR2A (7.661e-15)	HNRNPK (1.188e-14)
ENSG00000183598	HIST2H3D PPI subnetwork	ENSG00000178458	ENSG00000178458 PPI subnetwork	7.10E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	SMARCD2 (2.40e-32)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)
ENSG00000203811	HIST2H3C PPI subnetwork	ENSG00000178458	ENSG00000178458 PPI subnetwork	7.10E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	SMARCD2 (2.40e-32)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)
ENSG00000143368	SF3B4 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	7.23E-05	<0.01	RBM12 (6.00e-52)	RBM39 (9.20e-51)	SF3B4 (8.80e-50)	DDX42 (1.47e-38)	FTSJ3 (6.30e-32)	FUBP3 (6.32e-25)	DDX27 (4.40e-24)	TRA2A (5.52e-24)	NCL (1.35e-18)	FNBP4 (2.88e-17)
ENSG00000116957	TBCE PPI subnetwork	ENSG00000204197	KIFC1 PPI subnetwork	7.24E-05	<0.01	CENPW (4.800e-40)	SNRPC (6.800e-40)	DYNLRB1 (3.600e-24)	PSMC3 (4.950e-19)	PTRHD1 (3.450e-18)	TOP2A (1.110e-16)	TACC3 (1.110e-16)	TUBG1 (7.690e-12)	STIL (5.393e-11)	MNF1 (1.965e-10)
ENSG00000085872	CHERP PPI subnetwork	ENSG00000085872	CHERP PPI subnetwork	7.26E-05	<0.01	RBM12 (6.000e-52)	SF3B4 (8.800e-50)	TRA2A (5.520e-24)	FNBP4 (2.880e-17)	POLR2A (7.661e-15)	N4BP2L2 (3.016e-11)	ZNF592 (1.265e-10)	PTP4A2 (4.866e-09)	SNIP1 (1.376e-08)	TLN1 (1.460e-08)
MP:0000547	short limbs	MP:0003662	abnormal long bone epiphyseal plate proliferative zone	7.29E-05	<0.01	COLGALT2 (2.880e-50)	SCUBE3 (2.960e-28)	NFATC4 (1.920e-21)	IHH (1.600e-20)	ACAN (1.200e-19)	OMD (4.441e-16)	ASPN (4.441e-16)	ISLR (9.437e-15)	CRISPLD1 (3.308e-14)	SLC39A13 (5.951e-14)
ENSG00000096063	SRPK1 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	7.41E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	CCDC47 (4.200e-39)	DDX42 (1.470e-38)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)
MP:0004471	short nasal bone	MP:0000088	short mandible	7.72E-05	<0.01	HHIP (1.960e-66)	ADAMTSL3 (9.600e-29)	SCUBE3 (2.960e-28)	ACAN (1.200e-19)	TBX2 (9.960e-17)	OMD (4.441e-16)	CRISPLD1 (3.308e-14)	TBX4 (3.690e-13)	FAM101A (1.259e-12)	IGF2 (3.257e-12)
ENSG00000119718	EIF2B2 PPI subnetwork	ENSG00000093217	XYLB PPI subnetwork	7.80E-05	<0.01	CDK5RAP1 (1.200e-27)	RNF25 (1.760e-20)	MNAT1 (3.000e-16)	TRMT61A (6.006e-14)	NPM1 (5.040e-12)	GNL3 (6.115e-12)	ISCA2 (6.800e-12)	TMEM69 (2.398e-11)	MLX (5.107e-11)	QTRT1 (1.721e-10)
ENSG00000177084	POLE PPI subnetwork	GO:0044427	chromosomal part	7.96E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	ZNF367 (8.00e-33)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)
ENSG00000072501	SMC1A PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	8.24E-05	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	TRA2A (5.520e-24)	NCL (1.350e-18)	NUP160 (2.430e-17)	FNBP4 (2.880e-17)	SLBP (6.000e-17)	POLR2B (9.992e-16)	CSE1L (2.220e-15)	POLR2A (7.661e-15)
ENSG00000141034	C17orf39 PPI subnetwork	ENSG00000196787	HIST1H2AG PPI subnetwork	8.50E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	HEXIM1 (4.56e-26)
ENSG00000187837	HIST1H1C PPI subnetwork	ENSG00000153187	HNRNPU PPI subnetwork	8.90E-05	<0.01	HIST1H2AE (4.140e-73)	HIST1H1D (4.410e-66)	HIST1H4G (2.240e-63)	RBM12 (6.000e-52)	RBM39 (9.200e-51)	HIST1H1E (2.170e-28)	TRA2A (5.520e-24)	FNBP4 (2.880e-17)	HIST1H1A (2.030e-16)	HIST1H2BB (3.331e-16)
ENSG00000108590	MED31 PPI subnetwork	ENSG00000164758	MED30 PPI subnetwork	8.94E-05	<0.01	TRIM13 (4.000e-25)	ANAPC10 (1.500e-24)	RNF25 (1.760e-20)	PTRHD1 (3.450e-18)	ATP5SL (2.000e-16)	MNAT1 (3.000e-16)	GTF2B (4.885e-15)	EIF4E2 (1.032e-12)	ABT1 (8.286e-10)	VPS25 (8.416e-10)
GO:0005539	glycosaminoglycan binding	GO:0005539	glycosaminoglycan binding	9.31E-05	<0.01	HHIP (1.960e-66)	COLGALT2 (2.880e-50)	ADAMTSL3 (9.600e-29)	LOXL1 (1.020e-19)	ACAN (1.200e-19)	FBLN5 (3.220e-19)	IGFBP4 (1.650e-16)	OMD (4.441e-16)	ASPN (4.441e-16)	FBLN2 (9.992e-16)
MP:0010029	abnormal basicranium morphology	MP:0010029	abnormal basicranium morphology	9.67E-05	<0.01	GDF5 (1.400e-59)	SCUBE3 (2.960e-28)	IHH (1.600e-20)	ACAN (1.200e-19)	ID4 (3.331e-16)	OMD (4.441e-16)	CRISPLD1 (3.308e-14)	FAM101A (1.259e-12)	IGF2 (3.257e-12)	CYTL1 (1.636e-10)
ENSG00000177700	POLR2L PPI subnetwork	ENSG00000005075	POLR2J PPI subnetwork	9.78E-05	<0.01	RBM12 (6.000e-52)	SF3B4 (8.800e-50)	AAR2 (2.250e-26)	FUBP3 (6.320e-25)	DDX27 (4.400e-24)	TRA2A (5.520e-24)	NUP160 (2.430e-17)	FNBP4 (2.880e-17)	SSSCA1 (9.992e-16)	KDM1A (5.329e-15)
GO:0048705	skeletal system morphogenesis	GO:0048704	embryonic skeletal system morphogenesis	9.91E-05	<0.01	GDF5 (1.400e-59)	SCUBE3 (2.960e-28)	NFATC4 (1.920e-21)	ACAN (1.200e-19)	OMD (4.441e-16)	ISLR (9.437e-15)	CRISPLD1 (3.308e-14)	FAM101A (1.259e-12)	HMGA2 (4.031e-12)	FGF18 (1.165e-10)
CENPA:CONTAINING N	DEPOSITION OF NEW CENPA:CONTAINING NUCLEOSOMES AT THE	GO:0034080	CenH3-containing nucleosome assembly at centromere	9.99E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	NCAPG (1.17e-57)	CENPW (4.80e-40)	ZNF367 (8.00e-33)	CENPO (1.26e-30)	HIST1H1E (2.17e-28)
OME NUCLEOSOME AS	REACTOME_NUCLEOSOME_ASSEMBLY	GO:0034080	CenH3-containing nucleosome assembly at centromere	9.99E-05	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	NCAPG (1.17e-57)	CENPW (4.80e-40)	ZNF367 (8.00e-33)	CENPO (1.26e-30)	HIST1H1E (2.17e-28)
ENSG00000162521	RBBP4 PPI subnetwork	ENSG00000116478	HDAC1 PPI subnetwork	1.00E-04	<0.01	HIST1H2AE (4.140e-73)	HIST1H2BG (2.200e-67)	HIST1H2BH (3.520e-67)	HIST1H1D (4.410e-66)	HIST1H1E (2.170e-28)	HIST1H2BD (2.170e-28)	H1FX (3.080e-24)	HIST1H2BB (3.331e-16)	STAG1 (1.998e-15)	HIST1H4I (4.807e-14)
ENSG00000172660	TAF15 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.01E-04	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	CCDC47 (4.200e-39)	DDX42 (1.470e-38)	SMARCD2 (2.400e-32)	TRA2A (5.520e-24)	FNBP4 (2.880e-17)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)	DDX6 (5.962e-14)
ENSG00000174243	DDX23 PPI subnetwork	REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	1.04E-04	<0.01	RBM12 (6.000e-52)	RBM39 (9.200e-51)	SF3B4 (8.800e-50)	TRA2A (5.520e-24)	NCL (1.350e-18)	FNBP4 (2.880e-17)	POLR2B (9.992e-16)	KDM1A (5.329e-15)	HNRNPK (1.188e-14)	NASP (1.781e-12)
ENSG00000164032	H2AFZ PPI subnetwork	ENSG00000080603	SRCAP PPI subnetwork	1.07E-04	<0.01	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.70e-27)	HIST1H2AC (2.61e-26)	H1FX (3.08e-24)

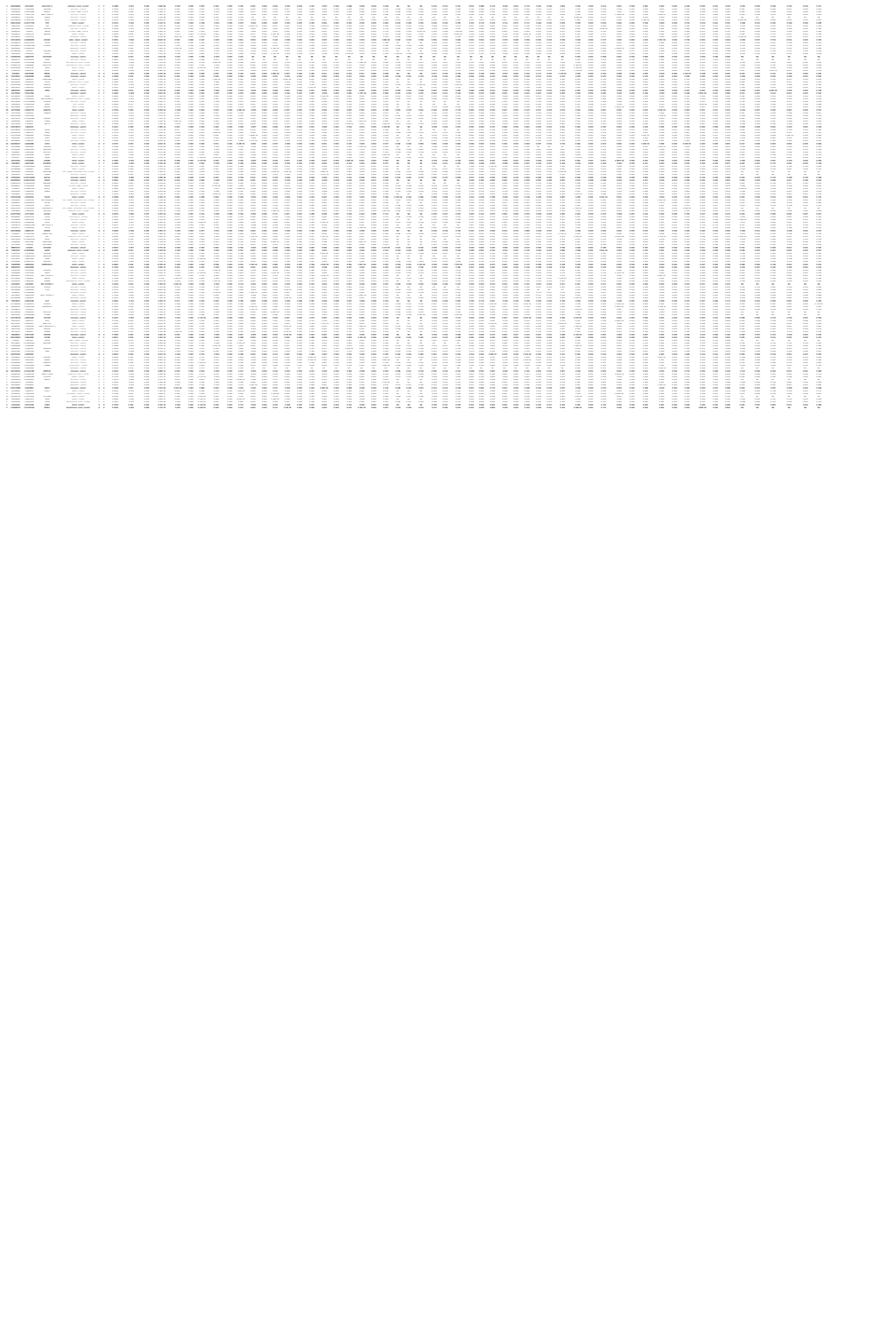
ENSG00000196924	FBP4A PPI subnetwork	ENSG00000172780	RAB43 PPI subnetwork	1.00E-03	<0.05	SF3B4 (8.800e-50)	AP3D1 (4.800e-27)	DDX27 (4.400e-24)	PAN2 (6.217e-15)	POLR2A (7.661e-15)	SMARCA5 (1.011e-10)	ILF3 (1.102e-10)	TSC2 (1.267e-10)	DHX38 (1.640e-09)	SART1 (2.409e-09)				
ENSG00000151211	EIF2B4 PPI subnetwork	ENSG00000093217	XYLB PPI subnetwork	1.01E-03	<0.05	CPNE1 (6.000e-52)	CDK5RAP1 (1.200e-27)	AAR2 (2.250e-26)	RNF25 (1.760e-20)	EIF4E2 (1.012e-12)	STYL (2.477e-12)	TMEM69 (2.388e-11)	CHD1L (3.226e-10)	NDUFAF1 (1.143e-09)	PNO1 (5.831e-09)				
RIBONUCLEOPROTEIN:TOME TRANSPORT OF RIBONUCLEOPROTEINS INTO THE HOST NUI		ENSG00000163002	NUP35 PPI subnetwork	1.01E-03	<0.05	RBM12 (6.000e-52)	CDK5RAP1 (1.200e-27)	PKN2 (5.040e-19)	NUP160 (2.430e-17)	POLR2B (9.992e-16)	UTP6 (1.665e-15)	CSE1L (2.220e-15)	PDS5B (1.669e-11)	TSFM (1.305e-09)	C18orf8 (4.148e-09)				
GO:0051604	protein maturation	GO:0016485	protein processing	1.01E-03	<0.05	CSNE (3.560e-42)	GHZ (1.560e-42)	GHI (7.200e-41)	SI46 (1.500e-34)	UHX1 (1.100e-28)	POMC (6.000e-25)	GHSR (5.160e-21)	ANKDB (5.418e-14)	PGGC (1.551e-13)	TMBIM4 (1.020e-09)				
ENSG00000136045	PWP1 PPI subnetwork	ENSG00000188205	DDX18 PPI subnetwork	1.02E-03	<0.05	FTSJ3 (6.300e-32)	AHCY (8.400e-28)	DDX27 (4.400e-24)	EXOSC5 (8.500e-21)	BCS1L (2.080e-20)	NCL (1.350e-18)	NOL8 (1.221e-15)	UTP6 (1.665e-15)	TRMT61A (6.006e-14)	NPM1 (5.040e-12)				
ENSG00000150347	ARIH2B PPI subnetwork	ENSG00000130803	ZNF317 PPI subnetwork	1.03E-03	<0.05	ZNF142 (2.640e-20)	ALPPL2 (2.900e-20)	NSG1 (1.277e-14)	IST2 (4.576e-11)	BOLA1 (1.924e-10)	CCNJ (3.058e-10)	ATAD2B (1.685e-07)	MEPCE (3.304e-07)	TACR2 (4.684e-07)	SYNPR (8.470e-07)				
ENSG00000154473	BUB3 PPI subnetwork	ENSG00000134690	CDC40 PPI subnetwork	1.05E-03	<0.05	NOP2 (1.170e-57)	CENPW (4.800e-40)	ZNF367 (8.000e-33)	CENPO (1.260e-30)	MPHOSPH9 (6.000e-21)	E2F1 (3.300e-20)	TOP2A (1.110e-16)	TACC3 (1.110e-16)	CSE1L (2.220e-15)	HIST1H4I (4.807e-14)				
ENSG00000085415	SEH1L PPI subnetwork	ENSG00000134690	CDC40 PPI subnetwork	1.05E-03	<0.05	NCAPG (1.170e-57)	CENPW (4.800e-40)	ZNF367 (8.000e-33)	CENPO (1.260e-30)	MPHOSPH9 (6.000e-21)	E2F1 (3.300e-20)	TOP2A (1.110e-16)	TACC3 (1.110e-16)	CSE1L (2.220e-15)	CENPF (6.839e-14)				
GO:0005640	nuclear outer membrane	GO:0031965	nuclear membrane	1.05E-03	<0.05	GHI (7.200e-41)	UHX1 (1.100e-28)	PIGU (1.177e-27)	POMC (6.000e-25)	NCR3LG1 (8.065e-13)	NMUR1 (2.005e-12)	TMEM88 (3.439e-09)	TMED10 (1.102e-08)	FADS1 (1.237e-08)	AGPAT2 (4.062e-08)				
DK2:ASSOCIATED EVER REACTOME CYCLIN ACDK2:ASSOCIATED EVENTS AT S PHASE ENTR		IATED PHOSPHORYLATION ANC	CDK:MEDIATED PHOSPHORYLATION AND REMOVA	3.06E-03	<0.05	SNRPC (6.800e-40)	PSMC5 (1.800e-38)	PSMA3 (4.950e-19)	SDHB (8.800e-18)	BTN3A2 (2.880e-17)	SNF8 (4.441e-16)	H1NT1 (3.109e-15)	GTF2B (4.885e-15)	EIF4E2 (1.032e-12)	TUBG1 (7.690e-12)				
ENSG00000112851	MRPL2 PPI subnetwork	ENSG00000164934	DCAF13 PPI subnetwork	3.06E-03	<0.05	HIST1H2AE (4.140e-73)	HIST1H2I (6.410e-66)	HIST1H4G (2.240e-63)	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	EXOSC5 (8.500e-21)	NCL (1.350e-18)	RPA (4.300e-18)	HIST1H2BB (3.131e-16)	SSSCA1 (9.992e-16)				
MP:0005503	abnormal tendon morphology	MP:0008438	abnormal cutaneous collagen fibril morphology	3.08E-03	<0.05	LOXL1 (1.020e-19)	ACAN (1.200e-19)	FBLN5 (3.220e-19)	IGFBPL1 (1.650e-16)	OMD (4.441e-16)	ASPN (4.441e-16)	FBLN2 (9.992e-16)	LTBP3 (1.221e-15)	ECM2 (1.332e-15)	ISLR (9.437e-15)				
MP:0002027	lung adenocarcinoma	MP:0002022	increased lymphoma incidence	3.09E-03	<0.05	CEP250 (5.500e-121)	ZNF367 (8.000e-33)	B3GNTB (1.690e-19)	GFI1 (2.502e-11)	TBX21 (3.557e-08)	GZMA (1.466e-07)	NAT8 (4.906e-07)	AKAP9 (1.385e-06)	ADAMTSL1 (1.066e-05)	SYPA2 (2.395e-05)				
ENSG00000101558	VAPA PPI subnetwork	ENSG00000188205	DDX18 PPI subnetwork	3.09E-03	<0.05	UQCC (1.240e-112)	DDX27 (4.400e-24)	ARHGEF2 (8.400e-22)	NOL8 (1.221e-15)	UTP6 (1.665e-15)	TRMT61A (6.006e-14)	NPM1 (5.040e-12)	CAPZA1 (5.087e-12)	GNL3 (6.115e-12)	TMEM69 (2.198e-11)				
DC20 AND OTHER APC/	DEGRADATION OF CDC20 AND OTHER APCCCDH1 TARGETED PRO	IATED PHOSPHORYLATION ANC	CDK:MEDIATED PHOSPHORYLATION AND REMOVA	3.09E-03	<0.05	SNRPC (6.800e-40)	PSMC5 (1.800e-38)	PSMC3 (4.950e-19)	SDHB (8.800e-18)	BTN3A2 (2.880e-17)	SNF8 (4.441e-16)	SSSCA1 (9.992e-16)	H1NT1 (3.109e-15)	GTF2B (4.885e-15)	EIF4E2 (1.032e-12)				
ENSG00000100479	POLE2 PPI subnetwork	GO:0044427	chromosomal part	3.10E-03	<0.05	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	NCAPG (1.17e-57)	CENPW (4.80e-40)	ZNF367 (8.00e-33)	CENPO (1.26e-30)	HIST1H1E (2.17e-28)	HIST1H2AC (2.61e-26)				
ENSG00000042429	MED17 PPI subnetwork	ENSG00000164758	MED30 PPI subnetwork	3.11E-03	<0.05	TEFM (9.000e-41)	TRMT6 (4.000e-25)	RQCD1 (7.800e-21)	ZNF142 (2.640e-20)	DOT1L (2.160e-18)	SEC16A (2.103e-11)	MED20 (6.233e-10)	GDF81 (1.057e-09)	DCAKD (1.934e-08)	DCAF7 (1.983e-07)				
ENSG00000117395	EBNA1BP2 PPI subnetwork	ENSG00000188205	DDX18 PPI subnetwork	3.12E-03	<0.05	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	EXOSC5 (8.500e-21)	NCL (1.350e-18)	NOL8 (1.221e-15)	UTP6 (1.665e-15)	TRMT61A (6.006e-14)	SDCCAG3 (1.029e-13)	NPM1 (5.040e-12)	GNL3 (6.115e-12)				
GO:0005518	collagen binding	GO:0031012	extracellular matrix	3.12E-03	<0.05	ADAMTSL3 (9.600e-29)	SCUBE3 (2.960e-28)	LOXL1 (1.020e-19)	ACAN (1.200e-19)	FBLN5 (3.220e-19)	OMD (4.441e-16)	ASPN (4.441e-16)	FBLN2 (9.992e-16)	LTBP3 (1.221e-15)	ECM2 (1.332e-15)				
ENSG00000080608	KIAA0020 PPI subnetwork	ENSG00000188205	DDX18 PPI subnetwork	3.15E-03	<0.05	HIST1H2AE (4.14e-73)	HIST1H2BG (2.20e-67)	HIST1H2BH (3.52e-67)	HIST1H1D (4.41e-66)	HIST1H4G (2.24e-63)	DDX42 (1.47e-38)	FTSJ3 (6.30e-32)	HIST1H1E (2.17e-28)	HIST1H2BD (2.17e-28)	HIST1H1T (2.75e-27)				
ENSG00000138092	CENPO PPI subnetwork	ENSG00000134690	CDC40 PPI subnetwork	3.16E-03	<0.05	NCAPG (1.170e-57)	CENPW (4.800e-40)	ZNF367 (8.000e-33)	CENPO (1.260e-30)	MPHOSPH9 (6.000e-21)	E2F1 (3.300e-20)	TOP2A (1.110e-16)	TACC3 (1.110e-16)	HIST1H4I (4.807e-14)	CENPF (6.839e-14)				
ENSG00000066654	THUMPD1 PPI subnetwork	IATED PHOSPHORYLATION ANC	CDK:MEDIATED PHOSPHORYLATION AND REMOVA	3.17E-03	<0.05	PSMC5 (1.800e-38)	ZNF341 (1.540e-37)	PSMC3 (4.950e-19)	PTRH2I (3.450e-18)	SDHB (8.800e-18)	HAGHL (2.554e-15)	EIF4E2 (1.032e-12)	IPI0K3 (2.126e-11)	CHRND (1.023e-09)	PSMD4 (1.762e-07)				
ENSG00000123219	CENPK PPI subnetwork	ENSG00000134690	CDC40 PPI subnetwork	3.19E-03	<0.05	NCAPG (1.170e-57)	CENPW (4.800e-40)	ZNF367 (8.000e-33)	CENPO (1.260e-30)	MPHOSPH9 (6.000e-21)	E2F1 (3.300e-20)	TOP2A (1.110e-16)	TACC3 (1.110e-16)	HIST1H4I (4.807e-14)	CENPF (6.839e-14)				
ENSG00000076242	MLH1 PPI subnetwork	ENSG00000122512	PMS2 PPI subnetwork	3.19E-03	<0.05	NCAPG (1.170e-57)	ZNF367 (8.000e-33)	USP37 (8.600e-21)	E2F1 (3.300e-20)	NOL8 (1.221e-15)	CSE1L (2.220e-15)	BMI1 (1.378e-13)	RBL1 (3.093e-13)	PSMC3IP (4.364e-12)	FAND (1.388e-11)				
ENSG00000211456	SACM1L PPI subnetwork	ENSG00000142892	PIGK PPI subnetwork	3.21E-03	<0.05	CCDC47 (4.200e-39)	ITCH (3.200e-23)	EIF2AK3 (5.200e-22)	RNF25 (1.760e-20)	CD164 (1.000e-16)	NUCB2 (2.959e-13)	RSRC1 (2.630e-12)	FBXPL (1.354e-11)	CNPY4 (5.284e-11)	FAM114C (1.280e-10)				
ENSG00000058091	CDK14 PPI subnetwork	GO:0000307	cyclin-dependent protein kinase holoenzyme complex	3.21E-03	<0.05	EPB41L1 (6.600e-34)	STAU1 (2.200e-24)	GATAD1 (1.470e-22)	LUZP1 (9.500e-20)	BICD2 (5.551e-15)	CHRND (1.023e-09)	ARHGAP21 (1.355e-08)	PTPN9 (4.115e-08)	RTN4 (4.018e-07)	CFL1 (1.521e-06)				
ENSG00000174547	MRPL11 PPI subnetwork	ENSG00000173867	ENSG00000137867 PPI subnetwork	3.22E-03	<0.05	TEFM (9.000e-41)	TACO1 (7.500e-25)	SDHB (8.800e-18)	ANAPC13 (1.121e-14)	PNRD (2.042e-12)	USCA2 (6.800e-12)	ATP13A1 (1.983e-11)	SFXN4 (7.840e-11)	DTRT1 (1.721e-10)	BOLA1 (1.924e-10)				
:TOME SIGNALING BY	REACTOME_SIGNALING_BY_PDGF	E DOWNSTREAM SIGNA	TREAM_DOWNSTREAM_SIGNAL_TRANSDUCTION	3.24E-03	<0.05	C6orf106 (2.449e-40)	LCHL1 (1.022e-19)	ACAN (1.200e-19)	ASPN (4.441e-16)	FBLN2 (9.992e-16)	LTBP3 (1.221e-15)	EHBP1L1 (1.443e-15)	ISLR (9.437e-15)	OGN (7.494e-14)	FAM101A (1.259e-12)				
URE MRNAS DERIVED I	TRANSPORT OF MATURE MRNAS DERIVED FROM INTRONLESS TR	ENSG00000163002	NUP35 PPI subnetwork	3.24E-03	<0.05	RBM12 (6.000e-52)	CDK5RAP1 (1.200e-27)	DTL0d (2.400e-20)	NUP160 (2.430e-17)	POLR2B (9.992e-16)	UTP6 (1.665e-15)	CSE1L (2.220e-15)	EXOSC9 (1.171e-11)	PDS5B (1.669e-11)	SEC16A (2.103e-11)				
ENSG00000166582	CENPV PPI subnetwork	ENSG00000130803	ZNF317 PPI subnetwork	3.24E-03	<0.05	RNF25 (1.760e-20)	ZNF142 (2.640e-20)	AUPP1Z (2.900e-20)	NSG1 (1.277e-14)	ZNF574 (5.513e-12)	IST2 (4.576e-11)	MEPCE (3.304e-07)	TACR2 (4.684e-07)	SYNPR (8.470e-07)	L3MYPDH (1.159e-06)				
ENSG00000177302	TDP3A PPI subnetwork	ENSG00000132383	RPA1 PPI subnetwork	3.25E-03	<0.05	CEP250 (5.500e-121)	ZNF367 (8.000e-33)	CCDC51 (1.760e-29)	FANCE (2.640e-25)	USP37 (8.600e-21)	E2F1 (3.300e-20)	SUZ12 (5.340e-14)	RMI1 (1.378e-13)	RBL1 (3.093e-13)	PSMC3IP (4.364e-12)				
GO:0060389	pathway-restricted SMAD protein phosphorylation	GO:0060389	pathway-restricted SMAD protein phosphorylation	3.27E-03	<0.05	BMP6 (2.700e-38)	FBOX3 (1.800e-31)	DYNI (8.400e-28)	SMAD6 (2.485e-09)	FAM20B (4.743e-09)	BMPR2 (1.421e-08)	SMAD7 (5.410e-08)	C16orf92 (1.272e-07)	GOLM1 (1.713e-07)	SLC2A8 (3.941e-05)				
ENSG00000124383	MPHOSPH10 PPI subnetwork	ENSG00000164934	DCAF13 PPI subnetwork	3.28E-03	<0.05	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	EXOSC5 (8.500e-21)	NCL (1.350e-18)	SSSCA1 (9.992e-16)	NOL8 (1.221e-15)	UTP6 (1.665e-15)	TRMT61A (6.006e-14)	NPM1 (5.040e-12)	GNL3 (6.115e-12)				
ENSG00000204356	RDBP PPI subnetwork	, POLYMERASE II TRANSCRIPTI	TOME RNA POLYMERASE II TRANSCRIPTION ELONG	3.28E-03	<0.05	RDMD1 (5.400e-52)	SMARCD2 (2.400e-32)	FUBP3 (6.320e-25)	SNF8 (4.441e-16)	SSSCA1 (9.992e-16)	SNAPC4 (3.069e-11)	ABT1 (8.286e-10)	WRAP53 (1.588e-09)	SART1 (2.409e-09)	SF3B14 (5.084e-09)				
ENSG00000206358	RDBP PPI subnetwork	, POLYMERASE II TRANSCRIPTI	TOME RNA POLYMERASE II TRANSCRIPTION ELONG	3.28E-03	<0.05	RDMD1 (5.400e-52)	SMARCD2 (2.400e-32)	FUBP3 (6.320e-25)	SNF8 (4.441e-16)	SSSCA1 (9.992e-16)	SNAPC4 (3.069e-11)	ABT1 (8.286e-10)	WRAP53 (1.588e-09)	SART1 (2.409e-09)	SF3B14 (5.084e-09)				
ENSG00000206357	RDBP PPI subnetwork	, POLYMERASE II TRANSCRIPTI	TOME RNA POLYMERASE II TRANSCRIPTION ELONG	3.28E-03	<0.05	RDMD1 (5.400e-52)	SMARCD2 (2.400e-32)	FUBP3 (6.320e-25)	SNF8 (4.441e-16)	SSSCA1 (9.992e-16)	SNAPC4 (3.069e-11)	ABT1 (8.286e-10)	WRAP53 (1.588e-09)	SART1 (2.409e-09)	SF3B14 (5.084e-09)				
ENSG00000198925	ATG9A PPI subnetwork	GO:0008135	translation factor activity, nucleic acid binding	3.29E-03	<0.05	FTSJ3 (6.300e-32)	DDX27 (4.400e-24)	NOL8 (1.221e-15)	TRMT61A (6.006e-14)	GNL3 (6.115e-12)	HIGAIP (7.119e-12)	SUGP1 (3.598e-11)	TWISTNB (8.711e-11)	SMARCA5 (1.013e-10)	C10orf12 (1.161e-10)				
ENSG00000138433	CIR3 PPI subnetwork	GO:0008380	RNA splicing	3.31E-03	<0.05	RBM39 (9.200e-51)	ANAPC10 (1.150e-24)	TRA2A (5.520e-24)	FNBP4 (2.880e-17)	MMAT3 (3.000e-16)	SENP6 (2.676e-14)	RSBN1L (7.837e-13)	DX39CS (1.173e-11)	SMARCA5 (1.013e-10)	CCDC6 (2.259e-09)				
GO:0030880	RNA polymerase complex	KEGG_RNA_POLYMERASE	KEGG_RNA_POLYMERASE	3.32E-03	<0.05	RDMD1 (5.400e-52)	DYNLRB1 (1.600e-24)	EXOSC5 (8.500e-21)	ATP5SL (2.000e-16)	SSSCA1 (9.992e-16)	TRMT61A (6.006e-14)	ZNF326 (1.805e-13)	SMRAM (2.460e-11)	C10orf12 (1.161e-10)	FAM195A (2.145e-10)				
ENSG00000097046	CDC7 PPI subnetwork	ENSG00000135336	ORC1 PPI subnetwork	3.32E-03	<0.05	NCAPG (1.17e-57)	CENPW (4.80e-40)	ZNF367 (8.00e-33)	CENPO (1.26e-30)	RQCD1 (7.80e-21)	USP37 (8.60e-21)	E2F1 (3.30e-20)	NUP160 (2.43e-17)	SLBP (6.00e-17)	SFXN5TI (9.60e-17)				
ENSG00000134697	GNL2 PPI subnetwork	ENSG00000188205	DDX18 PPI subnetwork	3.33E-03	<0.05	DDX42 (1.470e-38)	FTSJ3 (6.80e-32)	DDX27 (4.40e-24)	EXOSC5 (8.500e-21)	NCL (1.350e-18)	SSSCA1 (9.992e-16)	NOL8 (1.221e-15)	UTP6 (1.665e-15)	TRMT61A (6.006e-14)	NPM1 (5.040e-12)				
ENSG00000175279	ARTS1 PPI subnetwork	ENSG00000134690	CDC40 PPI subnetwork	3.33E-03	<0.05	NCAPG (1.17e-57)	CENPW (4.80e-40)	ZNF367 (8.00e-33)	CENPO (1.26e-30)	MPHOSPH9 (6.00e-21)	E2F1 (3.30e-20)	TOP2A (1.11e-16)	TACC3 (1.11e-16)	HIST1H4I (4.807e-14)	CENPF (6.839e-14)				
ENSG00000132341	RAN PPI subnetwork	ENSG00000163002	NUP35 PPI subnetwork	3.33E-03	<0.05	GTUD4 (2.400e-20)	UTP6 (1.665e-15)	CSE1L (2.220e-15)	KPNA3 (8.216e-14)	TUBG1 (7.690e-12)	PDS5B (1.669e-11)	SMARCA5 (1.013e-10)	ILF3 (1.102e-10)	IARS (5.688e-10)	THADA (4.461e-09)				
ENSG00000077514	POLD3 PPI subnetwork	:TOME LAGGING STRAND SYNT	REACTOME_LAGGING_STRAND_SYNTHESIS	3.34E-03	<0.05	ZNF367 (8.000e-33)	CENPO (1.260e-30)	PIGU (1.177e-27)	FANCE (2.640e-25)	EXOSC5 (8.500e-21)	USP37 (8.600e-21)	E2F1 (3.300e-20)	NUP160 (2.430e-17)	SLBP (6.000e-17)	CENPF (6.839e-14)				

Supplementary Table 23. Associations between the height variants and body mass index (BMI), waist-to-hip ratio (WHR), HDL-cholesterol (HDL), LDL-cholesterol (LDL), triglycerides (TG), total cholesterol (TC), myocardial infarction (MI), coronary artery disease (CAD), systolic blood pressure (SBP), diastolic blood pressure (DBP), age at menopause, age at menarche, type 2 diabetes (T2D), fasting glucose (FG), fasting insulin (FI), 2-hour glucose (2hGlu), and glycosylated hemoglobin (HbA1c). We highlight in pink P-values <2e-7 and in yellow pleiotropic coding variants with MAF <5%. The direction of the effect (BETA) and effect allele frequency (EAF) is given for the alternate (Alt) allele.

Chr	Pos (hg19)	rsID	Gene	VEP annotation	Ref	Alt	EAF (Alt allele)	HEIGHT BETA	HEIGHT SE	HEIGHT PVAL	BMI BETA	BMI SE	BMI PVAL	WHR BETA	WHR SE	WHR PVAL	HDL BETA	HDL SE	HDL PVAL
12	57146069	rs2277339	*PRIM1*	missense_variant	T	G	0.1049	-0.031	0.004	4.22E-16	-0.005	0.004	0.164	0.014	0.004	0.001	-0.006	0.004	1.14E-01
[illegible]																			
6	105378954	rs7759938	-	intergenic_variant	C	T	0.6784	-0.044	0.003	2.78E-59	0.001	0.002	0.680	-0.010	0.003	0.001	0.005	0.003	9.87E-02
9	108967088	rs2090409	-	intergenic_variant	C	A	0.3266	-0.023	0.003	2.95E-18	0.007	0.002	0.002	-0.005	0.003	0.122	-0.007	0.003	8.66E-03
[illegible]																			

rsID	LDL BETA	LDL SE	LDL PVAL	TG BETA	TG SE	TG PVAL	TC BETA	TC SE	TC PVAL	MI BETA	MI SE	MI PVAL	CAD BETA	CAD SE	CAD PVAL	SBP BETA	SBP SE	SBP PVAL	DBP BETA	DBP SE	DBP PVAL
rs2277339	-0.003	0.004	0.477	0.011	0.004	0.007	-0.002	0.004	0.628	0.017	0.017	0.322	0.031	0.015	0.038	-0.011	0.093	0.905	-0.075	0.055	0.174
[illegible]																					
rs7759938	0.003	0.003	0.293	-0.010	0.003	4.56E-04	0.002	0.003	0.359	NA	NA	NA	0.013	0.010	0.206	-0.034	0.062	0.590	0.006	0.037	0.863
rs2090409	0.005	0.003	0.079	0.003	0.003	0.220	0.004	0.003	0.120	0.002	0.011	0.870	0.001	0.010	0.898	0.080	0.063	0.206	0.025	0.038	0.514
[illegible]																					

rsID	T2D BETA	T2D SE	T2D PVAL	HbA1c BETA	HbA1c SE	HbA1c PVAL	FI BETA	FI SE	FI PVAL	FG BETA	FG SE	FG PVAL	2hGlu BETA	2hGlu SE	2hGlu PVAL	Menarche BETA	Menarche SE	Menarche PVAL	Menopause BETA	Menopause SE	Menopause PVAL
rs2277339	0.034	0.020	0.043	0.001	0.002	0.780	0.008	0.003	0.033	0.004	0.003	0.275	0.045	0.014	4.55E-04	-0.001	0.010	0.893	-0.312	0.035	1.78E-19
[illegible]																					
rs7759938	-0.010	0.016	0.995	-3.26E-04	0.002	0.926	-0.008	0.002	0.001	-0.010	0.002	1.15E-05	-0.019	0.010	0.039	-0.118	0.005	7.83E-110	-0.047	0.022	0.030
rs2090409	0.002	0.015	0.973	4.32E-04	0.001	0.639	-0.002	0.002	0.217	-0.002	0.002	0.234	0.025	0.010	0.011	-0.089	0.005	2.30E-63	-0.023	0.022	0.296
[illegible]																					



Supplementary Table 24. Biological information for genes with rare or low-frequency variants associated with height (see Tables 1 and 2 in the main text).

rsid	Gene	Function	Function (NCBI Gene)	Expression pattern (GTEx)	OMIM/Animal model
rs147445258; rs775421 62	*ABCB6*	missense; missense	The membrane-associated protein encoded by this gene is a member of the superfamily of ATP-binding cassette (ABC) transporters. ABC proteins transport various molecules across extra- and intra-cellular membranes. ABC genes are divided into seven distinct subfamilies (ABC1, MDR/TAP, MRP, ALD, OABP, GCN20, White). This protein is a member of the MDR/TAP subfamily. Members of the MDR/TAP subfamily are involved in multidrug resistance as well as antigen presentation. This half-transporter likely plays a role in mitochondrial function. Localized to 2q26, this gene is considered a candidate gene for lethal neonatal	Relatively high expression in all tissues, except whole blood.	Lan blood group, dominant iris and chorioretinal coloboma, dominant dyschromatosis universalis hereditaria
rs16942341	*ACAN*	synonymous	This gene is a member of the aggrecan/versican proteoglycan family. The encoded protein is an integral part of the extracellular matrix in cartilagenous tissue and it withstands compression in cartilage. Mutations in this gene may be involved in skeletal dysplasia and spinal degeneration.	Higher expression in arteries.	Osteochondritis dissecans, short stature, and early-onset osteoarthritis
rs7636	*ACHE*	synonymous	Acetylcholinesterase hydrolyzes the neurotransmitter, acetylcholine at neuromuscular junctions and brain cholinergic synapses, and thus terminates signal transmission. It is also found on the red blood cell membranes, where it constitutes the Yt blood group antigen. Acetylcholinesterase exists in multiple molecular forms which possess similar catalytic properties, but differ in their oligomeric assembly and mode of cell attachment to the cell surface. It is encoded by the single ACHE gene, and the structural diversity in	Hiegher expression in the CNS.	Yt blood group
rs141374503	*ADAMTS3*	missense	This gene encodes a member of the ADAMTS [a disintegrin and metalloproteinase with thrombospondin motifs] protein family. Members of the family share several distinct protein modules, including a propeptide region, a metalloproteinase domain, a disintegrin-like domain, and a thrombospondin type 1 (TS) motif. Individual members of this family differ in the number of C-terminal TS motifs, and some have unique C-terminal domains. The protein encoded by this gene is the major procollagen II N-propeptidase. A deficiency	Ubiquitous low expression.	
rs61736454	*ADAMTS6*	missense	This gene encodes a member of the ADAMTS [a disintegrin and metalloproteinase with thrombospondin motifs] protein family. Members of the family share several distinct protein modules, including a propeptide region, a metalloproteinase domain, a disintegrin-like domain, and a thrombospondin type 1 (TS) motif. Individual members of this family differ in the number of C-terminal TS motifs, and some have unique C-terminal domains.	Ubiquitous low expression.	
rs138059525	*AMOTL1*	missense	The protein encoded by this gene is a peripheral membrane protein that is a component of tight junctions or TJs. TJs form an apical junctional structure and act to control paracellular permeability and maintain cell polarity. This protein is related to angiomotin, an angiostatin binding protein that regulates endothelial cell migration and capillary formation.	Relatively high expression in all tissues, except whole blood and EBV-lymphocytes.	
rs13141	*ANAPC5*	missense	This gene encodes a tetratricopeptide repeat-containing component of the anaphase promoting complex/cyclosome (APC/C), a large E3 ubiquitin ligase that controls cell cycle progression by targeting a number of cell cycle regulators such as B-type cyclins for 26S proteasome-mediated degradation through ubiquitination. The encoded protein is required for the proper ubiquitination function of APC/C and for the interaction of APC/C with transcription coactivators. It also interacts with polyA binding protein and represses internal ribosome entry site-mediated translation.	High expression in all tissues	
rs137852591	*AR*	missense	The androgen receptor gene is more than 90 kb long and codes for a protein that has 3 major functional domains: the N-terminal domain, DNA-binding domain, and androgen-binding domain. The protein functions as a steroid-hormone activated transcription factor. Upon binding the hormone ligand, the receptor dissociates from accessory proteins, translocates into the nucleus, dimerizes, and then stimulates transcription of androgen responsive genes. This gene contains 2 polymorphic trinucleotide repeat segments	Highest expression in reproductive tissues, and moderate expression in heart and liver.	Aminal models have studies the AR gene with respect to several diseases, including Spinal and Bulbar Muscular Atrophy,body size, litter size, prostate cancer, just to name a few. For exampe, Abel et al. (2001) created transgenic mice that developed many of the motor symptoms of SBMA and had a truncated, highly expanded AR gene driven by the neurofilament light chain (162280) promoter. McManamny et al. (2002) developed a transgenic model of SBMA expressing a full-length human AR cDNA carrying 65 (AR-65) or 120 CAG repeats (AR-120), with widespread expression driven by the cytomegalovirus promoter. Mice carrying the AR-120 transgene displayed behavioral and motor dysfunction, while mice carrying 65 CAG repeats showed a mild phenotype. Sato et al. (2003)
rs141923065	*ARMC5*	splice_acceptor	This gene encodes a member of the ARM (armadillo/beta-catenin-like repeat) superfamily. The ARM repeat is a tandemly repeated sequence motif with approximately 40 amino acid long. This repeat is implicated in mediating protein-protein interactions. The encoded protein contains seven ARM repeats. Mutations in this gene are associated with primary bilateral macronodular adrenal hyperplasia, which is also known as ACTH-independent macronodular adrenal hyperplasia 2.	Modest expression across all tissues	ACTH-independent macronodular adrenal hyperplasia 2
rs3208856	*CBLC*	missense	This gene encodes a member of the Cbl family of E3 ubiquitin ligases. Cbl proteins play important roles in cell signaling through the ubiquitination and subsequent downregulation of tyrosine kinases.	No expression in the CNS. Expression in several tissues, including bladder, stomach, skin, etc.	
rs33966734	*CCND3*	stop-gained	The protein encoded by this gene belongs to the highly conserved cyclin family, whose members are characterized by a dramatic periodicity in protein abundance through the cell cycle. Cyclins function as regulators of CDK kinases. Different cyclins exhibit distinct expression and degradation patterns which contribute to the temporal coordination of each mitotic event. This cyclin forms a complex with and functions as a regulatory subunit of CDK4 or CDK6, whose activity is required for cell cycle G1/S transition. This protein has been shown to interact with and be involved in the phosphorylation of tumor suppressor	Modest expression across all tissues	
rs4072796	*CD163L1*	missense	This gene encodes a member of the scavenger receptor cysteine-rich (SRCR) superfamily. Members of this family are secreted or membrane-anchored proteins mainly found in cells associated with the immune system. The SRCR family is defined by a 100-110 amino acid SRCR domain, which may mediate protein-protein interaction and ligand binding. The encoded protein contains twelve SRCR domains, a transmembrane region and a cytoplasmic domain. Alternative splicing results in multiple transcript variants encoding different isoforms.	Almost no expression in all tissues, except moderate expression in spleen and low expression in colon.	
rs17480616	*CNOT4*	missense	The protein encoded by this gene is a subunit of the CCR4-NOT complex, a global transcriptional regulator. The encoded protein interacts with CNOT1 and has E3 ubiquitin ligase activity.	Modest expression across all tissues, but low in whole blood.	
rs148934412; rs1496615348	*CRISPLD2*	missense; missense	Chiquet et al (2011) reported that variation in CRISPLD2 is associated with nonsyndromic cleft lip and palate. Both *CRISPLD1* and *CRISPLD2* are expressed in murine craniofacies. They could play a role in the folic acid pathway and cartilage formation.	High expression in all tissues, except the CNS and EBV-lymphocytes.	
rs11722554	*CYTL1*	missense	C17 is a cytokine-like protein specifically expressed in bone marrow and cord blood mononuclear cells that bear the CD34 surface marker.	High expression in aorta ateries.	Jeon et al. (2011) found that Cytl1 -/- mice were viable and showed normal postnatal growth and development of lung, heart, and long bones. Cytl1 -/- mice exhibited normal cartilage development and endochondral ossification. Chondrogenesis of Cytl1 -/- mesenchymal cells induced by micromass cultures was normal. Cytl1 expression was reduced in a mouse model of osteoarthritis, and deletion of Cytl1 enhanced osteoarthritis cartilage destruction. Jeon et al. (2011) concluded that CYTL1 is not essential for induction of chondrogenesis, but that it may be required for maintenance of cartilage homeostasis.
rs9838238	*DCBLD2*	missense	Discoidina neuropilin-like membrane protein. Potentially implicated in tumorogenesis and protein degradation.	Higher expression in transformed fibroblasts.	
rs7757648	*DDR1*	intron	Receptor tyrosine kinases play a key role in the communication of cells with their microenvironment. These kinases are involved in the regulation of cell growth, differentiation and metabolism. The protein encoded by this gene belongs to a subfamily of tyrosine kinase receptors with homology to Dictyostelium discoideum protein discoidin I in their extracellular domain, and that are activated by various types of collagen.	Expression of this protein is restricted to epithelial cells, particularly in the kidney, lung, gastrointestinal tract, and brain.	
rs7571816	*DIS3L2*	intron	The protein encoded by this gene is similar in sequence to 3'/5' exonucleolytic subunits of the RNA exosome. The exosome is a large multimeric ribonucleotide complex responsible for degrading various RNA substrates.	Modest expression in all tissues, but low in whole blood.	Mutated in Perlman syndrome (similarities with BWS)
rs144673025	*DISP1*	missense	The pattern of cellular proliferation and differentiation that leads to normal development of embryonic structures often depends upon the localized production of secreted protein signals. Cells surrounding the source of a particular signal respond in a graded manner according to the effective concentration of the signal, and this response produces the pattern of cell types constituting the mature structure. A novel segment-polarity gene known as dispatched has been identified in Drosophila and its protein product is	Modest expression in all tissues, but low in whole-blood and EBV-lymphocytes.	
rs2066674	*DLEU1*	intron	One of 2 long non-coding RNA genes (DLEU1 and DLEU2) that map to chr band 13Q14.3 that is recurrently deleted in solid tumors and hematopoietic malignancies like chronic lymphocytic leukemia (Gardina A et al. Plos Genet 2013).	Low expression in all tissues	
rs41274586	*DLG5*	missense	This gene encodes a member of the family of discs large (DLG) homologs, a subset of the membrane-associated guanylate kinase (MAGUK) superfamily. The MAGUK proteins are composed of a catalytically inactive guanylate kinase domain, in addition to PDZ and SH3 domains, and are thought to function as scaffolding molecules at sites of cell-cell contact. The protein encoded by this gene localizes to the plasma membrane and cytoplasm, and interacts with components of adherens junctions and the cytoskeleton. It is	Relatively high expression in all tissues, except in whole blood and EBV-lymphocytes.	
rs34471628	*DUSP1*	missense	The expression of DUSP1 gene is induced in human skin fibroblasts by oxidative/heat stress and growth factors. It specifies a protein with structural features similar to members of the non-receptor-type protein-tyrosine phosphatase family, and which has significant amino-acid sequence similarity to a Tyr/Ser-protein phosphatase encoded by the late gene H1 of vaccinia virus. The bacterially expressed and purified DUSP1 protein has intrinsic phosphatase activity, and specifically inactivates mitogen-activated protein (MAP)	High expression in all tissues, except modest in CNS and low in EBV-lymphocytes	
rs41511151	*ELN*	missense	This gene encodes a protein that is one of the two components of elastic fibers. The encoded protein is rich in hydrophobic amino acids such as glycine and proline, which form mobile hydrophobic regions bounded by crosslinks between lysine residues. Deletions and mutations in this gene are associated with supravalvular aortic stenosis (SVAS) and autosomal dominant cutis laxa. Multiple transcript variants encoding different isoforms have been found for this gene.	Low expression in all tissues, except moderate expression in aorta, coronary and tibial arteries.	Li et al. (1998) defined the role of elastin in arterial development and disease by generating mice lacking elastin. These mice died of an obstructive arterial disease that resulted from subendothelial cell proliferation and reorganization of smooth muscle. These cellular changes were similar to those seen in atherosclerosis; however, lack of elastin was not associated with endothelial damage, thrombosis, or inflammation, which occur in models of atherosclerosis. Disruption of elastin was enough to induce subendothelial proliferation of smooth muscle and may contribute to obstructive arterial disease. ELN hemizygosity in mice and humans induces a compensatory increase in the number of rings of elastic lamellae and smooth muscle during arterial development. Humans are exquisitely sensitive to reduced ELN expression, developing profound arterial thickening and markedly increased risk of obstructive vascular disease. Lee et al. (2007) studied the immune responses of age-matched smokers with and without emphysema and found that differential responsiveness of T cells to elastin peptides, but not to collagenor albumin, correlated with emphysema severity. They concluded that antielastin autoimmunity possibly resulting from secretion of proteolytic enzymes induced by cigarette smoke exposure is associated with an inflammatory response
rs116858574	*EMC4*	missense	ER membrane protein complex subunit 4	Moderate expression acorss all tissues.	
rs41292521	*EPS15*	missense	This gene encodes a protein that is part of the EGFR pathway. The protein is present at clatherin-coated pits and is involved in receptor-mediated endocytosis of EGF. Notably, this gene is rearranged with the HRX/ALL/MLL gene in acute myelogeneous leukemias.	High expression in all tissues	
rs78727187	*FBN2*	missense	The protein encoded by this gene is a component of connective tissue microfibrils and may be involved in elastic fiber assembly. Mutations in this gene cause congenital contractural arachnodactyly	High expression in transformed fibfoblasts	Contractural arachnodactyly, congenital; Macular degeneration, early-onset
rs138273386	*FIBIN*	missense	fin bud initiation factor homolog (zebrafish);protein coding;	High expression in Tibial Nerve and Artery Aorta	
rs28925904	*GAB1*	missense	The protein encoded by this gene is a member of the IRS1-like multisubstrate docking protein family. It is an important mediator of branching tubulogenesis and plays a central role in cellular growth response, transformation and apoptosis. Two transcript variants encoding different isoforms have been found for this gene.	Modest expression across all tissues;high in Tibial Nerve	Vasyutina et al. (2005) found that Cxcr4 (162643)-positive muscle progenitor cells reach the anlage of the tongue in Gab1-null or Cxcr4-null mouse embryos, but not in Cxcr4/Gab1 double mutants, suggesting that these proteins interact during progenitor cell migration.To reveal the functions of Gab1 in vivo, Itoh et al. (2000) generated mice lacking Gab1 by gene targeting. Gab1-deficient embryos died in utero and displayed developmental defects in the heart, placenta, and skin, which were similar to phenotypes observed in mice lacking signals of the hepatocyte growth factor (142409), platelet-derived growth factor (e.g., 173430), and epidermal growth factor (131530) pathways. Consistent with these observations, extracellular signal-regulated kinase mitogen-activated protein kinase (ERK MAPK) was activated at much lower levels in cells from Gab1-deficient embryos in response to these growth factors or to stimulation of
rs77169818	*GALR1*	missense	The neuropeptide galanin elicits a range of biological effects by interaction with specific G-protein-coupled receptors. Galanin receptors are seven-transmembrane proteins shown to activate a variety of intracellular second-messenger pathways. GALR1 inhibits adenylyl cyclase via a G protein of the Gi/Go family. GALR1 is widely expressed in the brain and spinal cord, as well as in peripheral sites such as the small intestine and heart.	Low expression in all tissues;high in Pituitary	Galanin (137035) is an important neuromodulator present in the brain, gastrointestinal system, and hypothalamopituitary axis. It is a 30-amino acid non-C-terminally amidated peptide that potently stimulates growth hormone secretion, inhibits cardiac vagal slowing of heart rate, abolishes sinus arrhythmia, and inhibits postprandial gastrointestinal motility. The actions of galanin are mediated through interaction with specific membrane receptors that are members of the 7-transmembrane family of G protein-coupled receptors. Walli et al. (1994) identified and biochemically characterized a specific receptor for galanin in various areas of human brain. Habert-Ortoli et al. (1994) also cloned a functional human galanin receptor
rs117801489	*GLT8D2*	missense	glycosyltransferase 8 domain containing 2;protein coding	High to moderate expression in most tissues;highest in Artery Aorta	
rs34354104	*GMPR2*	missense	It is a Protein Coding gene. Among its related pathways are Metabolism and Purine metabolism (REACTOME). GO annotations related to this gene include GMP reductase activity. An important paralog of this gene is IMPDH2.	High expression in all tissues;highest in Adrenal Gland	
rs34815962	*GRAMD2*	missense	GRAM domain containing 2	Low expression in all tissues;highest in Thyroid and Lung	

rs141308595	*HAPLN3*	missense	This gene belongs to the hyaluronan and proteoglycan binding link protein gene family. The protein encoded by this gene may function in hyaluronic acid binding and cell adhesion.	Moderate to low expression; highest in Artery Aorta	
rs140385822	*HSD11B2*	missense	There are at least two isozymes of the corticosteroid 11-beta-dehydrogenase, a microsomal enzyme complex responsible for the interconversion of cortisol and cortisone. The type I isozyme has both 11-beta-dehydrogenase (cortisol to cortisone) and 11-oxoreductase (cortisone to cortisol) activities. The type II isozyme, encoded by this gene, has only 11-beta-dehydrogenase activity. In aldosterone-selective epithelial tissues such as the kidney, the type II isozyme catalyzes the glucocorticoid cortisol to the inactive metabolite cortisone, thus preventing illicit activation of the mineralocorticoid receptor. In tissues that do not express	low expression;highest in Colon Transverse, Kidney and Small Instestine	Kotelevtsev et al. (1999) generated Hsd11b2-null mice. All of the mice appeared normal at birth, but about 50% showed motor weakness and died within 48 hours. Male and female survivors were fertile but exhibited hypokalemia, hypotonic polyuria, and apparent mineralocorticoid activity of corticosterone. Young adult Hsd11b2-null mice were markedly hypertensive with hypertrophy and hyperplasia of the epithelium of the distal tubules of the nephron; the histologic changes did not reverse with mineralocorticoid receptor antagonism. Kotelevtsev et al. (1999) concluded that Hsd11b2-null mice provide a model for the human syndrome of apparent mineralocorticoid excess
rs142036701	*IHH*	missense	This gene encodes a member of the hedgehog family of secreted signaling molecules. Hedgehog proteins are essential regulators of a variety of developmental processes including growth, patterning and morphogenesis. The encoded protein specifically plays a role in bone growth an differentiation. Mutations in this gene are the cause of brachydactyly type A1 which is characterized by shortening or malformation of the phalanges. Mutations in this gene are also the cause of acrocapitofemoral dysplasia.	low expression;highest in Colon Transverse, Small Instestine and Stomach	Acrocapitofemoral dysplasia;Brachydactyly, type A1
rs4252548	*IL11*	missense	The protein encoded by this gene is a member of the gp130 family of cytokines. These cytokines drive the assembly of multisubunit receptor complexes, all of which contain at least one molecule of the transmembrane signaling receptor IL6ST (gp130). This cytokine is shown to stimulate the T cell-dependent development of immunoglobulin-producing B cells. It is also found to support the proliferation of hematopoietic stem cells and megakaryocyte progenitor cells. Alternatively spliced transcript variants encoding distinct isoforms have been found for this gene.	low expression	IL13 (147683) is a major stimulator of inflammation and tissue remodeling at sites of Th2 inflammation. Chen et al. (2005) found that transgenic mice overexpressing Il13 specifically in lung showed upregulation of both Il11 and Il11ra (600939), but not Il6r (147880), as well as upregulation of other IL6 (147620)-type cytokines and a modest increase in gp130 (IL6ST; 600694). Il13 transgenic Il11ra -/- mice exhibited a decrease in the inflammatory response seen in Il13 transgenic Il13ra +/+ mice, as well as reduced fibrosis, hyaluronic acid accumulation, chemokine production, and alveolar remodeling response. Il13 transgenic Il11ra -/- mice also survived significantly longer than Il13 transgenic Il11ra +/+ mice. Chen et al. (2005) concluded that IL11RA plays a key role in the pathogenesis of IL13-induced inflammation and remodeling. They proposed that IL11, which is induced simultaneously with IL13 in inflammatory
rs11575580	*IL11RA*	missense	Interleukin 11 is a stromal cell-derived cytokine that belongs to a family of pleiotropic and redundant cytokines that use the gp130 transducing subunit in their high affinity receptors. This gene encodes the IL-11 receptor, which is a member of the hematopoietic cytokine receptor family. This particular receptor is very similar to ciliary neurotrophic factor, since both contain an extracellular region with a 2-domain structure composed of an immunoglobulin-like domain and a cytokine receptor-like domain. Multiple alternatively spliced transcript variants have been found for this gene.	moderate expression;higher in Artery Aorta, Colon Sigmoid and Thyroid	IL13 (147683) is a major stimulator of inflammation and tissue remodeling at sites of Th2 inflammation. Chen et al. (2005) found that transgenic mice overexpressing Il13 specifically in lung showed upregulation of both Il11 and Il11ra, but not Il6r, as well as upregulation of other IL6 (147620)-type cytokines and a modest increase in gp130. Il13 transgenic Il11ra -/- mice exhibited a decrease in the inflammatory response seen in Il13 transgenic Il13ra +/+ mice, as well as reduced fibrosis, hyaluronic acid accumulation, chemokine production, and alveolar remodeling response. Il13 transgenic Il11ra -/- mice also survived significantly longer than Il13 transgenic Il11ra +/+ mice. Chen et al. (2005) concluded that IL11RA plays a key role in the pathogenesis of IL13-induced inflammation and remodeling. They proposed that IL11, which is induced simultaneously with IL13 in inflammatory disorders such as asthma, may mediate
rs150341307	*IQCC*	missense	IQCC (IQ Motif Containing C) is a Protein Coding gene.	low expression;highest in Testis	
rs34343821	*KIAA0922*	missense	Also known as TMEM131L. Isoform 1: Membrane-associated form that antagonizes canonical Wnt signaling by triggering lysosome-dependent degradation of Wnt-activated LRP6. Regulates thymocyte proliferation.	low expression;highest in EBV transformed lymphocytes	KIAA0922, or TMEM131L, is a regulator of intrathymic proliferation and differentiation and an antagonist of the Wnt (see 164820) signaling pathway (Maharzi et al., 2013)
rs79485039	*KIAA1614*	missense	Protein coding gene with unknown function.	Varied, but mostly moderate expression across all tissues with highest expression in the brain cerebellum and cerebellar hemisphere.	
rs117295933	*KLHL28*	missense	The Kelch-like (KLHL) gene family encodes a group of proteins that generally possess a BTB/POZ domain, a BACK domain, and five to six Kelch motifs. BTB domains facilitate protein binding and dimerization. The BACK domain has no known function yet is of functional importance since mutations in this domain are associated with disease. Kelch domains form a tertiary structure of β-propellers that have a role in extracellular functions, morphology, and binding to other proteins. Presently, 42 KLHL genes have been identified by the HUGO Gene Nomenclature Committee (HGNC), and they can be found across multiple human		
rs35713889	*LAMB2*	missense	Laminins, a family of extracellular matrix glycoproteins, are the major noncollagenous constituent of basement membranes. They have been implicated in a wide variety of biological processes including cell adhesion, differentiation, migration, signaling, neurite outgrowth and metastasis. Laminins, composed of 3 non identical chains: laminin alpha, beta and gamma (formerly A, B1, and B2, respectively), form a cruciform structure consisting of 3 short arms, each formed by a different chain, and a long arm composed of all 3 chains. Each laminin chain is a multidomain protein encoded by a distinct gene. Several isoforms of each	moderate to high expression;highest in Ovary and Artery Aorta	Nephrotic syndrome, type 5, with or without ocular abnormalities;Pierson syndrome
rs62623707	*LECT2*	missense	This gene encodes a secreted, 16 kDa protein that acts as a chemotactic factor to neutrophils and stimulates the growth of chondrocytes and osteoblasts. This protein has high sequence similarity to the chondromodulin repeat regions of the chicken myb-induced myeloid 1 protein. A polymorphism in this gene may be associated with rheumatoid arthritis	low expression;highest in Liver	Yamagoe et al. (1998) stated that LECT2 is the same as bovine chondromodulin II, a positive regulator of chondrocyte proliferation, and is highly related to chicken mim1, a myeloblastosis-induced myeloid protein (see 189990) and CEBPB (189965) target gene.
rs8052655	*LRRC36*	missense	LRRC36 (Leucine Rich Repeat Containing 36) is a Protein Coding gene. An important paralog of this gene is CEP72	low expression;highest in Testis	
rs34821177	*MARCH3*	missense	This gene encodes a member of the membrane-associated RING-CH (MARCH) family. The encoded protein is an E3 ubiquitin-protein ligase that may be involved in regulation of the endosomal transport pathway.	Ubiquitous expression.	
rs52826764	*MATN3*	missense	This gene encodes a member of von Willebrand factor A domain containing protein family. This family of proteins is thought to be involved in the formation of filamentous networks in the extracellular matrices of various tissues. This protein contains two von Willebrand factor A domains; it is present in the cartilage extracellular matrix and has a role in the development and homeostasis of cartilage and bone. Mutations in this gene result in multiple epiphyseal dysplasia.	Low expression except in the lungs and tibial nerves.	Multiple Epiphyseal Dysplasia. Spondyloepimetaphyseal Dysplasia. To assess the function of matrilin-3 during skeletal development, Ko et al. (2004) generated Matn3-null mice. Homozygous mutant mice appeared normal, were fertile, and showed no obvious skeletal malformations. Histologic and ultrastructural analysis revealed endochondral bone formation indistinguishable from that of wildtype animals. Northern blot, immunohistochemical, and biochemical analyses indicated no compensatory upregulation of any other member of the matrilin family. Ko et al. (2004) hypothesized that matrilins are functionally redundant and that the phenotypes of MED disorders are not caused by the absence of matrilin-3 in cartilage.
rs11580946	*MCL1*	missense	This gene encodes an anti-apoptotic protein, which is a member of the Bcl-2 family. The longest gene product (isoform 1) enhances cell survival by inhibiting apoptosis while the alternatively spliced shorter gene products (isoform 2 and isoform 3) promote apoptosis and are death-inducing.	High expression across all tissues. Higher expression in whole blood, adipose, and liver	MCL1 as an attractive candidate for regulation of hematopoietic stem cell homeostasis that is highly expressed in hematopoietic stem cells and regulated by growth factor signals. Inducible deletion of Mcl1 in mice resulted in ablation of bone marrow.
rs147348682	*MEI1*	missense	meiotic double-stranded break formation protein 1. Required for normal meiotic chromosome synapsis. May be involved in the formation of meiotic double-strand breaks (DSBs) in spermatocytes (By similarity).	Relative low expression, although the highest expression is in teh testis	Libby et al. (2003) found that homozygous Mei1-null mice were sterile due to meiotic arrest caused by defects in chromosome synapsis. There was a lack of zygotene Rad51 (179617) foci and, presumably, defects in the production of genetically programmed double-strand breaks, similar to the phenotype seen in Spo11 (605114)-null mice.
rs17880989	*MMP14*	missense	Proteins of the matrix metalloproteinase (MMP) family are involved in the breakdown of extracellular matrix in normal physiological processes, such as embryonic development, reproduction, and tissue remodeling, as well as in disease processes, such as arthritis and metastasis. Most MMP's are secreted as inactive proproteins which are activated when cleaved by extracellular proteinases. However, the protein encoded by this gene is a member of the membrane-type MMP (MT-MMP) subfamily; each member of this subfamily contains a potential transmembrane domain sequence that, when mutated or removed, it thus cell surface	Ubiquotuos expression effect in brain tissues and whole blood	Mmp14 deficiency caused craniofacial dysmorphism, arthritis, osteopenia, dwarfism, and fibrosis of soft tissues due to ablation of a collagenolytic activity that is essential for modeling of skeletal and extraskeletal connective tissues. These findings demonstrated the pivotal function of MMP14 in connective tissue metabolism and illustrated that modeling of the soft connective tissue matrix by resident cells is essential for the development and maintenance of the hard tissues of the skeleton
rs145659444	*MTMR11*	missense	Myotubularin Related Protein 11. GO annotations related to this gene include phosphatase activity.	Relatively very low expression, highest expression in colon and intestine	
rs16859517	*NHEJ1*	intron	Double-strand breaks in DNA result from genotoxic stresses and are among the most damaging of DNA lesions. This gene encodes a DNA repair factor essential for the nonhomologous end-joining pathway, which preferentially mediates repair of double-stranded breaks. Mutations in this gene cause different kinds of severe combined immunodeficiency disorders.	Very low expression across all tissues	severe combined immunodeficiency with microcephaly, growth retardation, and sensitivity to ionizing radiation
rs921122	*NOL8*	missense	NOL8 binds Ras-related GTP-binding proteins (see MIM 608267) and plays a role in cell growth (Sekiguchi et al., 2004).	High expression across all tissues.	
rs146301345	*NPR3*	missense	This gene encodes one of three natriuretic peptide receptors. Natriuretic peptides are small peptides which regulate blood volume and pressure, pulmonary hypertension, and cardiac function as well as some metabolic and growth processes. The product of this gene encodes a natriuretic peptide receptor responsible for clearing circulating and extracellular natriuretic peptides through endocytosis of the receptor.	Really low expression in transformed fibrobalst	Hypertention salt resistence. In 1979, a mutation designated 'longjohn' (lgj), because affected mice displayed an exceptionally long body, arose in BALB/cJ mice at the Jackson Laboratory. A second allele, designated 'strigosus' (stri), which in Latin means 'long and emaciated,' was identified at the Institut Pasteur; it arose in 1989 in an outbred stock after chemical mutagenesis with ethylnitrosourea. The first and a third allele discovered at the Jackson Laboratory were spontaneous mutations. All 3 mutations were proven to be allelic by progeny testing. The phenotype was found to be recessive and to map to the proximal region of mouse chromosome 15. Analysis of skeletal preparations of stri/stri mice indicated that the endochondral ossification process was slightly delayed,
rs78247455; rs28932177	*NSD1*	missense; missense	This gene encodes a protein containing a SET domain, 2 LXXLL motifs, 3 nuclear translocation signals (NLSs), 4 plant homeodomain (PHD) finger regions, and a proline-rich region. The encoded protein enhances androgen receptor (AR) transactivation, and this enhancement can be increased further in the presence of other androgen receptor associated coregulators. This protein may act as a nucleus-localized, basic transcriptional factor and also as a bifunctional transcriptional regulator. Mutations of this gene have been	Moderate expression across all tissues being higher on brain	Sotos syndrome 1. Van Haelst et al. (2005) reported a 3-generation family with gigantism (Sotos syndrome) in whom they identified a missense mutation in the NSD1 gene
rs116807401	*PABPC4L*	missense	Poly(A) Binding Protein, Cytoplasmic 4-Like might bind RNA	Scarce expression across all tissues	
rs35658696	*PAM*	missense	This gene encodes a multifunctional protein. The encoded preproprotein is proteolytically processed to generate the mature enzyme. This enzyme includes two domains with distinct catalytic activities, a peptidylglycine alpha-hydroxylating monooxygenase (PHM) domain and a peptidyl-alpha-hydroxyglycine alpha-amidating lyase (PAL) domain. These catalytic domains work sequentially to catalyze the conversion of neuroendocrine peptides to active alpha-amidated products. Alternative splicing results in multiple	Very low expression across all tissues except moderately high expression in heart-atrial appendage. Also slightly higher expression in heart left ventricle and aortic artery compared to most other tissues.	
rs149385790	*PDE5A*	missense	This gene encodes a cGMP-binding, cGMP-specific phosphodiesterase, a member of the cyclic nucleotide phosphodiesterase family. This phosphodiesterase specifically hydrolyzes cGMP to 5'-GMP. It is involved in the regulation of intracellular concentrations of cyclic nucleotides and is important for smooth muscle relaxation in the cardiovascular system.	Moderate expression in Adipose tissue, lung, prostate. And higher on Arteries, esophagus and colon	Sebkhi et al. (2003) concluded that PDE5A inhibition attenuates the rise in pulmonary artery pressure and vascular remodeling when given before chronic exposure to hypoxia and when administered as a treatment during ongoing hypoxia-induced pulmonary hypertension
rs34667348	*PHKB*	stop-gained	Phosphorylase kinase is a polymer of 16 subunits, four each of alpha, beta, gamma and delta. The alpha subunit includes the skeletal muscle and hepatic isoforms, encoded by two different genes. The beta subunit is the same in both the muscle and hepatic isoforms, encoded by this gene, which is a member of the phosphorylase b kinase regulatory subunit family. The gamma subunit also includes the skeletal muscle and hepatic isoforms, encoded by two different genes. The delta subunit is a calmodulin and can be encoded by three different genes. The gamma isoforms contain the active site of the enzyme, whereas the alpha and	Moderate expression across all tissues particularly high in skeletal muscle, and visceral adipose tissue	
rs201226914	*PIEZO1*	missense	The protein encoded by this gene is a mechanically-activated ion channel that links mechanical forces to biological signals. The encoded protein contains 36 transmembrane domains and functions as a homotetramer. Defects in this gene have been associated with dehydrated hereditary stomatocytosis.	Moderate expression across all tissues particularly high in adipose tissue, breast, lung and colon	Dehydrated hereditary stomatocytosis with or without pseudohyperkalemia and/or perinatal edema. Lymphedema, hereditary, III
rs3136797	*POLB*	missense	The protein encoded by this gene is a DNA polymerase involved in base excision and repair, also called gap-filling DNA synthesis. The encoded protein, acting as a monomer, is normally found in the cytoplasm, but it translocates to the nucleus upon DNA damage. Several transcript variants of this gene exist, but the full-length nature of only one has been described to date.	Low expression across most tissues. Much higher expression in brain cerebellum and cerebellar hemisphere.	Because POLB and the clinical phenotype of Werner syndrome (WRN; 277700) map to the same region, 8p12-p11, Sadakane et al. (1994) investigated the POLB gene in 2 patients and found 107-bp insertions or 87-bp deletions in the catalytic domain. Further study was required to determine whether this is a primary or a secondary change, since somatic cells from Werner syndrome patients have a propensity to develop chromosomal aberrations. Chang et al. (1994) used fluorescence in situ hybridization to place the POLB gene centromeric to DBS135 at 8p11.2. This and other evidence presented by Chang et al. (1994) indicated that POLB is not the Werner syndrome gene. El-Andalousi et al. (2006) determined that human POLB formed a complex with and was
rs121434601	*PTH1R*	missense	The protein encoded by this gene is a member of the G-protein coupled receptor family 2. This protein is a receptor for parathyroid hormone (PTH) and for parathyroid hormone-like hormone (PTHLH). The activity of this receptor is mediated by G proteins which activate adenylyl cyclase and also a phosphatidylinositol-calcium second messenger system. Defects in this receptor are known to be the cause of Jansen's metaphyseal chondrodysplasia (JMC), chondrodysplasia Blomstrand type (BOCD), as well as	Moderate expression across tissues, Particularly high in kidney and no expression in whole blood, transformed fibroblast and transformed lymphoblasts	Chondrodysplasia, Blomstrand type, Eiken syndrome, Failure of tooth eruption, primary, Metaphyseal chondrodysplasia, Murk Jansen type
rs61730641	*PTPN13*	missense	The protein encoded by this gene is a member of the protein tyrosine phosphatase (PTP) family. PTPs are signaling molecules that regulate a variety of cellular processes including cell growth, differentiation, mitotic cycle, and oncogenic transformation. This PTP is a large intracellular protein. It has a catalytic PTP domain at its C-terminus and two major structural domains: a region with five PDZ domains and a FERM domain that binds to plasma membrane and cytoskeletal elements. This PTP was found to interact with, and	Moderate expression across several tissues, slightly higher in skin, ovary and nerve. No expression in whole blood, muscle and liver	
rs41286560	*RTL1*	missense	This gene is a retrotransposon-derived, paternally expressed imprinted gene that is highly expressed at the late fetal stage in both the fetus and placenta. It has an overlapping maternally expressed antisense transcript, which contains several microRNAs targeting the transcripts of this gene through an RNA interference (RNAi) mechanism. This gene is essential for maintenance of the fetal capillaries. The imprinted DLK1-MEG3 gene region on chromosome 14q32.2 alters susceptibility to type 1 diabetes.	Scarce expression in all tissues slightly higher in hippocampus	. They demonstrated that Rtl1 is essential for maintenance of the fetal capillaries and that both its loss and its overproduction cause late fetal and/or neonatal lethality in mice.
rs143365597; rs114233776	*SCMH1*	missense; missense	sex comb on midleg homolog 1. Among its related pathways are Cellular Senescence and Cellular Senescence. GO annotations related to this gene include sequence-specific DNA binding transcription factor activity.	Moderate expression across tissues being the lowest in whole blood	Both male and female Scmh1 -/- mice were viable and grew normally into adulthood, but they exhibited axial homeosis and premature senescence of murine embryonic fibroblasts, indicating an indispensable role for Scmh1 as a PRC1 component. Approximately half of male Scmh1 -/- mice were sterile.
rs28929474	*SERPINA1*	missense	serpin peptidase inhibitor, clade A. The protein encoded by this gene is secreted and is a serine protease inhibitor whose targets include elastase, plasmin, thrombin, trypsin, chymotrypsin, and plasminogen activator. Defects in this gene can cause emphysema or liver disease. Several transcript variants encoding the same protein have been found for this gene.	High expression in liver and whole blood	Emphysema due to AAT deficiency.Emphysema-cirrhosis, due to AAT deficiency. Hemorrhagic diathesis due to \"antithrombin\" Pittsburgh. (Pulmonary disease, chronic obstructive, susceptibility to)

rs76208147	*SETD2*	missense	SET domain containing 2. Huntington's disease (HD), a neurodegenerative disorder characterized by loss of striatal neurons, is caused by an expansion of a polyglutamine tract in the HD protein huntingtin. This gene encodes a protein belonging to a class of huntingtin interacting proteins characterized by WW motifs. This protein is a histone methyltransferase that is specific for lysine-36 of histone H3, and methylation of this residue is associated with active chromatin. This protein also contains a novel transcriptional activation domain, and has been found associated with hyperphosphorylated RNA polymerase II.	Moderate expression across tissues	While cigarette smoking is a major cause of COPD (see 606963), only 15% of smokers develop the disease, indicating major genetic influences. The most widely recognized candidate gene in COPD is SERPINA1, although it has been suggested that SERPINA3 (107280) may also play a role.
rs61743810	*SLC35E3*	missense	Solute carrier family 35, member E3;The SLC family includes approximately 300 genes that provide instructions for making proteins called solute carriers. Proteins in the SLC family transport various molecules across the membranes surrounding the cell and its component parts.	Low expression across all tissues, highest in adrenal gland	
rs41286548	*SLC8A3*	missense	This gene encodes a member of the sodium/calcium exchanger integral membrane protein family. Also, known as NCX3. Na+/Ca2+ exchange proteins are involved in maintaining Ca2+ homeostasis in a wide variety of cell types. The protein is regulated by intracellular calcium ions and is found in both the plasma membrane and intracellular organellar membranes, where exchange of Na+ for Ca2+ occurs in an electrogenic manner. Alternative splicing has been observed for this gene and multiple variants have been described.	Low expression across all tissues, highest in skeletal muscle tissue and brain	Sokolow et al. (2004) produced mice deficient in Ncx3. Ncx3-deficient mice presented a skeletal muscle fiber necrosis and a defective neuromuscular transmission, reflecting the absence of Ncx3 in the sarcolemma of the muscle fibers and at the neuromuscular junction. The defective neuromuscular transmission was characterized by the presence of electromyographic abnormalities. The findings indicated that NCX3 plays an important role in vivo in the control of Ca(2+) concentrations in skeletal muscle fibers and at the neuromuscular junction.
rs144712473	*SMG7*	missense	This gene encodes a protein that is essential for nonsense-mediated mRNA decay (NMD); a process whereby transcripts with premature termination codons are targeted for rapid degradation by a mRNA decay complex. The mRNA decay complex consists, in part, of this protein along with proteins SMG5 and UPF1. The N-terminal domain of this protein is thought to mediate its association with SMG5 or UPF1 while the C-terminal domain interacts with the mRNA decay complex. This protein may therefore couple changes in UPF1 phosphorylation state to the degradation of NMD candidate transcripts. Alternative splicing results in	Moderate expression across tissues, highest in brain (cerebellar hemisphere and testis)	
rs34427075	*SNRPC*	synonymous	This gene encodes one of the specific protein components of the U1 small nuclear ribonucleoprotein (snRNP) particle required for the formation of the spliceosome. The encoded protein participates in the processing of nuclear precursor messenger RNA splicing. snRNP particles are attacked by autoantibodies frequently produced by patients with connective tissue diseases. The genome contains several pseudogenes of this functional gene. Alternative splicing results in a non-coding transcript variant.	Moderate expression across tissues, highest in cells- transformed lymphocytes	
rs148833559	*STC2*	missense	This gene encodes a secreted, homodimeric glycoprotein that is expressed in a wide variety of tissues and may have autocrine or paracrine functions. The encoded protein has 10 of its 15 cysteine residues conserved among stanniocalcin family members and is phosphorylated by casein kinase 2 exclusively on its serine residues. Its C-terminus contains a cluster of histidine residues which may interact with metal ions. The protein may play a role in the regulation of renal and intestinal calcium and phosphate transport, cell metabolism, or cellular calcium homeostasis. Constitutive overexpression of human	Moderate expression across tissues, highest in cells- transformed fibroblasts	
rs61730011	*TBX15*	missense	This gene belongs to the T-box family of genes, which encode a phylogenetically conserved family of transcription factors that regulate a variety of developmental processes. All these genes contain a common T-box DNA-binding domain. Mutations in this gene are associated with Cousin syndrome	Low expression across tissues, highest in skeletal muscle and subsutaneous adipose tissue	Cousin syndrome; By targeted disruption of the Tbx15 gene in mice, Kuijper et al. (2005) and Singh et al. (2005) reproduced the spontaneous mouse mutant droopy ear (de), which exhibits a complex craniofacial malformation. The skeletal phenotype of the Tbx-inactivated mice includes small overall size, hypoplastic scapulae, moderate shortening of several long bones, and a dysmorphogenesis of cranial bones and cervical vertebrae, including vertical displacement of the supraoccipital bone, a small basioccipital bone, a small foramen magnum, and changes in the shape of the squamosum and of the first and second vertebrae.
rs148543891	*TIAM2*	missense	This gene encodes a guanine nucleotide exchange factor. A highly similar mouse protein specifically activates ras-related C3 botulinum substrate 1, converting this Rho-like guanosine triphosphatase (GTPase) from a guanosine diphosphate-bound inactive state to a guanosine triphosphate-bound active state. The encoded protein may play a role in neural cell development. Alternatively spliced transcript variants encoding different isoforms have been described.	Low expression in most tissues, highest expression in the testis. Moderate expression in brain tissues.	
rs113388806	*TNRC6A*	missense	This gene encodes a member of the trinucleotide repeat containing 6 protein family. The protein functions in post-transcriptional gene silencing through the RNA interference (RNAi) and microRNA pathways. The protein associates with messenger RNAs and Argonaute proteins in cytoplasmic bodies known as GW-bodies or P-bodies. Inhibiting expression of this gene delocalizes other GW-body proteins and impairs RNAi and microRNA-induced gene silencing.	Moderate expression across tissues, highest in brain and pituitary	
rs17277546	*TRIM4*	3'UTR	The protein encoded by this gene is a member of the tripartite motif (TRIM) family. The TRIM motif includes three zinc-binding domains, a RING, a B-box type 1 and a B-box type 2, and a coiled-coil region. The protein localises to cytoplasmic bodies. Its function has not been identified. Alternatively spliced transcript variants that encode different isoforms have been described.	Moderate expression across tissues	
rs71455793	*TSGA10IP*	missense	Also known as FAM161C. Testis specific, 10 interacting protein.	No expression except high in testis	
rs147996581	*TSPAN31*	missense	The protein encoded by this gene is a member of the transmembrane 4 superfamily, also known as the tetraspanin family. Most of these members are cell-surface proteins that are characterized by the presence of four hydrophobic domains. The proteins mediate signal transduction events that play a role in the regulation of cell development, activation, growth and motility. This encoded protein is thought to be involved in growth-related cellular processes. This gene is associated with tumorigenesis and osteosarcoma.	Moderate expression across tissues	
rs77885044	*TTC28*	missense	Tetratricopeptide repeat domain 28;The tetratricopeptide (TTC) repeat domain containing family includes genes that provide instructions for proteins containing regions (domains) of repeating sequences called tetratricopeptides.	Moderate expression across tissues, highest in ovary and uterus	
rs16866412	*TTN*	missense	Titin, or connectin, is a giant muscle protein expressed in the cardiac and skeletal muscles that spans half of the sarcomere from Z line to M line. Titin plays a key role in muscle assembly, force transmission at the Z line, and maintenance of resting tension in the I band region (Itoh-Satoh et al., 2002). Ti	Almost no expression in all tissues, except moderate expression in heart and high expression in skeletal muscle.	Garvey et al. (2002) identified the mdm mutation as a complex rearrangement that includes a deletion and LINE insertion in the titin gene. Mutant allele-specific splicing results in the deletion of 83 amino acids from the N2A region of TTN, a domain thought to bind CAPN3. Western blot analysis detected a 50 to 60% reduction in the amount of CAPN3 in affected muscles. Garvey et al. (2002) concluded that the mdm mouse is a model for tibial muscular dystrophy. The giant protein titin serves a primary role as a scaffold for sarcomere assembly; one potential mediator of this process is calpain-3 (CAPN3; 114240). To test the hypothesis that calpain-3 mediates remodeling during myofibrillogenesis, Kramerova et al. (2004) generated CAPN3 knockout (C3KO) mice. Titin distribution was normal in longitudinal sections from the C3KO mice; however, electron microscopy of muscle fibers showed misaligned A bands. In vitro studies revealed that calpain-3 can bind and cleave titin and that some mutations that are pathogenic in human muscular dystrophy result in reduced affinity of calpain-3 for titin. Huebsch et al. (2005) generated CAPN3 overexpressing transgenic (C3Tg) and C3KO mice and showed that overexpression of CAPN3 exacerbated mdm disease, leading to a shorter life span and more severe muscular dystrophy. However, C3KO/mdm double-mutant mice showed no change in the progression or severity of disease, indicating that aberrant CAPN3 activity is not a primary mechanism in this disease. The authors examined the treadmill locomotion of heterozygous +/mdm mice and detected a significant increase in stride time with a concomitant increase in stance time. These altered gait parameters were completely corrected by CAPN3 overexpression in C3Tg/+/mdm mice, suggesting a CAPN3-dependent role for the N2A domain of TTN in the dynamics of muscle contraction.
rs150494621	*WDR76*	missense	Protein coding gene of unknown function. Specifically binds 5-hydroxymethylcytosine (ShmC), suggesting that it acts as a specific reader of ShmC.	Low expression in most tissues but moderate expression in brain cerebellum and cereballar hemisphere. Highest expression in EBV transformed lymphcytes	
rs2229089	*XPC*	missense	This gene encodes a component of the nucleotide excision repair (NER) pathway. There are multiple components involved in the NER pathway, including Xeroderma pigmentosum (XP) A-G and V, Cockayne syndrome (CS) A and B, and trichothiodystrophy (TTD) group A, etc. This component, XPC, plays an important role in the early steps of global genome NER, especially in damage recognition, open complex formation, and repair protein complex formation. Mutations in this gene or some other NER components	Low expression across tissues, sightly higher in cell transformed fibroblasts	Xeroderma pigmentosum, group C; Sands et al. (1995) generated XPC-deficient mice by 'knockout' of the mouse homolog of the human XPC gene using embryonic stem cell technology. The deficient mice showed marked hyperplasia of the epidermis with focal areas of hyperkeratosis in varying degrees of dysplasia, acantholysis, and/or dyskeratosis, similar to the human lesions known as actinic or solar keratosis. Changes in the eye included severe keratitis and corneal ulceration.
rs141845046	*ZBTB7B*	missense	This gene encodes a zinc finger-containing transcription factor that acts as a key regulator of lineage commitment of immature T-cell precursors. It is necessary and sufficient for commitment of CD4 lineage, while its absence causes CD8 commitment. It also functions as a transcriptional repressor of type I collagen genes. Alternatively spliced transcript variants have been found for this gene.	Low expression across tissues, higher in skin	He et al. (2005) identified the HD locus as the zinc finger transcription factor Th-POK (ZBTB7B). They showed that expression of Th-POK in the thymus normally restricted the CD4 lineage, and that constitutive expression leads to redirection of class I-restricted thymocytes to the CD4 lineage. The HD mutation is an A-to-G transition at nucleotide 1165 resulting in an arg-to-gly substitution at amino acid 389. This arg-to-gly substitution occurs within the second of 4 zinc finger domains of Th-POK and affects a residue predicted to interact directly with DNA. He et al. (2005) concluded that Th-POK is a master regulator of lineage commitment.
rs75596750; rs112892337	*ZFAT*	missense; missense	This gene encodes a protein that likely binds DNA and functions as a transcriptional regulator involved in apoptosis and cell survival. This gene resides in a susceptibility locus for autoimmune thyroid disease (AITD) on chromosome 8q24. Alternative splicing results in multiple transcript variants encoding distinct isoforms.	High expression in esophagus and skeletal muscle	Autoimmune thyroid disease, susceptibility to, 3; Tsunoda et al. (2010) found that Zfat1 +/- mice were viable, fertile, and indistinguishable from wildtype mice, whereas Zfat -/- mice suffered early embryonic lethality. Zfat -/- placenta showed abnormal development of the spongiotrophoblast layer at embryonic day 8.0, and Zfat -/- yolk sacs were bloodless at embryonic day 9.5, with reduced number of blood islands and impaired differentiation of hematopoietic progenitor cells. Defects in hematopoietic differentiation were associated with profound reductions in expression of the direct Zfat targets Tal1 (187040), Lmo2 (180385), and Gata1 (305371) and in Tal1 downstream genes.
rs61733564	*ZNF500*	missense	zinc finger protein 500; may play a role in hES cell growth and differentiation.	Moderate expression across tissues, highest in ovary & uterus	
rs41291604	*ZNF518A*	missense	The protein encoded by this gene is a member of the krueppel C2H2-type zinc finger protein family. The encoded protein contains five zinc fingers and is likely a nuclear transcriptional regulator. Several transcript variants encoding two different isoforms have been found for this gene.	Moderate expression across tissues, highest in testis and thyroid	
rs147110934	*ZNF628*	missense	Zinc finger proteins (ZNFs), which bind nucleic acids, perform many key functions, the most important of which is regulating transcription. Genes in the ZNF family provide instructions for making zinc finger proteins, which are regulatory proteins that are involved in many cellular functions.	Low expression across tissues, except high in testis	